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**METACOMUNIDADE E OTIMIZAÇÃO DO  
BIOMONITORAMENTO DA BIODIVERSIDADE  
AQUÁTICA DE RIACHOS TROPICAIS**

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**METACOMUNIDADE E OTIMIZAÇÃO DO  
BIOMONITORAMENTO DA BIODIVERSIDADE  
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Tese apresentada ao Programa de Pós-Graduação  
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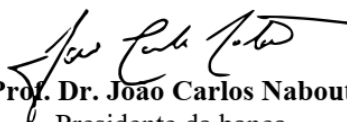
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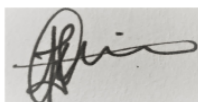
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## RESUMO

Ecossistemas terrestres estão cada vez mais impactados por conta das alterações antrópicas, principalmente sobre as coberturas vegetacionais, o que por sua vez causa mudanças profundas em ecossistemas aquáticos, principalmente dulcícolas. Os impactos são cada vez mais cumulativos e em múltiplas escalas espaciais, causando mudanças na estrutura, produtividade e como consequência em toda cadeia, impactando a abundância, riqueza e diversidade funcional. Em uma metacomunidade aquática, as espécies são diferentes e podem servir como base nos determinantes estruturais da comunidade, por esta razão neste trabalho nós avaliamos comunidades aquáticas submetidas a diferentes mudanças e impactos ambientais, dentro e ao entorno da Floresta Nacional de Silvânia, Goiás. Dessa forma, estruturamos a Tese em três capítulos, no CAPÍTULO I avaliamos como as comunidades de peixes de riacho são afetadas por fatores ambientais e espaciais através da desconstrução da metacomunidade, baseado em características relacionadas à dispersão. Utilizamos então, técnicas de partição de variação para testar os efeitos relativos dos fatores ambientais locais, espaciais e da paisagem. A abundância total das espécies foi fracamente explicada por variáveis ambientais e espaciais. A estrutura da comunidade de peixes nectobentônicos pequenos e de fluxo rápido, por sua vez, foi explicada pelo ambiente. Assim como, peixes nectobentônicos grandes e de água lenta, foram explicados por variáveis espaciais, e a paisagem apresentou explicabilidade para peixes de água lenta com diferentes capacidades de dispersão. No CAPÍTULO II utilizamos diferentes grupos biológicos e suas congruências para identificar a possibilidade de monitoramento de ecossistemas aquáticos. Nós avaliamos se a taxonomia, a resolução numérica e a congruência entre diferentes táxons podem ser usadas para otimizar custos e tempo para biomonitoramento. Para esse objetivo utilizamos análises de Mantel e Procrustes. Os resultados mostraram que os níveis taxonômicos e as resoluções numéricas foram fortemente correlacionados em todos os grupos taxonômicos ( $r > 0,70$ ), mas não entre os grupos biológicos. Diferentes conjuntos de variáveis ambientais explicaram diferentes composições de grupos biológicos distintos. Concluímos que o uso dos grupos como bioindicadores é mais informativo por meio de níveis taxonômicos mais elevados com dados de ocorrência, mas que avaliações multitaxa fornecem informações complementares no biomonitoramento. No CAPÍTULO III avaliamos os efeitos diretos e indiretos das variáveis de paisagem, ambientais locais e de produtividade sobre a riqueza taxonômica e funcional da comunidade peixes (entropia quadrática de Rao). Construimos um modelo teórico com utilização da modelagem de equações estruturais. Os nossos resultados indicaram uma forte relação das variáveis ambientais e produtividade sobre a riqueza e diversidade funcional. Além disso, os efeitos diretos e indiretos indicaram que a preservação do ambiente natural realmente está ligada a melhores condições de riqueza e diversidade funcional da comunidade de peixes.

Palavras-chave: metacomunidade, efeitos diretos e indiretos, riacho, Cerrado, monitoramento ambiental, pathway análise, diversidade funcional

## ABSTRACT

Terrestrial ecosystems are increasingly impacted by anthropogenic changes, especially on vegetation cover, which causes deep changes in aquatic ecosystems, especially freshwater. The impacts are increasingly cumulative and multiple spatial scales, causing changes in structure, productivity and consequently in the entire chain, impacting abundance, richness and functional diversity. In an aquatic metacommunity, the species are different and can serve as a basis for the structural determinants of the community, for this reason in this work we evaluate aquatic communities subjected to different environmental changes and impacts, within and around the National Forest of Silvânia, Goiás. Thus, we structured the Thesis into three chapters, in CHAPTER I we assess how stream fish communities are affected by environmental and spatial factors through the deconstruction of the metacommunity, based on characteristics related to dispersal. Then, we use variation partitioning techniques to test the relative effects of local, spatial, and landscape environmental factors. The total abundance of species was weakly explained by environmental and spatial variables. The community structure of small and fast-flowing nectobenthic fish, in turn, was explained by the environment. As well, large and slow-water nectobenthic fish were explained by spatial variables, and the landscape was explained by slow-water fish with different dispersal capabilities. In CHAPTER II we use different biological groups and their congruences to identify the possibility of monitoring aquatic ecosystems. We evaluated whether taxonomy, numerical resolution and congruence between different taxa can be used to optimize cost and time for biomonitoring. For this purpose, we used Mantel and Procrustes analyses. The results showed that taxonomic levels and numerical resolutions were strongly correlated across all taxonomic groups ( $r > 0.70$ ), but not across biological groups. Different sets of environmental variables explained different compositions of different biological groups. We conclude that the use of groups as bioindicators is more informative through higher taxonomic levels with occurrence data, but that multi-rate assessments provide additional information in biomonitoring. In CHAPTER III we evaluate the direct and indirect effects of landscape, local environmental and productivity variables on the taxonomic and functional richness of the fish community (Rao's quadratic entropy). We built a theoretical model using structural equation modeling. Our results indicated a strong relationship between environmental variables and productivity on richness and functional diversity. Furthermore, the direct and indirect effects indicated that the preservation of the natural environment is really linked to better conditions of richness and functional diversity of the fish community.

Keywords: metacommunity, direct and indirect effects, stream, Cerrado, environmental monitoring, pathway analysis, functional diversity

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# INTRODUÇÃO

Ecosistemas aquáticos de água doce tem importância local e global inestimadas, pois apresentam uma biodiversidade única e com serviços ambientais substanciais (Schroter et al., 2005). No entanto, estes habitats são globalmente afetados, e ao que tudo indica, os estados de degradação estão cada vez mais acentuados, exigindo uma demanda urgente de ações de conservação (Dudgeon et al., 2006). Um dos tipos mais comuns de mudanças no tipo uso de solo é a conversão da cobertura natural para agricultura ou pecuária, o que tem causado grande perda de vegetação nativa e conseqüentemente leva a um aumento na entrada de sedimentos no meio aquático durante períodos chuvosos, provocando um aumento dos sólidos totais e turbidez nos ecossistemas aquáticos (Liu et al., 2008).

A conversão da área natural para agricultura ou pastagem é por sua vez é uma das maiores ameaças à conservação de ambientes aquáticos e de espécies de peixes de água doce (Teresa *et al.*, 2012; Liu et al., 2008; Sweeney *et al.*, 2004), pois está relacionado com processo de assoreamento e turbidez, ocasionado pelo carregamento de material alóctone, reduzindo na profundidade e fluxo (Gregory *et al.*, 1991), o que está diretamente relacionada à abundância total de peixes de diferentes grupos funcionais (Ferrari *et al.*, 2018).

A destruição da vegetação ripária por sua vez leva à simplificação do habitat e conseqüentemente limita as comunidades aquáticas (Pinto *et al.*, 2006). Estudos observaram que ambientes com menor proporção de matas ripárias apresentam diminuição e substituição de peixes bentônicos por espécies tolerantes a sedimentos e às vezes invasoras (Jones et al., 1999). Além disso, as mudanças na estrutura da paisagem representam alterações na composição da comunidade nas paisagens ribeirinhas, o que corrobora com a teoria da metacomunidade em que condições locais causam efeitos no isolamento e conseqüentemente na riqueza, abundância e suas diversidades funcionais nos ecossistemas aquáticos (Brown & Swan, 2010; Harvey & Altermatt, 2019; Henriques-Silva et al., 2019; Schmera et al., 2018; Swan & Brown, 2017; Tonkin, Heino, et al., 2018).

Por outro lado, a preservação das zonas ripárias mantém as características originais do riacho (Sweeney *et al.*, 2004; Casatti *et al.*, 2009), exercendo a função de reter sedimentos e contaminantes das áreas adjacentes, atuando como um amortecedor contra os impactos do

desmatamento (Dudgeon, 2008), além de manter a heterogeneidade do habitat aquático (Naiman & Décamps, 1997). Compreendemos assim, que as variáveis locais podem ser influenciadas pelas características da paisagem ambiental, como uso do solo e tipo de cobertura, indicando um efeito direto ou indireto nas variáveis da paisagem e nas populações aquáticas locais (Miranda et al., 2014).

### ***Efeitos diretos e indiretos***

Os efeitos diretos são aqueles avaliados a partir de uma relação em que a mudança de uma variável está diretamente ligada a outra, como por exemplo a mudança da estrutura do habitat, como cobertura do solo, causaria alterações nas variáveis ambientais locais, como fluxo, temperatura e turbidez, assim como a mudança nas variáveis ambientais levariam a alterações nas comunidades locais (Pandit *et al.*, 2009; Casatti et al. 2009). Os efeitos indiretos por sua vez são demonstrados de forma que uma variável mais geral, como mudança na cobertura do solo, causaria mudanças nas comunidades de peixes (Pickett e Cadenasso 1995; Harborne *et al.*, 2011; Teresa *et al.*, 2012; Rees *et al.*, 2014), indicando que sempre que houver uma mudança no tipo de cobertura de solo poderemos identificar uma mudança nas comunidades locais.

Para riachos, as zonas ripárias tem função de reter sedimentos e contaminantes das áreas adjacentes, atuando como um amortecedor contra os impactos do desmatamento (Dudgeon, 2008), além de manter a heterogeneidade do habitat aquático (Naiman & Décamps, 1997). Portanto, a vegetação ripária tem influência em várias escalas em comunidades aquáticas, e influência em vários grupos da comunidade, como algas, fitoplâncton, zooplâncton, invertebrados e peixes, além da dinâmica trófica entre os grupos (Allan & Castillo 2007; Lorion & Kennedy, 2009). Um exemplo causado por mudanças nas condições ambientais, que interfere na dinâmica ecológica interespecífica e que pode acontecer em ambiente aquáticos alterados é o acelerado processo de eutrofização, causado por excesso de nutrientes (esgoto, agrotóxicos e fertilizantes), especificamente o nitrogênio e o fósforo, causando crescimento excessivo de algas e plantas aquáticas, comprometendo o corpo d'água (Barros, 2008).

A consequência da eutrofização é o desequilíbrio do balanço do oxigênio dissolvido na

água (OD), assim como a floração de cianobactérias, levando a alterações na turbidez da água e consequentemente a mortandade de peixes e outros animais (Von Sperling, 1994; Motta, 2006). Esse desequilíbrio compromete o corpo d'água (Barros, 2008; Trochine et al., 2017) e é agravado por momentos de maior precipitação (da Rocha Junior et al., 2018), aumento de atividades antrópicas locais (Meehl et al., 2007; Jung et al., 2016; Khan et al., 2018; Bae et al., 2020) e mudanças climáticas (IPCC, 2014). Para pequenos corpos d'água, no entanto, numerosos estudos mostram uma maior sensibilidade das comunidades aquáticas, não apenas para poluição, mas também para desmatamento das áreas ripícolas destes riachos (Waters, 1995).

Para peixes de riacho por exemplo, a vegetação ripária determina condições hidrológicas fundamentais para manutenção de variáveis como a temperatura, oxigênio dissolvido, contribuição do material alóctone para alimentação, refúgio e sítios de reprodução para as espécies de peixes (Schneider & Winemiller, 2008), além da alteração da composição e função da comunidade ao longo do gradiente fluvial (Vannote et al., 1980). Estudos indicam que ambientes com menor proporção de matas ripárias apresentam diminuição da abundância de espécies bentônicas, assim como sua substituição por espécies tolerantes a sedimentos e às vezes invasoras (Jones et al., 1999), o que seria um efeito indireto sobre a comunidade. Já para fitoplânctons e o zooplânctons a qualidade do ambiente é determinante, pois estes respondem rapidamente as alterações ambientais, o que os tornam importantes grupos utilizados para o biomonitoramento e análise da qualidade da água (Odemis & Evrendilek, 2007), pois passam por respostas a efeitos diretos na qualidade e condições hidrológicas.

Desta forma, a compreensão da integridade de áreas ripárias tem sido um componente importante nas estratégias de avaliação, monitoramento e manejo para a conservação da biodiversidade de rios, riachos e nascentes (Naiman & Décamps, 1997). Pois, dentro de um grupo taxonômico, espécies e populações podem ser ameaçadas de maneiras distintas frente aos diferentes tipos de uso do solo (Baker & King, 2010). Assim, a interação de diferentes formas de degradação como desmatamento, fragmentação e diferentes tipos de poluição, podem afetar a estrutura espacial das comunidades aquáticas tanto sob o aspecto de composição de espécies, como sob aspectos funcionais (Baker & King, 2010). Em geral, comunidades aquáticas estão relacionadas aos recursos disponíveis no ambiente e suas características podem estar sempre mudando, já que riachos são ambientes instáveis e sujeitos a constantes variações físicas (Manna et al., 2013). Assim, é importante compreender qual a

conexão entre os ecossistemas terrestres e aquáticos e de qual forma ambientes aquáticos, principalmente dulcícolas, respondem às influências periféricas, o que ainda é um paradigma importante na ecologia aquática (Ward, 1998).

### *Dinâmicas ecológicas e comunidades aquáticas*

Por ambientes de riachos apresentarem respostas mais rápidas e variações mais intensas na diversidade de vários grupos aquáticos (Casatti et al., 2009) por serem ambientes mais sensíveis as mudanças ambientais locais (Riseng et al., 2011), atualmente as pesquisas em ambientes aquáticos têm utilizado cada vez mais espécies ou grupos de organismos diferentes que possam responder de maneira eficiente a degradação do meio, tendo em vista que suas características ecológicas tendem a variar sistematicamente em relação às alterações no meio ambiente tanto no tempo como no espaço, fazendo com que possivelmente cada táxon responda de maneira distinta as modificações no meio (Juen & De Marco, 2012).

Para estudos ambientais aquáticos, a utilização de todos os táxons ao mesmo tempo para avaliação de qualidade ambiental é um dos gargalos de estudo de ambientes dulcícolas. Desta forma, uma das estratégias adotadas para minimizar o uso de todos os grupos aquáticos é a utilização de substitutos, que fornecem uma maneira mais rápida de medir a biodiversidade real ou estimada em uma escala local ou regional (Lindenmayer et al., 2015). Em geral, essas medidas são realizadas levando em conta a congruência entre os organismos e os ambientes que eles ocupam, correlacionando-os ao seu papel no ecossistema, que variará de acordo com processos ecológicos (Clayton et al., 2004). Por tanto, uma compreensão detalhada das dinâmicas ecológicas e interações interespecíficas desses organismos pode fornecer a informação de organismos dentro do ambiente que estão relacionados (Tilman, 2000).

Considerando que grupos de espécies respondem as perturbações antrópicas de uma forma geralmente complexa e fortemente influenciada por vários processos ecológicos, é difícil prever como um determinado ecossistema aquático de pequeno porte se comportará frente as mudanças locais (Hayes et al., 1996). Assim, compreender como diferentes grupos aquáticos, assim como, a congruência entre diferentes grupos reage local e espacialmente frente as mudanças ambientais, auxiliará em medidas mais rápidas de avaliações ambientais, assim como no planejamento voltado à conservação (Lindenmayer et al., 2015). Por tanto,

várias opções estão disponíveis como variáveis de resposta para monitorar a saúde dos sistemas aquáticos (Jørgensen et al., 2005).

Desta forma, é necessário que haja uma investigação mais profunda em cada ambiente para escolha das variáveis que melhor respondam as mudanças, e que gere uma maior facilidade ou custo de medição e análise, assim como, uma relação entre os componentes e funcionamento do ecossistema. Visando contribuir para reduzir essa lacuna, desenvolvemos este trabalho para avaliar efeitos diretos e indiretos da paisagem nas comunidades aquáticas, assim como avaliar a concordância espacial entre grupos taxonômicos para fins de monitoramento.

No primeiro capítulo, intitulado *Deconstruction of a Neotropical stream fish metacommunity based on dispersal-related traits* avaliamos a influência de preditores ambientais locais, espaciais e de paisagem na estrutura da metacomunidade de peixes de riachos utilizando uma abordagem de desconstrução da comunidade com base em atributos funcionais. capacidade de dispersão das espécies, tais como tamanho das espécies, tipo de habitat e tipo de mobilidade.

No segundo capítulo, intitulado *Shortcuts for biomonitoring programs of stream ecosystems: evaluating the taxonomic, numeric, and cross-taxa congruence in phytoplankton, periphyton, zooplankton, and fish assemblages* nós avaliamos diferentes métodos como substituição taxonômica, numérica e de grupos substitutos, de forma que diferentes grupos aquáticos possuem respostas similares ao gradiente ambiental e distância espacial.

No terceiro capítulo, intitulado *Efeitos diretos e indiretos do uso do solo, variáveis ambientais locais e produtividade na diversidade de peixes de riachos* nós verificamos os efeitos diretos e indiretos dos diferentes tipos de uso do solo (ambientes naturais, de agricultura e pastagem), e das diversas variáveis ambientais (tronco, areia e lama, fluxo, temperatura, clorofila, nitrato e folhiço) sobre a diversidade taxonômica e funcional de peixes em ambiente de riacho no Bioma Cerrado, levando em consideração que nossos pontos amostrais estão inseridos em diferentes níveis de ambientes impactados pela ação humana. Para chegarmos a esta resposta nós elaboramos três hipóteses: (I) a primeira é de que diferentes tipos de uso de solo causam efeitos diretos sobre variáveis ambientais locais, de forma que locais com menos vegetação natural tenham mudanças tanto nas variáveis locais, quanto nas estruturais, causando variações nos grupos da comunidade aquática, como algas,

fitoplâncton, zooplâncton e invertebrados, além da dinâmica trófica entre os grupos; Nossa (II) segunda hipótese é a de variáveis ambientais estarão relacionadas diretamente aos padrões de riqueza funcional e taxonômica da comunidade ictíica local, de forma que as condições ambientais locais do riacho (e.g.: temperatura, clorofila, fluxo etc.) são determinantes diretos sobre a comunidade de peixes locais; A terceira hipótese é de que (III) será possível identificar uma relação em cascata, de forma que o tipo de cobertura do solo afetará diretamente as variáveis ambientais e estruturais locais e que como consequência afetará a comunidade peixes fazendo com que assim possamos encontrar efeitos indiretos das mudanças da cobertura do solo sobre a diversidade taxonômica e funcional da comunidade de peixes.

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# CAPÍTULO I

## **Grouping a Neotropical stream fish metacommunity based on dispersal-related traits by different functional niche dimensions**

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## **Abstract**

The species within a metacommunity have different traits, which may be used as a basis to understand the determinants of community structure. This study aimed to understand how stream fish communities are affected by environmental and spatial factors by use of different functional niche dimensions based on dispersal-related traits, such as habitat use (i.e. benthic, nektobenthic, marginal, and surface), preference for water flow (i.e. fast, intermediate, and slow), and body size (i.e. small, medium, and large). We sampled 18 stream reaches in a dendritic network in the upper Paraná ecoregion, situated in Cerrado Biome in Brazil. We used a set of variation partitioning techniques to test the relative effects of local environmental, spatial and landscape factors on the different species groups defined according to the attributes associated with dispersal ability. The environmental and spatial variables weakly explained the variation in total community structure. However, based on different functional niche dimensions to explain the different species subsets, we found that the environment had an important relationship with community structure of nektobenthic, fast flow associated and small fish. Spatial variables were more related to the community structure of nektobenthic fishes, surface and marginal species, slow-water associated and large fish, while landscape variables explained more variation in the community structure of slow-water associated fish. We showed that the difference functional niche dimensions of a metacommunity based on species dispersal traits improved understanding of the community structure of stream fish, which may also be applied in the conservation of Cerrado streams and their riparian forests.

Keywords: Cerrado, community structure, functional composition, dispersal-related traits, habitat use, water flow, body size

## **Introduction**

Metacommunities are characterized by sets of local communities connected by dispersal of different species that can interact in diverse ways (Wilson 1992, Leibold et al. 2004). One of the main goals of metacommunity ecology is to understand how the structure of biotic communities is affected by local environmental factors (i.e. niche-based processes) and their spatial structure in a landscape (i.e. dispersal based-processes) (Leibold et al. 2004, Mihaljevic 2012). Therefore, the study scale and dispersal ability of organisms are recognized as significant factors affecting the structure of biotic communities (Lansac-Tôha et al. 2021). The scale of study may affect our perception of environmental and spatial factors, the key factors shape community structure, thereby resulting in scale-dependent findings of metacommunities (Heino and Peckarsky 2014, Heino et al. 2015). This issue of spatial scaling is also often related to other kinds of context dependency, such as the characteristics of each taxonomic group or sets of functional traits analyzed (Erős et al. 2012, Aspin et al. 2018, Crabot et al. 2019, Rocha et al. 2020). Thus, the different functional niche dimensions can determine how organisms respond to environmental and spatial variables (Algarate et al. 2014, Machado et al. 2016, Rocha et al. 2020).

Freshwater fish communities are restricted by the aquatic environment within a dendritic river network (Altermatt 2013, Tonkin et al. 2018). Within a river network, fish show great variation in dispersal capacity (Palheta et al. 2021) and rely on different dispersal means to reach a locality (Welcomme et al. 2006, Vasconcelos et al. 2014, Gonçalves et al. 2020). For example, fish species with strong dispersal capacity were mainly influenced by local environmental factors and weakly influenced by spatial variables, while species with poor dispersal capacity were weakly influenced by local

environmental variables (Palheta et al. 2021). Also, stream communities are shaped by environmental conditions at local scales (e.g. water depth, flow and quality) and landscape-level scales (e.g. land use and land cover in the catchment), which corroborates the metacommunity theory in which local conditions cause effects on isolation and consequently on richness, abundance and their functional diversities in aquatic ecosystems (Brown & Swan, 2010; Harvey & Altermatt, 2019), making streams an ideal system for studying the organization of aquatic metacommunities (Lorion and Kennedy 2009, Fernandes et al. 2012, Heino and Peckarsky 2014, Pérez-Mayorga et al. 2017).

Most stream fish studies have focused on the entire metacommunity simultaneously (Erős et al. 2012, 2019), which may limit understanding of metacommunity organization because groups of species sharing the same key features and may respond more consistently to the environment and show similar dispersal pathways compared with entire fish communities (Pérez-Mayorga et al. 2017). Thus, the different functional niche dimensions is a method that can evaluate the influence of different predictors (e.g., environmental variables or spatial filters) on groups of species sharing similar functional features, such as habitat use, body size, dispersal ability and more (Algarte et al. 2014, Li et al. 2019). For example, specialist and generalist species may exhibit distinct metacommunity organization (Alahuhta et al. 2014), with the community structure of specialist species being determined by niche processes because different species prefer different environmental conditions (Pandit et al. 2009). In contrast, the community structure of generalist species may be mainly driven by regional processes related to dispersal processes (Fernandes et al. 2013, Blanchet et al. 2014).

The habitat preference of a fish species is typically related to its dietary preferences, which can affect the occurrence and abundance of a species according to the local habitat conditions (Halpern et al. 2008, Henriques et al. 2016, 2017). For example, benthic fish are associated with the stream bottom (Oliveira et al. 2010), nektonic fish move freely in the water column (Lincoln et al. 1995), and pelagic fish are found mainly in lentic environments (Oliveira et al. 2010). Habitat use may also be associated with the dispersal propensity of fish. In addition, larger species may generally have greater dispersal capacity (Jenkins et al. 2007), as well as show greater persistence in local communities due to their dietary plasticity, longer life spans and wider environmental tolerances (Bender et al. 2013, Luiz et al. 2013).

The dispersal mode of fishes is one of the important tools that we can evaluate, because are various modes of dispersal in stream organisms, it can vary from aquatic passive dispersal (juvenile drift or accidental transport by flow), or an active dispersion, based on swimming capacity of fishes (express by behavioral motivation to engage in persistent directional movement) or specific behaviors that allow them to pass barriers (Carvajal-Quintero et al., 2015) what give than an active dispersal abilities (Jenkins et al., 2007), what can change according to their different body sizes (e.g. Soininen et al., 2011). Also, the fish dispersion can be limited by any factor (e.g. geomorphological, hydrological) that prevents species from dispersing to all localities within a region (Heino et al., 2015).

In this study, we evaluated if the influence of ecological processes on fish metacommunity organization differs among species groups divided by key traits, especially those related to dispersal capacity. We therefore grouping species by different functional traits based on their dispersal and habitat use traits, and subsequently evaluated how the variation in species composition can be explained by dispersal-based

and niche-based processes. 1) We expected that local environmental variables would be more important for the structure of entire stream fish communities (Pandit et al. 2009), since different land uses (natural landscapes, pasture, agriculture, and forestry) will directly interfere in the constitution of the aquatic habitat, thereby causing a change in species composition. 2) Following the approach of different functional niche dimensions, we expected the spatial component to be more important for groups of species with low dispersal capacity (Devictor et al. 2008, Barragán et al. 2011), such as for small benthic species. 3) We also expected environmental factors to be more important for species dependent on specific habitat conditions (Casatti et al. 2009), such as for small and slow-water species, species present under the banks, surface-dwelling species, as well as nektobenthic and benthic species. 4) Finally, we expected land use and local habitat characteristics to influence species with weak dispersal capacity (Flynn et al. 2009, Barragán et al. 2011), including small-sized and medium-sized species, and species with a preference for slow water flow. The expectations 2, 3 and 4 suggest that the change in habitat conditions will also result in a change in the species composition, enabling the reduction and replacement of benthic fish by sediment-tolerant and sometimes invasive species.

## **Material and Methods**

### **Study area and fish collection**

The study was carried out in the upper Paraná River basin, including the sub-basins of the Rivers Piracanjuba, Ribeirão Vermelho, Córrego Caidor and Rio dos Bois. The sampled reaches were situated in 1<sup>st</sup> to 4<sup>th</sup> order streams (Figure 1). Streams with the presence of artificial barriers or small hydroelectric plants (PCHs) were excluded

from our sampling and sampled sub-basins will only meet several km ahead, in rivers larger than 4<sup>th</sup> order. The region is comprised of a large vegetation mosaic, with a large protected area (39.66%), the Silvânia National Forest (FLONA, 486.67 ha), as well as urban areas (4.45%), pastures (33.76%), agriculture (21.03%) and forestry (1.08%).

The fieldwork was carried out during the dry season from August to September in 2017. Fish sampling was carried out in 18 stretches of 80 m length in each stream through electric fishing, using an alternating current generator (1000 W, 300–500 V, 1–3 A) with single-pass electric fishing. Fish samplings were performed by two people with a fishing net attached to the generator, followed by another person with a support net not attached to the generator. Electric fishing was carried out in the upstream direction, following a path that explored all types of microhabitats along the 80-meter stretch (Mazzoni et al. 2000). The captured fish were euthanized using clove oil (eugenol, C<sub>10</sub>H<sub>12</sub>O<sub>2</sub>) and fixed in 10% formalin solution and transferred to 70% ethanol after 72 hours. The species were identified to the lowest possible taxonomic level through specialized literature (Miranda and Mazzoni 2003, Claro-García and Shibatta 2013, Lima and Caires 2011).

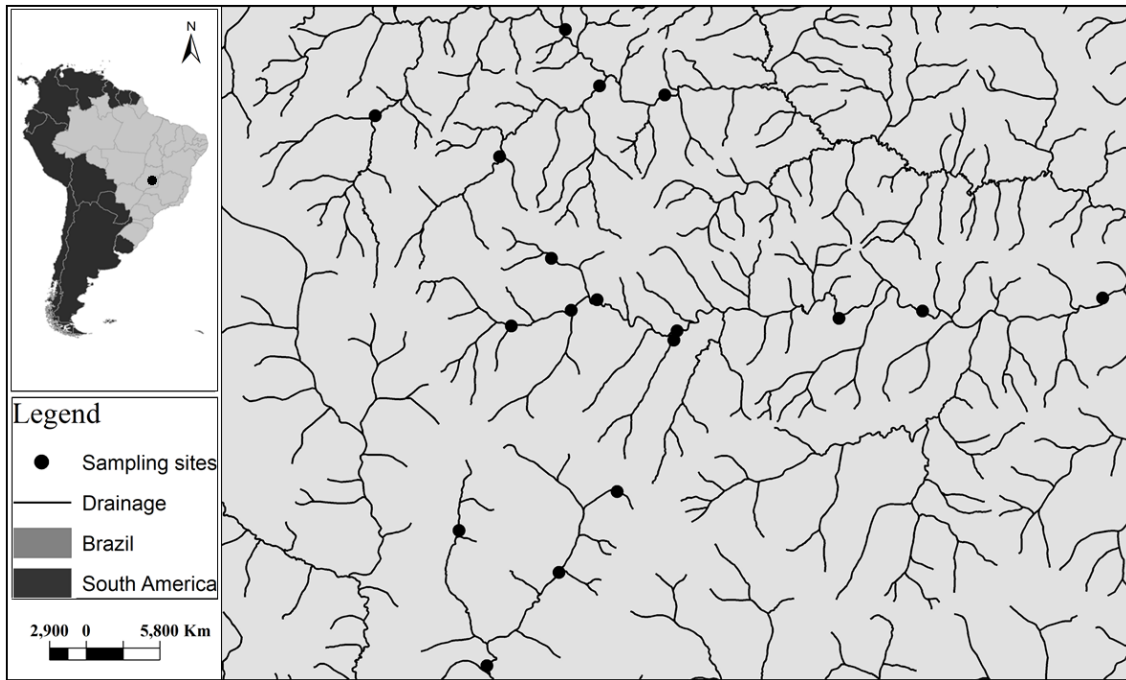


Figure 1. Location of the Silvânia National Forest (FLONA) and the 18 sampling points in the four sub-basins around it.

### **Fish community different functional traits**

The fish metacommunity was classified according to traits related to species' habitat use, water flow preference, and body size. Subsequently, a site-by-species matrix was built for each trait group (e.g. Lavorel et al. 2008) (Table 1).

Table 1: Biological traits used in grouping species by different functional traits.

Trait Group	Single Traits	Descriptions and interpretations
Habitat use		
	Benthic	Organisms living or associated with the stream bottom, species with dorsoventrally flattened bodies <sup>a</sup>
	Marginal	Species that prefer swimming close to the banks or amongst the marginal vegetation of water bodies <sup>a, b</sup>
	Nektobenthic	Species typically associated with river or stream bottoms but actively swim in the lower portion of the water column <sup>c</sup>
	Nektonic	Classified as species that swim or move freely in all layers of the water column <sup>c</sup>
	Surface	Surface or pelagic fish that have the body compressed laterally and are found in more structured and productive lentic environments <sup>a</sup>
Flow Preference		
	Fast water	Represented by species that prefer areas of fast water. These areas may represent more restricted environmental conditions, limiting the occurrence of several species, which results in highly similar fish communities <sup>d, e</sup>
	Intermediate water	Represented by low flow velocity and, consequently, places that are richer in food resources and formation of different mesohabitats <sup>f, g, h</sup>
	Slow water	Represented by areas of low water flow, indicating habitats composed of fine sediments and organic materials. In these habitats, pool formations are common as sites of substrate particle deposition zones <sup>e, i</sup>
Size		
	Large	Individuals larger than 150 mm <sup>e</sup> .
	Medium	Individuals between 50–150 mm <sup>e</sup> .
	Small	Individuals smaller than 50 mm <sup>e</sup> .

<sup>a</sup>Oliveira *et al.* (2010), <sup>b</sup>Brejão *et al.* (2013), <sup>c</sup>Lincoln *et al.* (1995), <sup>d</sup>Angermeier e Schlosser (1989), <sup>e</sup>Teresa e Casatti (2012), <sup>f</sup>Burhnheim (2002), <sup>g</sup>Angermeier and Karr (1983), <sup>h</sup>Langeani *et al.* (2005), <sup>i</sup>Moon (1939).

### **Local environmental variables**

The environmental variables related to the physical structure of the streams were measured in 9 equidistant transects (ten meters) within each sample section. We measured stream width (m), depth (cm) and flow (rotation per minute, General Oceanics ® flowmeter, model 2030) (Carvalho 2008). We also visually estimated the riparian forest features, type of substrate, and in-stream habitat structures, including the presence of consolidated and unconsolidated material, and the proportions of trunks, leaves, and other bottom components (i.e., the relative proportion of each substrate component) (see Cummins 1962). Subsequently, we calculated the mean values of the environmental variables for each study section (Table S1).

Water quality was measured once at each location in the field, including variables such as water temperature, transparency (cm), pH, conductivity ( $\mu\text{s cm}^{-1}$ ), dissolved oxygen (OD,  $\text{mg L}^{-1}$ ), turbidity (NTU) and chlorophyll-a ( $\mu\text{g L}^{-1}$ , using the Eureka Manta 2 Amphibian probe). Variables such as biochemical oxygen demand (BOD,  $\text{mg L}^{-1}$ ), oxidation potential reduction (redox, mV), dissolved oxygen ( $\text{mg L}^{-1}$ ), total solids ( $\text{mg L}^{-1}$ ), and total dissolved solids (TDS,  $\text{mg L}^{-1}$ ) were evaluated in the laboratory following the standard methods for the examination of water and wastewater (Apha 1998). The mean values are described in table S1.

### **Landscape variables**

The features of upstream drainage areas (i.e. total area and areas of different buffers), altitude and slope were estimated based on digital elevation models. We extracted information on land use and cover from these models, using images from TerraClass (Miranda 2018) for the Cerrado Biome (<http://www.dpi.inpe.br/tccerrado/>).

Landscape data were obtained for buffers based on the vegetation classification into natural landscapes (i.e. protected areas), pasture, agriculture and forestry (Brazil, 2015).

Previously, the buffers upstream of the sampling points were built with fixed widths of 50 m and 100 m, and with three different lengths of 100 m, 500m and the entire course of the stream (i.e. upstream basin area) (Dala-Corte et al. 2017, 2019, Ávila et al. 2018). For the buffers construction we were based on the Brazilian Forest Code (Law n. 12.651/2012) which considers a permanent preservation area around streams, ranging from 30 to 500 meters, related with stream width. Theoretically, because the buffer distance is used to understand the interface between the land and the stream, we used the same buffer widths for all sample sites (Watson and Chang 2018), and we did not consider the width of the streams (considering 1st to 4th order streams), thereby, we use the 100 m lengths for 500 m upstream and basin area.

### **Spatial variables**

As the distance between sampling sites can be a proxy for dispersal limitation, we used the river distance matrix to generate a set of spatial vectors (Table S2). Spatial vectors represent the spatial autocorrelation between sampling points along watercourses, which are typically more useful than simple linear distances for obligatory aquatic organisms like fish (Goslee and Urban 2020, Landeiro et al. 2014). We thus generated 9 PCNM (Principal Coordinates of Neighbor Matrices) (Bocard and Legendre 2002, Oksanen et al. 2011) spatial filters using the PCNM function in vegan (Oksanen et al. 2011) package of the R software (R Core Team 2016). (Table S3). PCNMs are spatial predictors that can be easily incorporated into regression or canonical ordination models (Bocard and Legendre 2002). In addition, each vector generated (i.e., spatial filter) has a distinct spatial structure, where the first spatial filters

are associated with large-scale spatial patterns, while the last spatial filters are associated with a fine-scale spatial patterns (Legendre and Legendre 2012).

### **Data analysis**

We constructed different matrices including site-by-species (i.e. all species and separately for each trait group), site-by-environmental variables (i.e. physical-chemistry), site-by-landscape variables (i.e. natural area, pasture, agriculture and forestry) and site-by-spatial (PCNMs) variables. Environmental variables (except pH) were log-transformed ( $X + 1$ ) and landscape variables (i.e. percentages) were transformed using arcsine square root transformation. These transformations are widely used in ecological studies (Legendre and Gallagher 2001, Machado et al. 2015). All statistical analyses were performed using the R software (R Core Team 2016).

Initially, environmental, landscape and spatial variables were screened based on Variance Inflation Factors (VIF) to remove collinear variables. We consider variables with  $VIF > 0.5$  to be collinear. The VIF was calculated using the "vifcor" function from the usdm package (Naimi, 2017). Thereafter, forward selection of spatial, environmental and landscape variables was performed separately, using the stopping criteria of significance level alpha ( $P < 0.05$ ), whereby the variables explaining significant variation in community composition were retained (Blanchet et al. 2008). Forward selection was used separately for all sets of variables (i.e. local environmental, landscape and spatial variables), so that the variables varied depending on the response matrix analyzed. We used the "forward.sel" function of the adespatial package (Dray et al. 2017) to select the explanatory variables.

A variation partitioning approach based on redundancy analysis (RDA) was then used to determine the relative importance of local environmental, landscape and spatial

components as adjusted  $R^2$  values (Legendre and Legendre 1998, Oksanen et al. 2011). Subsequently, different partial redundancy analyses (pRDAs) were performed based on selected predictor variables (spatial, environmental and landscape variables). The pure components thus were local environmental [Env], landscape [Land] and spatial [Spa] (Legendre and Legendre 1998, Peres-Neto et al. 2006). We performed variation partitioning for each response matrix analyzed (i.e. total community matrix, and matrices separately for different groups defined by habitat use, dispersal or body size) that was Hellinger transformed (Legendre and Gallagher 2001). The significance of each pure component [Env, Land, and Spa] was tested using the function `anova` from the `vegan` package. Redundancy analysis (RDA) and associated variation partitioning were run using the “`rda`” and “`varpart`” functions, respectively, from the `vegan` package (Oksanen et al. 2011).

## Results

We collected 1098 individuals of 33 species, belonging to six orders and 18 families: Characiformes (7 families), Siluriformes (6), Gymnotiformes (2), Cyprinodontiformes (1), Cichliformes (1) and Synbranchiformes (1). The most abundant species were *Bryconamericus turiuba*, *Piabina argentea* and *Poecilia reticulata*, comprising 40% of total abundance (Table S4).

The trait groups demonstrate a dominance of few traits in the area, with the largest number of fish species were benthic (14 species), fast-flow (10 species) and medium-sized species (18 species). However, the nektonic fish was the habitat group with the highest abundance (48% or 530 individuals), probably, because the two most abundant species were present in this group: *Bryconamericus turiuba* (18%) and *Piabina argentea* (12%). These species occurred in high numbers at points 3, 6, 17, 19

and 14 (in order of abundance), which were the 10 sampling points with the lowest rate of riparian vegetation cover.

The grouping species by different functional traits showed that environmental and spatial variables were generally important in explaining variation in different trait groupings (i.e. habitat use, flow preference and body size). For the species groups classified based on habitat use, we found that the environmental and spatial predictors based on riverine distance were both significant ( $P < 0.05$ ) for nektobenthic and surface species (Table 2). Although both fractions were significant, the environmental component was greater for nektobenthic species ( $R^2 \text{ adj.} = 0.26$ ,  $P < 0.05$ ), while the explanatory power of space was greater for marginal ( $R^2 \text{ adj.} = 0.28$ ,  $P < 0.05$ ) and surface ( $R^2 \text{ adj.} = 0.18$ ,  $P < 0.05$ ) species. The community structure of nektonic species was significantly explained only by the environmental predictors ( $R^2 \text{ adj.} = 0.075$ ,  $P < 0.05$ ), whereas benthic species were not significantly explained by any of the predictors. The environment predictors were mostly explained for nektobenthic species, indicating that the water quality and vegetation structure were important to group occurrence (Table 2).

The local environmental, landscape and spatial variables were important for different water flow preference groups. Local environmental variables were important for the groups of species with preference for fast, intermediate and slow water flow ( $R^2 \text{ adj.} = 0.15$ ,  $0.12$ , and  $0.14$ , respectively). Additionally, landscape variables, together with local environmental variables, explained significant variation in the species group with a preference for fast water flow. Spatial variables, together with the local environmental and landscape variables, contributed significantly to variation in the species group with a preference for slow water flow. The local environmental variables were slightly different for each species group, with depth and transparency (indicated by

the values of total dissolved solids and total solids) being important for the species groups with a preference for fast flow and slow flow. Chlorophyll-a was important in explaining the group of species with preference for intermediate water flow. Slow-flow species were also explained by one large-scale spatial variable (spatial filter 2). Land use was related to the species groups with preference for fast flow and slow flow, but with different significant predictor variables included in the models. The group of fast-flow species was associated with the presence of natural landscape features, while the group of slow-flow species was associated with pasture areas.

Regarding body size, spatial variables were important for the groups of large and small fish, with one large-scale spatial filter (2) being important for large fish ( $R^2_{adj}=0.13$ ) and one fine-scale spatial filter (6) being important for small fish ( $R^2_{adj}=0.10$ ). For small fish, chlorophyll-a, depth and consolidated substrate showed substantial explanatory power ( $R^2_{adj} = 0.23$ ), thus suggesting that these local environmental variables influenced the distributions of small species, such as *Curculionichthys insperatus*, *Piabarchus stramineus* and *Piabina argentea*.

Table 2: Relationship analysis between traits composition of habitat, fish dispersal and size with environmental, landscape (land use), and spatial variables, for the region of Silvânia, Goiás, Brazil, in 2017. The bold values indicates significant results (\*P<0.05). (TDS = Total dissolved solids). The "a" codon indicates the variation explained exclusively by the environment; codon "b" the variation explained exclusively by land use; the codon "c" is the variation explained exclusively by space; codons "a+b", indicate the variation explained by the environment and land use together; codons "a+c", indicate the variation explained by the environment and space together; codons "b+c", indicate the variation explained by land use and space together; codons "a+b+c", indicate the variation explained by the environment, land use and space together; while codon d indicates the residual variation, that is, it cannot be explained by any of the sets of variables used in the analysis. The values of F and P are not presented for shared fractions and residual, as it is not possible to test their significance.

	N Species	Environment	Landscape	Spatial Filters	Env (a)			Land (b)			Spa (c)			a+b	a+c	b+c	a+b+c	d
					R <sup>2</sup> adj	F	P	R <sup>2</sup> adj	F	P	R <sup>2</sup> adj	F	P	R <sup>2</sup> adj	R <sup>2</sup> adj	R <sup>2</sup> adj	R <sup>2</sup> adj	R <sup>2</sup> adj
<b>Entire fish community</b>	33	Chlorophyll-a, Depth	Natural	1, 2, 6	0.06	1.55	<b>0.03</b>	0.01	1.55	0.32	0.08	1.55	<b>0.02</b>	0.06	0.04	0.04	0	0.71
<b>TRAITS COMPOSITION</b>																		
<b>Habitat</b>																		
Benthic	14	Depth, TSD, Consolidated substrate	Natural	-	0.06	14.53	0.09	0.02	15.41	0.15	-	-	-	0.16	-	-	-	0.69
Marginal	6	Flow, Temperature	-	2, 5, 8	0.04	1.46	0.15	-	-	-	0.28	4.13	<b>0.005</b>	-	0.22	-	-	0.46
Nektobenthic	5	Chlorophyll-a, Riparian forest, Leaves, Total solids	-	1, 8	0.26	3.46	<b>0.001</b>	-	-	-	0.07	2.26	<b>0.04</b>	-	0.27	-	-	0.40
Nektonic	7	Chlorophyll-a	-	-	0.07	2.38	<b>0.03</b>	-	-	-	-	-	-	-	-	-	-	-
Surface	1	Depth	Basin Area	6	0.13	6.66	<b>0.02</b>	0	0.04	0.82	0.18	8.98	<b>0.01</b>	0.20	0.06	0	0.10	0.33
<b>FLOW PREFERENCE</b>																		
Fast water	10	Depth, Consolidated substrate, Total solids	Natural	-	0.15	2.30	<b>0.009</b>	0.06	2.45	<b>0.04</b>	-	-	-	0.12	-	-	-	0.67
Intermediate water	8	Chlorophyll-a	-	-	0.12	3.36	<b>0.02</b>	-	-	-	-	-	-	-	-	-	-	-
Slow water	15	Depth, TDS	Basin Area, Pasture	2	0.14	2.59	<b>0.007</b>	0.08	1.92	<b>0.04</b>	0.11	3.32	<b>0.007</b>	0.20	0.06	0	0.10	0.31
<b>SIZE</b>																		
Large	5	Flow, Temperature	-	2	0.08	2.17	0.10	-	-	-	0.13	4.65	0.01	-	0.23	-	-	0.55
Medium	18	STD, Depth, Flow	Natural, Natural 500m	1, 8	0.04	1.28	0.18	0.03	1.30	0.22	0.007	1.05	0.41	0.02	0.03	0.02	0.07	0.78
Small	10	Depth, Chlorophyll-a, Consolidated substrate	Basin Area	6	0.23	3.34	<b>0.003</b>	0.01	1.42	0.23	0.10	3.60	<b>0.01</b>	0.06	0.06	0	0.002	0.53

## **Discussion**

### ***Hypothesis 1 – Entire fish community***

The roles of different ecological factors on variation in community structure in Neotropical riverine ecosystems have been given increasing attention recently, considering different taxonomic groups and spatial scale (e.g., Borges et al. 2020, Oliveira et al. 2020, Benone et al. 2020, Lansac-Toha et al. 2021). Considering entire fish metacommunity, mainly environmental variables were significant, indicating the importance of species sorting for the variation in fish community structure (Borges et al. 2020). Previously, several studies that shown that environmental variables mainly affect variation in the community structure of stream fish (López-Delgado et al. 2019, Carvalho and Tejerina-Garro 2015, Sály et al. 2011, Vanormelingen et al. 2008, Magalhães et al. 2002), which is directly related to the occurrence of different species groups with different traits. The effect of environmental and spatial predictors on local communities can be explained by the fact that most species we captured are specialists, mostly of medium body size, and have efficient dispersal capacity. Specialist species were mainly affected by stream size, occurring in narrow headwater streams with few pools, thin substrates and plenty of woody debris (Scarnecchia 1988, O'Malley 2007, Pandit et al. 2009, Pease et al. 2015).

### ***Hypothesis 2 - Spatial components and different functional niche dimensions***

In general, our results show that spatial components demonstrate more influence in metacommunity for all traits composition than landscape use, for some groups both small and large scale filters were selected (marginal, nektobenthic and medium size). According to Pérez-Mayorga et al. (2017) spatial variables can distinctly influence the

occupancy and fish distributions, specifically in richness communities, it is more difficult to understand the relative importance of environmental versus spatial factors.

The expectation that slow-flow, marginal, surface, nektobenthic and benthic small species groups would be dependent on the local environmental conditions was partially corroborated, although spatial variables were important for some species groups. The importance of spatial variables varied among the trait groups, suggesting that the large and slow water fishes are being structured by dispersal limitation rather than mass effects (PCNM 2), on other hand, the small fishes that prefer surface were represented by intermediate scale (PCNM 6), demonstrating a finer selection, indicating that this groups can experience mass effects in greater intensity, because mass effects should increase in smaller spatial distances and smaller spatial extents (Heino et al., 2015).

Our hypothesis for the group of benthic fish was refuted because we found no relationship between these species and the environmental, landscape and spatial variables we examined. This may be because benthic species are more easily affected by local factors, such as the complexity of in-stream habitat (Harborne et al. 2011, Ferrari 2017) and food availability. These factors are associated with foraging strategies, such as the preference for feeding on invertebrates, algae or epilithon (Pickett and Cadenasso 1995, Casatti et al. 2015), for this reason, we indicate that other more specific variables such as food items (of origin) internal and external to the streams, distance and displacement capacity of the species, can offer clearer answers about this group, as well as its ability to swim and move in streams.

### **Hypothesis 3 – Environmental factors different functional niche dimensions**

For the species groups related to flow preference, we showed that slow-water fish (*Astyanax bockmanni*, *Hoplias malabaricus*, *Cichlasoma paranaense*, and *Poecilia reticulata*) responded to environmental factors. This species group showed significant relationships with all explanatory variable groups (i.e. environmental, landscape and spatial), but especially with variables related to riparian and pasture land uses. The group of species inhabiting fast-flow waters (*Aspidoras fuscoguttatus*, *Bryconamericus turiuba*, and *Cetopsorhamdia iheringi*) was affected by environmental factors, such as flow and depth, which are also directly related to their dispersal and swimming capacity. Stream depth is related to the total fish abundance, because the deeper the stream the greater its capacity to support larger number of individuals (Ferrari et al. 2018). Fish species present in intermediate water flows were mostly herbivores or omnivores (i.e. *Curculionichthys insperatus*, *Piabina argentea*, and *Rhamdia quelen*) and showed a significant relationship with chlorophyll-a, confirming the preference of this group for intermediate water flows with ample vegetation. However, species with preference to intermediate water flow typically requires forested streams with little agricultural and urban development in the catchment (Pease et al. 2015).

#### **Hypothesis 4 – Land use different functional niche dimensions**

In general, only environmental variables were selected in this work, this indicates that the conversion of natural habitat to pasture or agriculture is one of the strongest impacts for the aquatic environment, corroborating Heino (2013), indicating that the change in vegetation cover reduces connectivity, they prevent dispersal between locations and accelerate local extinctions (Pérez-Mayorga et al. 2017).

The loss of riparian vegetation indirectly influences stream biota by increasing siltation through the transport of allochthonous material, thus increasing turbidity and

reducing depth and flow (Gregory et al. 1991). This can impact the structure of fish communities (Wantzen and Mol 2013, Allard et al. 2016) by affecting fish survival via changes in habitat conditions and food availability (Jellyman et al. 2013). The occurrence of riparian forests is also directly related to species occurrences, since riparian vegetation is essential for maintaining the biological integrity of stream ecosystems (Sweeney et al. 2004, Casatti et al. 2009). This idea is corroborated by the relationship we found between species traits and environmental variables, such as depth, riparian forest, water flow and total solids.

## **Conclusion**

To conclude, use the approach of different functional niche dimensions demonstrated that entire stream fish communities of the Cerrado Biome are affected by both environmental and spatial variables. These variables together were responsible for explaining about 29% of the variation for overall metacommunity, even if for some functional traits groups the explicability has revealed higher values. Although we used variables commonly adopted in studies of stream fish metacommunities (e.g. Roa-Fuentes et al. 2020, Barbosa et al. 2019, Lemke and Suárez, 2013), we believe that other variables can also be important to the structuring of these communities, such as the interaction with other groups of organisms and geomorphologic characteristics of watershed, which were not considered in this study.

In general, five of the eleven trait groups were influenced by more than one explanatory variable group. However, environmental variables, such as features of riparian environments, water flow, stream depth and temperature, were most influential in shaping different trait groups. This finding suggests that preserving natural environmental conditions at the riparian and habitat scales should be important for

stream integrity in our study region. Our results also suggested that dispersal shaped the fish metacommunity we studied. This finding therefore suggests that guaranteeing free dispersal of fish between sites is also key in maintaining fish biodiversity in streams of the Cerrado Biome.

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### **Authors' contributions**

RCPF and JCN conceived of the presented idea. RCPF, PPB and KBM collected and analyzed the data. All authors discussed the results and contributed substantially to drafting the work or revising to improve the manuscript.

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Table S1 - Mean and standard deviation for the local environmental variables measured for each study section in the 18 streams in different sub-basins in the upper Paraná River basin, in the eastern portion of the State of Goiás.

Variable	Mean	Standard Deviation ( $\pm$ )
Temperature ( $^{\circ}\text{C}$ )	18.63	1.68
Transparency (cm)	0.8	0.31
pH	6.59	0.44
Conductivity ( $\mu\text{s cm}^{-1}$ )	41.18	23.2
Dissolved Oxygen ( $\text{mg L}^{-1}$ )	7.56	0.79
Turbidity (NTU)	69.8	165.78
Chlorophyll-a ( $\mu\text{g L}^{-1}$ )	1.35	1.58
Biochemical Oxygen Demand ( $\text{mg L}^{-1}$ )	1.74	1.68
Oxidation Potential Redox (mV)	268.93	73.2
Total Dissolved Solids ( $\text{mg L}^{-1}$ )	20.59	11.64
Total Solids ( $\text{mg L}^{-1}$ )	55.44	54.39
Unconsolidated Substrate (%)	91	1
Consolidated Substrate (%)	9	1
Width (m)	3.7	1.96
Depth (m)	0.33	0.079
Flow (rps)	216.56	126.12
Riparian Forest Width (m)	33.22	19.56

Table S2: Distance matrix created based on the River Distance Matrix from the geographical location of 18 points in different sub-basins in the upper Paraná River basin, in the eastern portion of the State of Goiás.

<b>RIVER DISTANCE MATRIX</b>																		
	<b>1</b>	<b>2</b>	<b>3</b>	<b>4</b>	<b>5</b>	<b>6</b>	<b>7</b>	<b>8</b>	<b>9</b>	<b>10</b>	<b>11</b>	<b>12</b>	<b>13</b>	<b>14</b>	<b>15</b>	<b>16</b>	<b>17</b>	<b>18</b>
<b>1</b>	0	4.78898	5.98081	8.86423	322.64	329.268	328.476	326.915	326.053	322.177	314.961	311.139	325.923	338.767	328.438	322.736	331.755	303.633
<b>2</b>	4.78898	0	9.80878	4.32153	327.429	334.057	333.265	331.704	330.842	326.966	319.75	315.928	330.712	343.556	333.227	327.525	336.544	308.422
<b>3</b>	5.98081	9.80878	0	13.884	328.621	335.249	334.457	332.896	332.034	328.158	320.942	317.12	331.904	344.748	334.418	328.717	337.736	309.613
<b>4</b>	8.86423	4.32153	13.884	0	331.505	338.132	337.34	335.779	334.917	331.042	323.825	320.003	334.787	347.631	337.302	331.6	340.619	312.497
<b>5</b>	322.64	327.429	328.621	331.505	0	7.2782	6.48615	4.92539	4.06309	0.46311	7.67967	11.5014	50.0757	62.92	52.5905	46.8888	55.9076	19.0078
<b>6</b>	329.268	334.057	335.249	338.132	7.2782	0	5.95386	2.90254	3.5308	7.09061	14.3072	18.1289	56.7032	69.5475	59.218	53.5163	62.5351	25.6353
<b>7</b>	328.476	333.265	334.457	337.34	6.48615	5.95386	0	3.60105	2.42306	6.29856	13.5151	17.3369	55.9111	68.7555	58.4259	52.7242	61.7431	24.8433
<b>8</b>	326.915	331.704	332.896	335.779	4.92539	2.90254	3.60105	0	1.17799	4.7378	11.9544	15.7761	54.3504	67.1947	56.8652	51.1635	60.1823	23.2825
<b>9</b>	326.053	330.842	332.034	334.917	4.06309	3.5308	2.42306	1.17799	0	3.8755	11.0921	14.9138	53.4881	66.3324	56.0029	50.3012	59.32	22.4202
<b>10</b>	322.177	326.966	328.158	331.042	0.46311	7.09061	6.29856	4.7378	3.8755	0	7.21656	11.0383	49.6126	62.4569	52.1274	46.4257	55.4445	18.5447
<b>11</b>	314.961	319.75	320.942	323.825	7.67967	14.3072	13.5151	11.9544	11.0921	7.21656	0	3.82177	42.396	55.2404	44.9108	39.2091	48.2279	11.3282
<b>12</b>	311.139	315.928	317.12	320.003	11.5014	18.1289	17.3369	15.7761	14.9138	11.0383	3.82177	0	38.5742	51.4186	41.089	35.3873	44.4062	7.50639
<b>13</b>	325.923	330.712	331.904	334.787	50.0757	56.7032	55.9111	54.3504	53.4881	49.6126	42.396	38.5742	0	14.0223	3.69269	3.18687	5.83194	31.0678
<b>14</b>	338.767	343.556	344.748	347.631	62.92	69.5475	68.7555	67.1947	66.3324	62.4569	55.2404	51.4186	14.0223	0	10.3296	16.0312	19.8542	43.9122
<b>15</b>	328.438	333.227	334.418	337.302	52.5905	59.218	58.4259	56.8652	56.0029	52.1274	44.9108	41.089	3.69269	10.3296	0	5.70167	9.52463	33.5826
<b>16</b>	322.736	327.525	328.717	331.6	46.8888	53.5163	52.7242	51.1635	50.3012	46.4257	39.2091	35.3873	3.18687	16.0312	5.70167	0	9.01881	27.881
<b>17</b>	331.755	336.544	337.736	340.619	55.9076	62.5351	61.7431	60.1823	59.32	55.4445	48.2279	44.4062	5.83194	19.8542	9.52463	9.01881	0	36.8998
<b>18</b>	303.633	308.422	309.613	312.497	19.0078	25.6353	24.8433	23.2825	22.4202	18.5447	11.3282	7.50639	31.0678	43.9122	33.5826	27.881	36.8998	0

Table S3: PCNM Matrix (Principal Coordinates of Neighbour Matrices) created from an AVR distance matrix (River Distance Matrix), resulting in 9 spatial filters for fish communities from different sub-basins in the upper Paraná River basin, in the eastern portion of the State of Goiás.

	<b>PCNM1</b>	<b>PCNM2</b>	<b>PCNM3</b>	<b>PCNM4</b>	<b>PCNM5</b>	<b>PCNM6</b>	<b>PCNM7</b>	<b>PCNM8</b>	<b>PCNM9</b>
<b>1</b>	-0.43267	0.600278	0.000205	2.29E-06	1.61E-09	1.52E-07	1.53E-07	3.27E-09	3.01E-08
<b>2</b>	-0.44252	-0.22272	-0.0002	-5.03E-05	0.186382	-1.95E-05	-0.00041	-0.79493	0.000343
<b>3</b>	-0.44251	-0.2227	-0.0002	-1.99E-05	-0.78163	-4.45E-06	7.77E-05	0.236058	-0.00011
<b>4</b>	-0.44251	-0.22274	-0.0002	-4.49E-05	0.595241	5.22E-06	0.00025	0.558886	-0.00024
<b>5</b>	0.130495	-0.04701	-0.21322	0.011	1.30E-06	-0.04423	-0.82531	0.000803	0.106054
<b>6</b>	0.130434	-0.04702	-0.28209	0.017568	-1.42E-05	0.680419	0.038924	-0.00012	-0.27709
<b>7</b>	0.130442	-0.04702	-0.27375	0.016343	-1.13E-05	-0.71418	0.130825	-5.92E-05	-0.06216
<b>8</b>	0.130458	-0.04702	-0.25795	0.016231	-9.41E-06	0.146921	0.336659	0.00032	0.833593
<b>9</b>	0.130466	-0.04701	-0.24914	0.015832	-7.91E-06	-0.0537	0.411821	2.99E-05	-0.45147
<b>10</b>	0.130499	-0.04701	-0.2088	0.011801	7.36E-07	-0.01465	-0.08335	0.000929	-0.06591
<b>11</b>	0.130546	-0.04701	-0.1335	0.003733	1.36E-05	-0.0112	-0.06122	-0.00084	-0.05294
<b>12</b>	0.130562	-0.04701	-0.09363	-0.00055	1.86E-05	-0.00939	-0.04998	-0.00154	-0.04637
<b>13</b>	0.130408	-0.04713	0.30792	-0.10646	-3.21E-06	0.007099	0.039395	0.000449	0.00724
<b>14</b>	0.130223	-0.0472	0.435546	0.663874	4.27E-06	-0.00035	-0.00625	-3.48E-05	-0.00135
<b>15</b>	0.130377	-0.04715	0.333357	0.119825	1.46E-06	0.005883	0.032399	0.000208	0.006065
<b>16</b>	0.130443	-0.04712	0.275551	-0.04068	4.17E-06	0.006612	0.038193	-0.00014	0.004921
<b>17</b>	0.130328	-0.04715	0.360084	-0.72839	-2.48E-05	0.000777	-0.00202	-1.35E-05	-0.00058
<b>18</b>	0.064528	0.679747	5.40E-06	1.14E-08	3.56E-05	6.02E-10	2.77E-09	1.76E-06	-5.58E-10

Table S4: Fish species found in our study streams, along with their functional traits related to habitat use, dispersal, and body size.

<b>Species</b>	<b>Habitat use</b>	<b>Velocity preference</b>	<b>Size</b>	<b>Order</b>	<b>Family</b>	<b>Genus</b>
<i>Aspidoras fuscoguttatus</i>	Benthic	Fast	Small	Siluriformes	Callichthyidae	Aspidoras
<i>Astyanax bockmanni</i>	Nektonic	Slow	Medium	Characiformes	Characidae	Astyanax
<i>Astyanax fasciatus</i>	Nektonic	Slow	Medium	Characiformes	Characidae	Astyanax
<i>Astyanax lacustris</i>	Nektonic	Slow	Medium	Characiformes	Characidae	Astyanax
<i>Bryconamericus turiuba</i>	Nektonic	Intermediate	Medium	Characiformes	Characidae	Bryconamericu
<i>Cetopsis gobioides</i>	Benthic	Fast	Medium	Siluriformes	Cetopsidae	Cetopsis
<i>Cetopsorhamdia iheringi</i>	Benthic	Fast	Medium	Siluriformes	Heptapteridae	Cetopsorhamdia
<i>Characidium zebra</i>	Benthic	Intermediate	Medium	Characiformes	Crenuchidae	Characidium
<i>Characidium gomesi</i>	Benthic	Fast	Medium	Characiformes	Crenuchidae	Characidium
<i>Cichlasoma paranaense</i>	Nektobenthic	Slow	Medium	Cichliformes	Cichlidae	Cichlasoma
<i>Curculionichthy sp</i>	Marginal	Intermediate	Small	Siluriformes	Loricariidae	Curculionichthys
<i>Curculionichthys insperatus</i>	Marginal	Intermediate	Small	Siluriformes	Loricariidae	Curculionichthys
<i>Eigenmannia virescens</i>	Marginal	Intermediate	Large	Gymnotiformes	Sternopygidae	Eigenmannia
<i>Gymnotus carapo australis</i>	Marginal	Slow	Large	Gymnotiformes	Gymnotidae	Gymnotus
<i>Hasemania hanseni</i>	Nektonic	Slow	Small	Characiformes	Characidae	Hasemania
<i>Hoplias malabaricus</i>	Margins	Slow	Large	Characiformes	Erythrinidae	Hoplias
<i>Hypostomus ancistroides</i>	Benthic	Intermediate	Medium	Siluriformes	Loricariidae	Hypostomus
<i>Hypostomus sp</i>	Benthic	Fast	Medium	Siluriformes	Loricariidae	Hypostomus
<i>Imparfinis schubarti</i>	Benthic	Fast	Medium	Siluriformes	Heptapteridae	Imparfinis
<i>Leporinus sp</i>	Nektobenthic	Slow	Medium	Characiformes	Anostomidae	Leporinus
<i>Leporinus spl</i>	Nektobenthic	Slow	Medium	Characiformes	Anostomidae	Leporins
<i>Parodon nasus</i>	Benthic	Fast	Medium	Characiformes	Parodontidae	Parodon

<i>Phenacorhamdia tenebrosa</i>	Benthic	Fast	Medium	Siluriformes	Heptapteridae	Phenacorhamdia
<i>Piabarchus stramineus</i>	Nektonic	Intermediate	Small	Characiformes	Characidae	Piabarchus
<i>Piabina argentea</i>	Nektonic	Intermediate	Small	Characiformes	Characidae	Piabina
<i>Pimelodella gracilis</i>	Benthic	Slow	Medium	Siluriformes	Heptapteridae	Pimelodella
<i>Pimelodus sp</i>	Benthic	Fast	Large	Siluriformes	Pimelodidae	Pimelodus
<i>Poecilia reticulata</i>	Surface	Slow	Small	Cyprinodontiformes	Poeciliidae	Poecilia
<i>Prochilodus lineatus</i>	Nektobenthic	Slow	Large	Characiformes	Prochilodontidae	Prochilodus
<i>Rhamdia quelen</i>	Benthic	Slow	Medium	Siluriformes	Heptapteridae	Rhamdia
<i>Rhyacoglanis paranensis</i>	Benthic	Fast	Medium	Siluriformes	Pseudopimelodidae	Rhyacoglanis
<i>Steindachnerina insculpta</i>	Nektobenthic	Slow	Medium	Characiformes	Curimatidae	Steindachnerina
<i>Synbranchus marmoratus</i>	Marginal	Slow	Large	Synbranchiformes	Synbranchidae	Synbranchus

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## CAPÍTULO II

**Shortcuts for biomonitoring programs of stream ecosystems: evaluating the taxonomic, numeric, and cross-taxa congruence in phytoplankton, periphyton, zooplankton, and fish assemblages**

**Short title: Shortcuts for biomonitoring program of stream ecosystems**

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## **Abstract**

Different biological groups can be used for monitoring aquatic ecosystems because they can respond to variations in the environment. However, the evaluation of different bioindicators may demand multiple financial resources and time, especially when abundance quantification and species-level identification are required. In this study, we evaluated whether taxonomic, numerical resolution and cross-taxa can be used to optimize costs and time for stream biomonitoring in Central Brazil (Cerrado biome). For this, we sampled different biological groups (fish, zooplankton, phytoplankton, and periphyton) in stream stretches distributed in a gradient of land conversion dominated by agriculture and livestock. We used the Mantel and Procrustes analyses to test the association among different taxonomic levels (species to class), the association between incidence and abundance data (numerical resolution), and biological groups. We also assessed the relative effect of local environmental and spatial predictors on different groups. The taxonomic levels and numerical resolutions were strongly correlated in all taxonomic groups ( $r > 0.70$ ). We found no correlations among biological groups. Different sets of environmental variables were the most important to explain the variability in species composition of distinct biological groups. Thus, we conclude that monitoring the streams in this region using bioindicators is more informative through higher taxonomic levels with occurrence data than abundance. However, different biological groups provide complementary information, reinforcing the need for a multi-taxa approach in biomonitoring.

Keywords: biological surrogates; Cerrado; ecological classification; environmental monitoring;

## **Introduction**

The biodiversity of aquatic freshwater ecosystems is of great local and global importance, which has experienced more pronounced declines than terrestrial environments [1]. Besides, aquatic environments are linked directly to peripheral terrestrial ecosystems. Therefore, structural changes in terrestrial environments [2, 3] can promote changes in the physical-chemical characteristics of the water and physical structure of the aquatic habitat [4], negatively affecting the aquatic biodiversity [5, 6, 7]. For this reason, urgent actions are necessary to protect freshwater ecosystems [8], in addition to methods that improve the assessment and biomonitoring of aquatic biodiversity [9].

Biomonitoring assessments often use bioindicator species or communities with specific requirements, together with a set of chemical and physical variables of the environment. Thus, changes in these variables can lead to changes in the species presence-absence and abundance, besides morphological, physiological, and behavioral interferences, or even local extinction [10]. Usually, biomonitoring research and programs focus on a single or a set of taxonomic groups. Thus, phytoplankton [11, 12, 13], periphyton [14, 15, 16], zooplankton [17, 18, 13], macroinvertebrates [19], and fish [20, 21], can be used alone or together with other taxonomic groups to assess the responses of different levels of environmental degradation in aquatic ecosystems [22].

Aspects related to implementation, such as low-cost sampling and identification and simplification of protocols, are crucial for determining the ideal tools for monitoring [23]. In this sense, strategies that seek to reduce costs and shortcut the monitoring program while guaranteeing the efficiency of aquatic biodiversity biomonitoring become essential [24], including the correlations among taxonomic levels [taxonomic resolution; e.g. 25, 75, 26, 27], between species abundance and

presence-absence data of each biological group [numerical resolution; e.g. 11, 28, 29], and correlations between biological groups and their trophic subdivisions [cross-taxa; e.g. 30, 31, 32].

Taxonomic resolution represents the use of coarser taxonomic levels (e.g., genus and family) instead of more detailed identification at the species level, without significant loss of information [33, 34, 11, 27]. Thus, adopting the taxonomic resolution method brings benefits such as reduced time for identification and, consequently, costs [35, 28]. That can facilitate the development of studies with reliable information and accelerate the performance of biomonitoring programs [36]. The numerical resolution aims to replace species abundance with presence-absence data [28, 37, 29]. This method has demonstrated concordant results when using presence-absence data and the complete dataset [38]. Another advantage of using this method is the speed in the counting process, making biomonitoring faster to be performed and decreasing costs [36, 28, 39].

For aquatic groups, congruence is expected mainly for groups that respond similarly to environmental and spatial gradients [40]. In this sense, some groups such as phytoplankton and periphyton may show high congruence because of their similar environmental requirements [41] and dispersal capacity. Besides, high congruence is expected for groups linked directly through the trophic web [42], such as phytoplankton and zooplankton [43], algae (phytoplankton and epilithic algal community), herbivorous fish [44], and even macroinvertebrates and fish.

For biomonitoring purposes, detecting concordant groups and assessing one or few groups would reduce the demand for people and resources without reducing the quality of information [24, 46, 9]. However, some groups may differ in their responses to the environment, and the assessment of all these groups could help capture more

detailed information on environmental variations [47]. Therefore, the multi-taxa approach [47, 42, 48] allows us to understand the concordance between groups and their response to environment and landscape variables, helping to guide optimized biomonitoring strategies.

Changes in riparian vegetation could drive changes in congruence patterns, as bioindicators from different taxonomic groups may have different tolerance thresholds to vegetation loss [e.g. 5]. For streams, the riparian forest protects the watercourse and retains sediment and contaminants from adjacent areas, acting as a buffer against the impacts of deforestation [49], in addition to maintaining the heterogeneity of aquatic habitats [50]. Many studies show a higher sensitivity of aquatic communities, not only to pollution but also to deforestation of stream riparian areas [51].

Biomonitoring is based on the assumption that bioindicators respond to environmental variations. However, this assumption is not necessarily valid, since dispersal-related processes may overcome niche processes influencing community structure and, consequently, the bioindicator responses [53]. Dispersal influences may be stronger enough to override the environmental signal captured by biological communities, making bioindicator responses unreliable [54, 55]. Thus, a crucial step in biomonitoring is identifying bioindicators less influenced by spatial processes and selecting those with stronger environmental signals [56].

Therefore, in this study, we aim to evaluate the different surrogacy methods (taxonomic, numerical, and cross-taxa) in streams, considering distinct aquatic groups. Besides, we aim to investigate whether these different levels (taxonomic and numerical) or groups have similar responses to the environmental gradient and spatial patterns. Thus, for taxonomic surrogacy (i), we expect the congruence between species and genus will be greater than between species and coarser levels (family, order, class) [11,

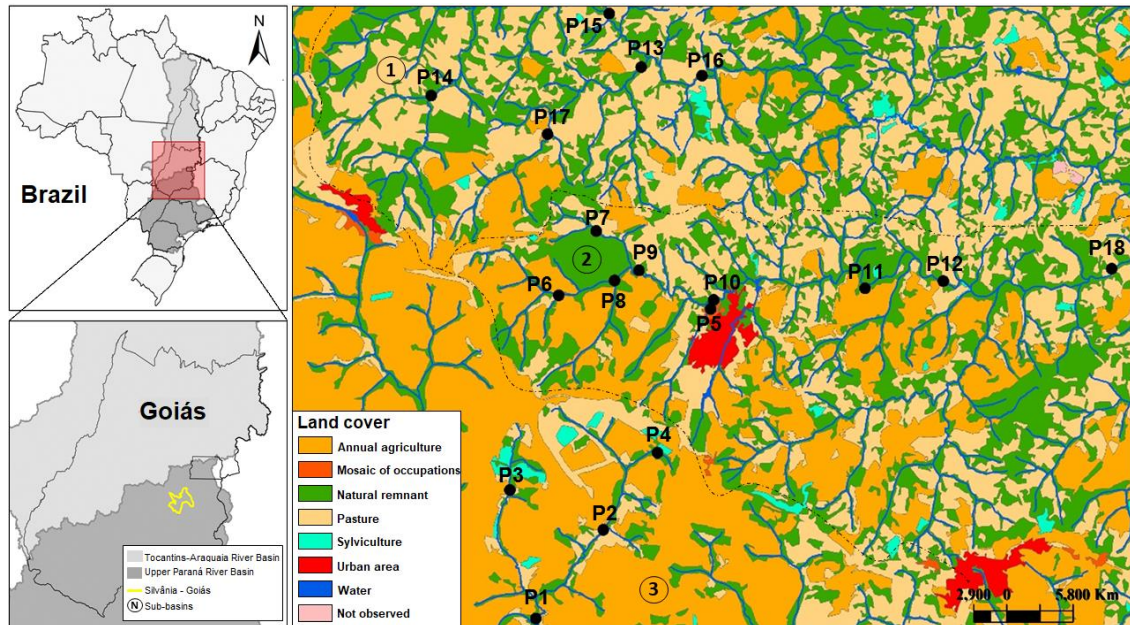
27]. For numerical resolution (ii), we expect the surrogacy of species abundance for presence-absence data to be highly concordant in all biological groups [26]. For the cross-taxa method (iii), we expect the cross-taxa congruence to occur between (a) phytoplankton and periphytic communities because of their similar environmental requirements, such as nutrients and luminosity [57, 58, 59]. Moreover, we expect high congruence between (b) algae (phytoplankton and periphyton) and herbivorous zooplankton [43, 27], between (c) carnivorous fish and zooplankton [60, 61], and between (d) algae (phytoplankton and periphyton) and herbivorous fish [44], due to the direct relationships established between these organisms through the food chain.

## **Material and Methods**

### **Study area**

The study was carried out in 18 streams of the upper Paraná River basin, including the sub-basins of Piracanjuba, Ribeirão Vermelho and Rio dos Bois. We used first- to fourth-order streams naturally shallow, narrow, and close to water sources (Figure 1). The streams are shallow, narrow, with a pH close to neutral, low concentrations of nutrients, and predominance of unconsolidated substrates. However, they show a high variation in flow and turbidity (Table S1). The average altitude and temperature of the region are 900 m and 26 °C, respectively [62]. The region climate is classified as Aw, according to Köppen's classification [63], being humid tropical with well-defined dry (April to September) and rainy (October to March) seasons. The region is part of the Cerrado biome with notable landscape heterogeneity, containing a preserved area with native vegetation (Silvânia National Forest - FLONA) and different land-use types (agricultural and pasture). The region surrounding the analyzed streams is constituted of a large vegetation mosaic (Figure 1), with a large and protected area

(39.66%), the Silvânia National Forest (FLONA, 486.67 ha), as well as urban areas (4.45%), pastures (33.76%), agriculture (21.03%), and forestry (1.08%).



**Fig 1. Location of the 18 sampling points in the three sub-basins, (1) Piracanjuba, (2) Ribeirão Vermelho, and (3) Rio dos Bois in the municipality of Silvânia, State of Goiás, Brazil.**

### **Collection and identification of biological material**

Phytoplankton, periphyton, zooplankton, and fish samplings were carried out during the same field campaign, within an 80-meter stream stretch, during the dry season (between August and September 2017). Phytoplankton was collected in areas with puddle formation on the subsurface (0.3 m) of streams, in which the water had less flow and higher light intensity. Water samples were stored in 100 ml amber glass bottles and preserved with acetic Lugol [64]. Individuals were then counted through the sedimentation technique [65], using an inverted optical microscope (Zeiss Axiovert 25) with 400x magnification. Individuals were counted in random fields until no new

species were added [66]. The density was expressed in individuals per ml (ind. ml<sup>-1</sup>), and the individuals identified up to the lowest possible taxonomic resolution and classified taxonomically according to the system proposed by Round [67, 68, 69].

Samples of the periphytic community were collected by scraping stones, leaves, and branches with a higher visual concentration of the superficial periphytic community. Scraping was performed using a plate with a central opening of 5 cm<sup>2</sup>, a brush, and distilled water. After scraping and washing, the resulting content was stored in a 100 ml amber flask and fixed with acetic Lugol [64]. Periphyton samples were subsampled and counted following the same protocol applied for phytoplankton, using the sedimentation technique [65]. The individuals were identified and classified according to Round [67, 68, 69].

Zooplankton sampling was performed using a plankton net with 68µm mesh size, in which 300L of water was filtered at each sampling point. The water collected for filtering zooplankton was always around two meters above and below the phytoplankton collection points. Each sample was buffered in 5% formalin and concentrated to a volume of 100 ml in 250 ml white flasks. Quantitative analysis was performed using three 10 ml subsamples, counting at least 200 individuals from each large group (testate amoebae, copepods, cladocerans, and rotifers) in a Sedgewick-Rafter chamber under an optical microscope [70]. The total density was expressed in individuals per m<sup>3</sup> (ind. m<sup>3</sup>). Zooplankton identification was performed based on specialized literature for different groups, such as testate amoebae [71, 72, 73] rotifers [74, 75, 76], cladocerans [77, 78], and copepods [79, 80]. Zooplankton was further classified according to their food preference in herbivores and carnivores, according to [81].

Fish were caught through electrofishing, using an alternating current generator

(1,000 W, 300–500 V, 1–3 A) with two fishing net connect to electrical current, plus an additional net, without electricity. Electrofishing was carried out upstream, following a trajectory that explored all types of microhabitats over 80 meters [82]. After capture, the fish were anesthetized in water and Eugenol solution and then transferred to 10% formalin. After 72 hours, they were deposited in 70% alcohol to preserve them [83, 84, 85, 82]. Individuals were identified using unpublished identification keys provided by a taxonomist (Fernando Rogério de Carvalho, Universidade Federal do Mato Grosso do Sul, Brazil). Fish were also categorized according to their trophic category into herbivores or carnivores [86]. The data used here corresponds to (Sistema de Autorização e Informação em Biodiversidade) SISBIO and (Instituto Chico Mendes de Conservação da Biodiversidade) ICMBio authorization for scientific activities number 59077-1.

### **Environmental and spatial data**

At each sampling point, limnological variables such as water temperature, transparency (m), pH, oxygen (O<sub>2</sub>), conductivity, dissolved oxygen (DO), turbidity, and chlorophyll-a were measured using the Eureka Manta 2 Amphibian probe. Other measurements were carried out in the laboratory, using water samples collected at the site, which were tested following Standard Methods for the Examination of Water and Wastewater [87]. The variables measured in the laboratory were biochemical oxygen demand (BOD), oxidation-reduction (redox), total solids (TS), total dissolved solids (TDS), nitrate, total nitrogen, ammonia nitrogen, total phosphorus, total organic carbon, and iron.

The habitat characterization was carried out based on measurements obtained in nine equidistant transects (10 m) within the 80-meter stretch sample. The following

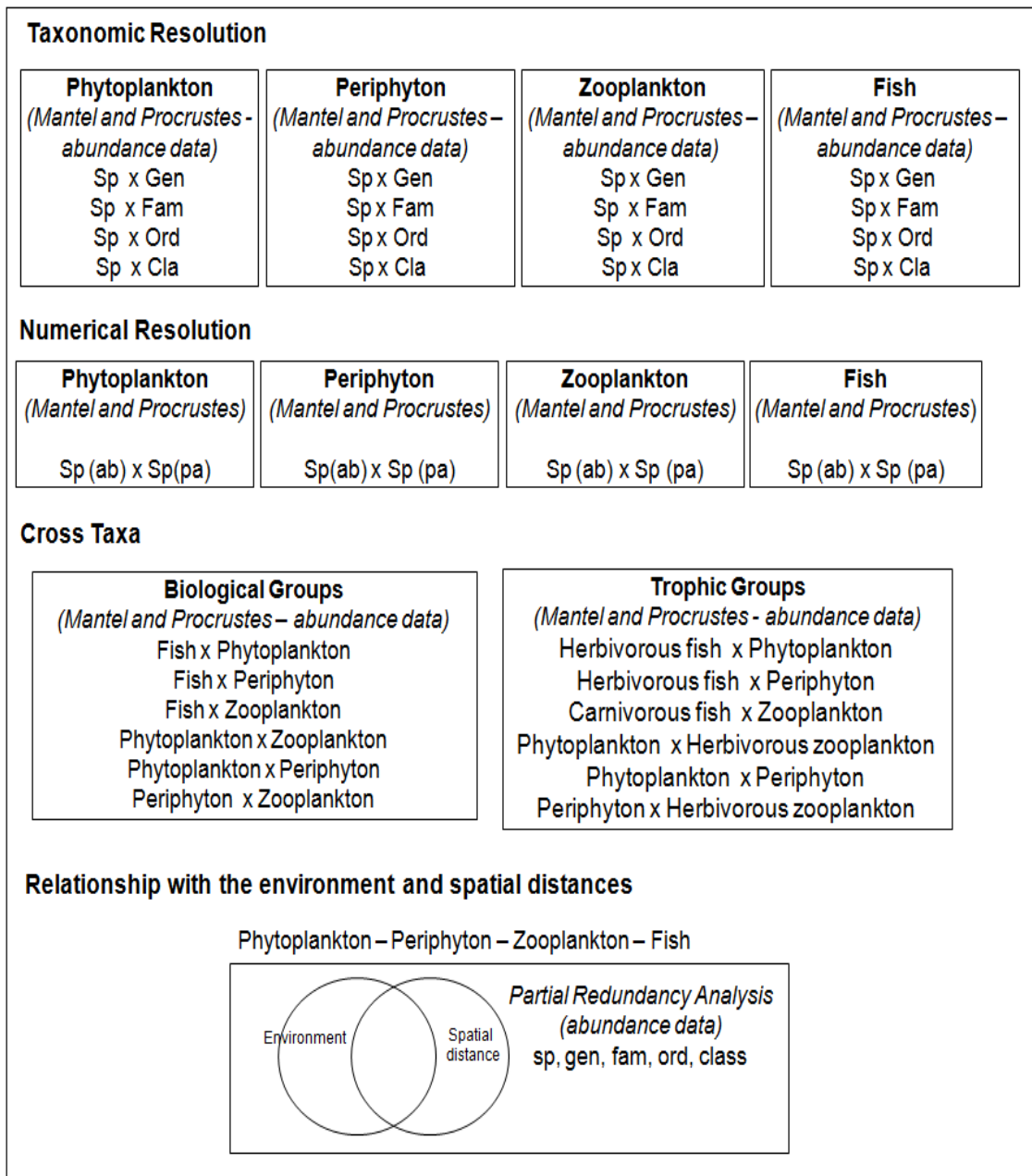
variables were obtained for each transect: stream width, mean depth represented by five points equidistant from one margin to another; flow, measured using the General Oceanics ® flowmeter, model 2030; riparian forest width, estimated visually up to 30 meters on each bank; stable (rocks and logs) and unstable (sand and mud) substrate composition, estimated visually as the proportion of each substrate component [88]. We then calculated the mean values and variation (standard deviation) of the environmental variables of each sampling location.

Spatial data were obtained using a distance matrix from the sampling points following the streamflow. The distances were used to create spatial vectors representing the autocorrelation among sampling points [89, 90]. From the analysis, we generated ten PCNM spatial filters (Principal coordinates of neighbor matrices) [91, 92] that were later included in our data analysis.

## **Data analysis**

Mantel and Procrustes analyses [93] were used to assess the congruence among taxonomic levels (i.e., species with higher levels such as genus, family, order, and class), numerical data types (species abundance and occurrence - Table S1), biological groups (phytoplankton, periphyton, zooplankton, and fish), and trophic levels (herbivorous fish, carnivorous fish, and herbivorous zooplankton). Both tests assess the correlation between multivariate datasets [94]. Mantel is a correlation test between two pairwise matrices [95] and Procrustes is a correlation test between ordination analysis axes [96]. The result interpretation in both tests is similar, in which statistic  $r$  varies between 0 (no congruence) and 1 (perfect congruence). We consider that correlations (Mantel and Procrustes) higher than 0.7 [24] suggest a strong concordance among the taxonomic levels, numerical data, biological groups, and trophic categories evaluated.

For all correlations, the significance of  $r$  values was tested using the Monte Carlo method with 10,000 random permutations. All analyses were performed using the vegan package [97] in the R software [98]. A summary of the analyses performed in this study is present in Figure 2.



**Fig 2. Analyses used to assess the taxonomic, numerical, and cross-taxa congruence and the effect of environmental and spatial variables for phytoplankton,**

**periphyton, zooplankton, and fish communities in 18 streams of the sub-basins Piracanjuba, Ribeirão Vermelho, and Rio dos Bois, in the municipality of Silvânia, State of Goiás, Brazil. sp = species; gen = genus; fam = family, ord = order; cla = class; ab = abundance; pa = presence or absence.**

## **Taxonomic resolution**

The abundance (for fish) and density (for zooplankton, phytoplankton, and periphyton) data were log-transformed ( $\log X + 1$ ) to remove the effect of high abundant species [99]. The abundance matrices for the different taxonomic levels (species, genus, family, order, and class) were converted into Bray-Curtis distance matrices and correlated using the Mantel's test. Subsequently, the Bray-Curtis distance matrices for each taxonomic level were submitted individually to Non-Metric Multidimensional Scaling analysis (NMDS). The literature suggests using the number of axes with the best fits [100]; thus, we selected the first two NMDS axes generated for each taxonomic level and correlated them using the Procrustes analysis.

## **Numerical resolution**

In this step, two types of datasets were used for each biological group individually (phytoplankton, periphyton, zooplankton, and fish). They are matrices of species composition based on abundance and occurrence (presence and absence). The abundance data were log-transformed ( $\log X + 1$ ) and converted to Bray-Curtis distance matrices, while the occurrence data were converted to Jaccard distance matrices. Subsequently, these matrices were correlated among them for each biological level individually using Mantel's test. They were then used to perform the NMDS, whose first two axes generated for each matrix type were correlated using the Procrustes

analysis.

### **Cross-taxa congruence**

We used matrices of species composition based on abundance data for each biological group and its trophic subdivisions to assess the surrogate groups. To fulfill our hypotheses, the fish group was categorized into total fish (considering the abundance of all sampled individuals), herbivorous fish, and carnivorous fish. Similarly, the zooplankton group was categorized into total zooplankton (considering the abundance of all sampled individuals) and herbivorous zooplankton (considering the abundance of herbivorous individuals only). The phytoplankton and periphyton groups were not categorized into subgroups. All data were log-transformed ( $\log X + 1$ ) and converted into Bray-Curtis distance matrices per biological or trophic groups. These matrices were correlated through the Mantel's test and used to perform the NMDS, whose first two axes, generated for a given biological group or its trophic subdivision, were correlated with the axes generated for the others, contemplating all possible combinations.

### **Relationship with the environment and spatial patterns**

A partial redundancy analysis (pRDA) was used to evaluate the influence of environmental variables and spatial patterns on the abundance of species, genera, families, orders, and classes. We considered all the biological groups previously evaluated because they show responses similar to the environmental gradient or the dispersal patterns throughout the streams.

For pRDA, different environmental variables were selected according to each group analyzed (fish, phytoplankton, periphyton, and zooplankton), based on the

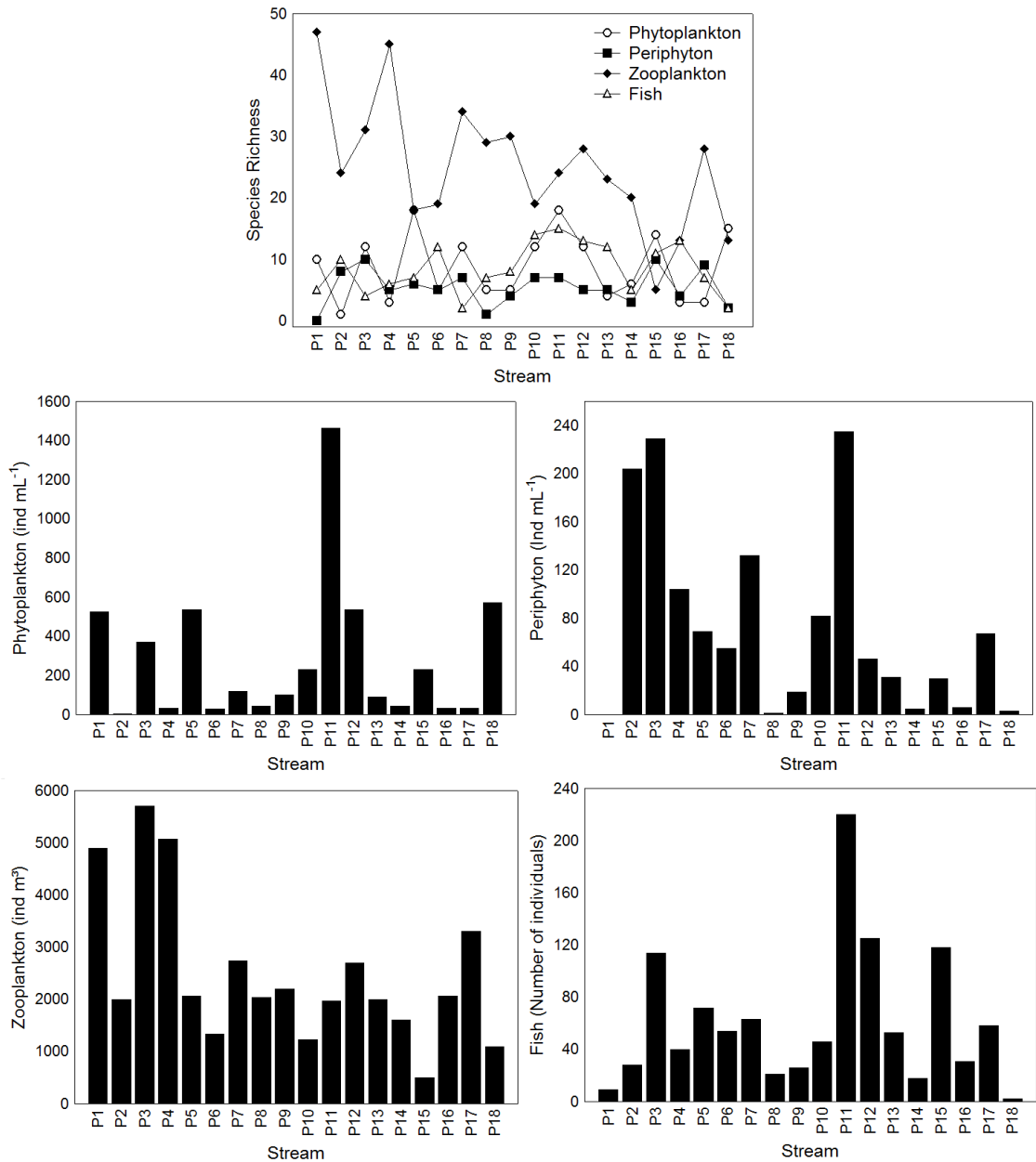
ecological relationships of groups with the environment already observed in the literature. The Variance Inflation Factors (VIF) was calculated to remove collinear variables. We consider variables with  $VIF > 0.5$  to be collinear. The VIF was calculated using the "vifcor" function from the usdm package [136]. The environmental variables (except pH) were log-transformed ( $\log X + 1$ ) to obtain a normal distribution or closer to normal for variables.

We used the forward selection function of the adespatial package [101] to select the explanatory variables. In forward selection, we utilized the different environmental variables selected previously according to VIF analysis and all PCNM filters previously generated. The selection of environmental and spatial predictors was performed individually using two stopping criteria, (1) the pre-selected significance level ( $P < 0.05$ ) and (2) the global model statistic, where the predictors explain the significance in which the variation in community composition was maintained ( $P < 0.05$ ) [102]. The forward selection was used individually for the taxonomic categories (species, genus, family, order, and class) so that the predictors varied depending on the response variable used.

A variation partitioning approach with adjusted R<sup>2</sup>-based redundancy analysis (RDA) was carried out to determine the relative importance of local environmental and spatial components [92, 93]. Subsequently, different pRDAs were performed based on the selected predictive, spatial, and environmental variables [93, 103]. The significance of each variation component was tested using the anova function, while RDA and pRDA were performed using the rda and varpart functions, respectively, of the vegan package [92]. All statistical analyses were performed in the R software [98], considering a 5% significance level ( $P$  values  $< 0.05$ ).

## Results

We identified 33 fish species, distributed into 26 genera, 18 families, and six orders, totalizing 1098 individuals. The lowest species richness and abundance was observed in point 18 and the highest in point 11 (Figure 3). The most abundant species were *Bryconamericus turiuba*, *Piabina argentea*, and *Poecilia reticulata*, corresponding to 40% of total fish abundance (Table S2). For phytoplankton, we identified 68 species, 39 genera, 28 families, 19 orders, and ten classes. The lowest species richness and total density was observed in point 2 and the highest in point 11 (Figure 2). The species with the highest density of individuals were *Monoraphidium griffithii*, *Navicula* sp., and *Chroococcus minimus* (Table S2). The periphytic community had 41 species, 29 genera, 25 families, 19 orders, and eight classes. The lowest species richness was observed in point 8 and the highest in points 3 and 15 (Figure 2). The lowest total density was observed in point 8 and the highest in point 11 (Figure 2). In total, we observed 1318 periphyton individuals, of which the most abundant species were *Sellaphora* sp., *Navicula* sp., *Pseudonabaena* sp., and *Gloeocapsopsis* sp., respectively (Table S2). For zooplankton, we identified 88 species, 33 genera, 23 families, six orders, and six classes. The lowest species richness was observed at point 15 and the highest at point 1 (Figure 2). The lowest total density was observed at point 15 and the highest at point 3 (Figure 2). The most abundant species were *Moina micrura*, *Bosminopsis deitersi*, and *Thermocyclops minutus* (Table S2).



**Fig 3. Species richness and total abundance or density observed for phytoplankton, periphyton, zooplankton, and fish in 18 streams of the sub-basins Piracanjuba, Ribeirão Vermelho, and Rio dos Bois in the municipality of Silvânia, State of Goiás, Brazil. ind = individuals.**

In general, the Mantel and Procrustes analyses (Table 1; Figure 1S-4S in supplementary material) showed concordant results. The comparison by taxonomic resolution showed that, the species level is congruent with the genus level for all groups

(phytoplankton, periphyton, zooplankton, and fish). We found values higher than 0.9 (for Mantel and Procrustes) for the fish group. This congruence indicates that species and genus levels have similarity patterns over the sampling units. This result was slightly less consistent for the phytoplankton group since only Mantel's test suggests congruence of species and genus. Besides, for all groups, the congruence values decreased with the increase in the taxonomic resolution level.

**Table 1. Mantel's and Procrustes tests using abundance (ab) and presence-absence (pa) matrices for taxonomic groups of fish, phytoplankton, periphyton, and zooplankton. Significant r values above 0.7 were highlighted.**

	Mantel		Procrustes	
	r	P	r	P
<b>Fish taxonomic resolutions (ab)</b>				
Species vs. Genus	<b>0.92</b>	<0.001	<b>0.93</b>	<0.001
Species vs. Family	<b>0.83</b>	<0.001	<b>0.88</b>	<0.001
Species vs. Order	<b>0.78</b>	<0.001	<b>0.78</b>	<0.001
Species vs. Class	0.39	0.01	0.405	0.08
<b>Phytoplankton taxonomic resolutions (ab)</b>				
Species vs. Genus	<b>0.81</b>	<0.001	0.61	<0.001
Species vs. Family	<b>0.75</b>	<0.001	0.58	0.001
Species vs. Order	<b>0.76</b>	<0.001	0.66	<0.001
Species vs. Class	0.69	<0.001	0.54	0.01
<b>Periphyton taxonomic resolutions (ab)</b>				
Species vs. Genus	<b>0.88</b>	<0.001	<b>0.782</b>	<0.001
Species vs. Family	<b>0.88</b>	<0.001	<b>0.787</b>	<0.001

Species vs. Order	<b>0.87</b>	<0.001	<b>0.83</b>	<0.001
Species vs. Class	0.61	<0.001	0.53	0.01
<b>Zooplankton taxonomic resolutions (ab)</b>				
Species vs. Genus	<b>0.76</b>	<0.001	<b>0.705</b>	<0.001
Species vs. Family	<b>0.72</b>	<0.001	0.63	<0.001
Species vs. Order	0.54	<0.001	0.56	0.001
Species vs. Class	0.51	<0.001	0.52	0.005
<b>Numerical resolutions</b>				
Fish species (ab) vs. Fish species (pa)	<b>0.89</b>	<0.001	<b>0.87</b>	<0.001
Phytoplankton species (ab) vs. Phytoplankton species (pa)	<b>0.97</b>	<0.001	<b>0.97</b>	<0.001
Periphyton species (ab) vs. Periphyton species (pa)	<b>0.89</b>	<0.001	<b>0.94</b>	<0.001
Zooplankton species (ab) vs. Zooplankton species (pa)	<b>0.98</b>	<0.001	<b>0.94</b>	<0.001
<b>Biological substitute group - Total</b>				
Fish (ab) vs. Phytoplankton (ab)	0.04	0.34	0.21	0.76
Fish (ab) vs. Periphyton (ab)	0.22	0.05	0.39	0.16
Fish (ab) vs. Zooplankton (ab)	-0.006	0.49	0.32	0.36
Phytoplankton (ab) vs. Zooplankton (ab)	-0.02	0.53	0.25	0.64
Phytoplankton (ab) vs. Periphyton (ab)	0.13	0.14	0.45	0.07
Periphyton (ab) vs. Zooplankton (ab)	-0.13	0.83	0.25	0.62
<b>Biological surrogate group - Trophic</b>				
Herbivorous fish (ab) vs. Phytoplankton (ab)	-0.02	0.52	0.23	0.69
Herbivorous fish (ab) vs. Periphyton (ab)	0.22	0.07	0.31	0.38
Carnivorous fish (ab) vs. Zooplankton (ab)	-0.01	0.52	0.209	0.75

Phytoplankton (ab) vs. Herbivorous zooplankton (ab)	-0.05	0.69	0.35	0.27
Phytoplankton (ab) vs. Periphyton (ab)	0.13	0.14	0.45	0.07
Periphyton (ab) vs. Herbivorous zooplankton (ab)	0.08	0.21	0.36	0.22

In the numerical resolution (Table 1), all biological groups showed a correlation above 0.8, indicating that the patterns of sampling units using abundance data were similar to the ordination of sampling units using presence-absence data. Thus, it is possible to use presence-absence data as a surrogate of species abundance for all groups studied. However, we found no significant correlations between biological and trophic groups (Table 1).

Fish and zooplankton were significantly correlated with the environmental variables, but not with spatial patterns (Table 2). For fish, conductivity and ORP were significant for species level and width was significant for genus level; while for zooplankton, pH and dissolved oxygen were the most important variable for most taxonomic resolutions. For phytoplankton, none of the environmental variables were significant for species, genus, family, order, and class (Table 2), but spatial patterns explained 3% and 17% of the composition identified at the genus and order level, respectively. For periphyton, spatial patterns significantly explained all levels of taxonomic identification (except species). In this group, fine scale (6, and 10) and large-scale (1 and 3) spatial patterns were significant. Considering the taxonomic resolution, the class category had the highest predictability, with 55% of its variability explained by the spatial variables.

**Table 2. Relationship analysis between fish, phytoplankton, periphyton, and zooplankton with environmental and spatial variables for the region of Silvânia, Goiás, Brazil, in 2017. The code “-“ indicate that no variable was selected in the global model by the forward selection function (see details in Methods), and it was not possible to proceed with the analysis. Significant values (\*P<0.05) indicate what environmental (ENV.) or spatial variables (S.V.) were associated with the variation in each species group. N indicates the number of different organisms in a given level of taxonomic identification. No analyses were performed for the class category since all fish sampled belong to the class Actinopterygii.**

<b>Group</b>	<b>N. Category</b>	<b>Environment</b>	<b>Spatial filters</b>	<b>R<sup>2</sup> adjusted [Environment]</b>	<b>R<sup>2</sup> adjusted [Spatial]</b>	<b>P [Env.]</b>	<b>P [S.V.]</b>
<b>Fish species</b>	33	Conductivity, ORP	-	0.08	-	0.01*	-
<b>Fish genus</b>	26	Width	-	0.05	-	0.01*	-
<b>Fish family</b>	18	-	-	-	-	-	-
<b>Fish order</b>	6	-	-	-	-	-	-
<b>Phytoplankton species</b>	68	-	-	-	-	-	-

<b>Phytoplankton genus</b>	40	-	1	-	0.03	-	0.05
<b>Phytoplankton family</b>	28	-	-	-	-	-	-
<b>Phytoplankton order</b>	19	-	1,2,3	-	0.17	-	0.002*
<b>Phytoplankton class</b>	10	-	-	-	-	-	-
<b>Periphyton species</b>	42	STD	1,3	-0.01	0.03	0.61	0.17
<b>Periphyton genus</b>	29	-	1,6	-	0.16	-	0.001*
<b>Periphyton family</b>	25	-	1,6	-	0.16	-	0.003*
<b>Periphyton</b>	19	-	1.6	-	0.22	-	0.001*

<b>order</b>							
<b>Periphyton class</b>	8	-	1,3,6,10	-	0.55	-	0.002*
<b>Zooplankton species</b>	88	-	-	-	-	-	-
<b>Zooplankton genus</b>	33	pH, DO	-	0.13	-	0.003*	-
<b>Zooplankton family</b>	23	pH, DO	-	0.16	-	0.001*	-
<b>Zooplankton order</b>	6	pH	-	0.17	-	0.002*	-
<b>Zooplankton class</b>	6	pH	-	0.17	-	0.006*	-

## **Discussion**

In this study, we found a high congruence among the taxonomic levels of all the biological groups evaluated, as well as between the species occurrence and abundance data. These results indicate that all biological groups showed a strong congruence between species identification and higher taxonomic levels and between presence-absence and abundance data, corroborating predictions i and ii. However, we did not find cross-taxa congruence between biological or trophic groups, contradicting the prediction iii. Therefore, replacing one group with another would result in loss of significant information since the groups showed complementary responses, capturing different aspects of the environmental variation of streams. In this sense, the simplification in the taxonomic levels or numerical resolution may result in cutting expenses of multiple collection campaigns, specialized taxonomists, and labor-intensive and time-consuming processes, without interfering with the quality of the process [105, 106, 26, 107]. Thus, future studies can estimate how much can be saved by applying simplification protocols in this region [e.g. 135].

## **Taxonomic Resolution**

Taxonomic resolution analysis with Mantel's test showed a high correlation ( $r > 0.7$ ) for all groups (fish, phytoplankton, periphyton, and zooplankton), indicating that species-level classification can be replaced by genus and even family, without significant loss of biological information. Thus, higher taxonomic levels (genus, family, and order) also represent the diversity of local species and may act as surrogates for environmental assessments [34]. These results corroborate several studies proposed for different aquatic groups, such as phytoplankton [13, 25, 27, 26], periphyton [16], macroinvertebrates [108], and fish [16, 109, 110, 26], indicating that the taxonomic resolution can be applied even for assessment of environmental impact [111].

Fish and periphyton groups had the highest correlation values (Mantel's  $r > 0.9$ ) for the genus level. For the periphyton, this high correlation remained for family (Mantel's  $r > 0.9$ ) and order (Mantel's  $r > 0.8$ ) levels. These results corroborate studies involving periphyton and fish [24, 20]. They show a high level of community concordance in small geographical areas, representing a community structure [24], a fact corroborated in this study for fish and periphyton. That also indicates that groups with more ability to choose or stay in habitats (e.g. fish and periphyton) showed higher correlation values than those carried more easily by the water flow (e.g. phytoplankton and zooplankton). These results can be explained by the fact that most fish species captured were specialists with efficient dispersal abilities; or because the periphyton species remain attached to a substrate, controlling its dispersion and spatial variation.

In general, the use of coarser taxonomic resolutions for stream environments is also a reliable and robust option for rapid bioassessment studies that require fewer resources [112]. They are used principally for groups with multiple families and genera (e.g., periphyton) and robust taxonomic congruence data [16]. Moreover, taxonomic identification at the species level requires specialists for different groups, which is not always available and can take a long time [50], especially in regions with high diversity [16, 113]. For this reason, the use of coarser taxonomic resolutions is a viable possibility for rapid bioassessment. However, it is necessary to emphasize that this surrogacy must be done with caution, because many species may still be unknown, mainly in regions of high biodiversity [16], if possible, the biomonitoring should be done with multiple taxonomic groups, and this approach is not efficient to propose, select, and monitor areas for conservation purposes [114]. In these regions, other factors must be taken into account, such as functional similarity [114, 115].

## **Numerical Resolution**

The numerical resolution aims to use presence-absence data as a surrogate for species abundance, which can speed up the assessment of communities, and consequently, the biomonitoring. Our results showed the possibility of surrogacy for all groups (fish, phytoplankton, periphyton, and zooplankton), with a high correlation ( $r > 0.8$ ).

Moreover, the use of presence-absence data can simplify and reduce time and effort in the biomonitoring of aquatic ecosystems since all groups mentioned in this study have been used as bioindicators of these ecosystems [116]. Presence-absence data remove abundance differences, and as a consequence, reduce the effect of dominant species regarding the ordination [38,117]. Furthermore, rare species can be as significant as common species in studies of species-environment relationships [118, 119]. Abundance data, on the other hand, demand more time for individuals counting. However, when necessary, these data allow a more distinct assessment of the most subtle ecological patterns in the community structure [120, 38] and niche selection [121], which is not easily observed with presence-absence data.

## **Surrogate Groups**

The concordance between biological groups and trophic divisions was not significant for any studied biological groups. Therefore, the ordination patterns recorded for one group did not correspond to other groups, even those with similar environmental requirements (e.g., phytoplankton and periphyton) or related in the food chain (e.g., periphyton and herbivorous fish). Thus, no biological or trophic group can be used as a surrogate for another in the region evaluated. This pattern corroborates other studies [45, 26] and highlights the particular importance of each biological group in environmental monitoring and biodiversity assessments [61, 122] since different groups respond to different scales of spatial and temporal impacts. For example, some groups may respond to limnological variables and others to hydrological variables, such as the presence or absence of riparian forest, while

others are responding to changes over time [123, 124, 38].

The lack of cross-taxa congruence may occur due to different responses of the groups to the distinct spatial scale variations in their core area [125, 126], as well as the life history of species [127, 128]. Despite the small number of streams studied, we covered a large part of the conservation unit area, contemplating a reasonable environmental variation in the region. Furthermore, the biodiversity sampled in the region is in accordance with the biodiversity found in other studies developed in the Brazilian Cerrado streams [e.g. 26, 104]. Thus, the small spatial scale and the significant anthropogenic influence on the study area may be interfering with the congruence among different groups.

Therefore, in this region, the use of cross-taxa may not be the most suitable for stream biomonitoring and small-scale assessments. Heino [24] also shows that the fish community assessment may depend on multiple environmental variables, according to their different environmental requirements. Besides, Barbosa *et al.* [26] indicate that for monitoring purposes, different groups must be evaluated in different ways, covering different strata of local trophic levels since these do not demonstrate a possibility of surrogacy among distinct communities. In fact, while assessing the fish's responses to environmental conditions, they were more associated with structural variables in streams, such as width and flow. The phytoplankton and periphyton was not directly associated with any of the evaluated environmental variables, while zooplankton was associated with physicochemical variables, such as dissolved oxygen and pH. These results indicate the need for complementarity of groups on aquatic biodiversity biomonitoring, mainly between fish and phytoplankton, fish and periphyton, and fish and zooplankton, since they respond to different environmental characteristics.

The trophic groups did not corroborate the expected responses. In this case, the ecological functions may be more strongly connected with changes in habitats and

environmental interference on the ichthyic stream assemblage [5, 129]. Thus, by grouping the fishes into broad categories, we may have lost the diet variation in quantitative terms that may be more connected to the impact on phytoplankton and zooplankton groups. These environments are small and strongly impacted by the maintenance or not of riparian areas, which can directly reflect the community's dietary conditions, yet not considered in this study. Other parameters, such as biomass of bacteria and fungi in the periphery (important for zooplanktons) and entry of allochthonous material (important for fishes), could also influence the responses.

### **Relationship with the environment and spatial patterns**

The importance of environmental gradients to predict responses for the species level are recurrent in many studies [e.g. zooplankton; 130]. This taxonomic level shows specific criteria for survival, which may be linked to the heterogeneity of aquatic ecosystems and environmental variables, which directly influence species composition [131, 52]. However, we emphasize that our results demonstrate correlation with environmental variables for species and genus of fish; genus, family, order and class of zooplankton; higher importance of spatial patterns for the most taxonomic resolutions of periphyton, and absence of environmental and spatial explanation for most taxonomic levels of phytoplankton.

Furthermore, the dynamics and structure of communities are not defined only by environmental variables. Instead, other factors such as spatial pattern [132], climate [133], biological interactions, and dispersal limitation [134] may play important roles in communities. However, our results showed significant relationships among the taxonomic levels and that these respond similarly to the environmental variables or spatial patterns. That allows us to use surrogate taxonomic categories within the same group, for example, by replacing species level with a higher taxonomic category, which would facilitate

biomonitoring. However, surrogacy among groups is not possible because they are not correlated, probably because they are influenced by different environmental variables and spatial patterns.

## **Conclusion**

Given the ecological importance of stream communities, biomonitoring is fundamental to understand the anthropogenic effect and plan efficient management for ecosystem conservation and restoration. Our results showed high congruence, especially for taxonomic and numerical resolutions. Thus, in general, the four groups evaluated (phytoplankton, periphyton, zooplankton, and fish) have a high biomonitoring potential on local scales. Moreover, the biological groups showed complementary responses to environmental gradients. Therefore, our results support the multi-taxa approach, using less detailed taxonomic and numerical resolutions in biomonitoring programs. The possibility of simplification in the sampling protocols found in our study can reduce costs for monitoring in this region. In this sense, future studies can focus on estimating how much this simplification can bring to biomonitoring.

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**Shortcuts for biomonitoring programs of stream ecosystems: evaluating the taxonomic, numeric, and cross-taxa congruence in phytoplankton, periphyton, zooplankton, and fish assemblages**

**Short title: Shortcuts for biomonitoring programs of stream ecosystems**

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**SUPPORTING INFORMATION 1**

S1 Table. Mean and standard deviation for the environmental variables measured in the 18 streams of sub-basins Piracanjuba, Ribeirão Vermelho, and Rio dos Bois in the municipality of Silvânia, State of Goiás, Brazil. DO = Dissolved Oxygen, Chl-a = Chlorophyll-a, BOD = biochemical oxygen demand, ORP = oxidation-reduction potential, TDS = total dissolved solids, T. Solids = Total Solids, T. Nitrogen = Total Nitrogen, A. Nitrogen = Ammoniacal Nitrogen, T. Phosphorus = Total Phosphorus, T. Org. Carbon = Total Organic Carbon, US = Unstable Substrate, SS = Stable Substrate, Width (m), and Riparian FW = Riparian Forest Width.

	<i>Mean</i>	<i>Stand. Dev.</i>	<i>P1</i>	<i>P2</i>	<i>P3</i>	<i>P4</i>	<i>P5</i>	<i>P6</i>	<i>P7</i>	<i>P8</i>	<i>P9</i>	<i>P10</i>	<i>P11</i>	<i>P12</i>	<i>P13</i>	<i>P14</i>	<i>P15</i>	<i>P16</i>	<i>P17</i>	<i>P18</i>
<i>Temperature (°C)</i>	18.63	1.68	17.7	19.92	17.63	20.59	19.12	19.38	19.35	19.76	16.55	19.19	16.45	17.4	18.5	16.86	21.75	21.12	18.33	15.8
<i>Transparency (%)</i>	0.80	0.31	1	1	1	1	0.1	1	1	1	1	1	1	0.95	1	1	0.5	0	1	1
<i>pH</i>	6.59	0.44	6.05	5.62	6	6.47	6.84	6.56	7.25	7.43	6.84	6.93	6.4	6.68	6.63	6.43	7.03	6.7	6.54	6.47
<i>Oxygen*</i>	7.60	0.79	7.94	7.6	5.94	6.88	7.33	8.08	5.48	7.86	8.57	7.79	7.51	8	7.76	8.41	7.87	7.73	8.26	7.8
<i>Conductivity#</i>	41.18	23.20	16.4	8.01	15.8	9.5	82	26.6	64.03	24	28.7	40.1	75.07	76.5	46.7	43.94	43.7	39.4	39.6	62.27
<i>DO*</i>	7.56	0.79	7.9	7.6	5.9	6.9	7.3	8.0	5.4	7.8	8.5	7.7	7.5	8.0	7.7	8.4	7.8	7.7	8.2	7.8
<i>Turbidity (NTU)</i>	69.80	165.78	5.47	4.63	10.58	4.8	118.9	15.49	10.1	6.15	4.95	14.56	6.09	5.75	4.62	4.78	16.52	604.1	3.01	4.18
<i>Chl-a*</i>	1.35	1.58	2.81	0.17	1.25	0.17	2.54	0.34	1.25	0.3	0.38	0.37	6.56	2.11	0.49	0.237	0.507	2.65	1.29	0.95
<i>BOD*</i>	1.74	1.68	0.4	4.50	4.20	2.10	0.90	1.70	4.60	5.00	0.34	0.90	0.10	0.30	0.90	0.10	1.30	2.40	1.00	0.60
<i>ORP (mV)</i>	268.93	73.20	358.8	256.03	330	185.6	304.8	216.2	108.05	194.4	311.1	215.4	339.5	325.3	325	186.2	226.7	294	289.8	374
<i>TDS*</i>	20.59	11.64	7.72	4.00	7.90	4.75	41.00	13.30	32.01	11.00	14.30	21.20	37.50	38.25	23.35	21.97	21.85	19.70	19.80	31.13
<i>T. Solids*</i>	55.44	54.39	15.00	10.00	32.00	16.00	89.00	31.00	48.00	117.00	33.00	34.00	52.00	47.00	35.00	42.00	51.00	248.00	42.00	56.00
<i>Nitrate*</i>	0.66	0.742	0.30	0.30	0.30	0.30	1.20	0.30	0.80	0.30	0.30	0.40	1.20	0.50	0.40	0.70	0.40	3.40	0.30	0.60
<i>T. Nitrogen*</i>	0.89	1.12	0.342	0.344	0.346	0.353	1.761	0.114	1.555	0.225	0.344	0.525	1.564	0.594	0.563	0.893	0.544	4.968	0.375	0.744
<i>A. Nitrogen*</i>	0.24	0.37	0.04	0.04	0.24	0.05	0.54	0.03	0.75	0.03	0.04	0.12	0.36	0.08	0.16	0.09	0.11	1.55	0.07	0.14
<i>T. Phosphorus*</i>	0.020	0.03	0.003	0.003	0.011	0.003	0.020	0.003	0.126	0.003	0.003	0.003	0.116	0.051	0.003	0.003	0.003	0.016	0.003	0.003
<i>T. Org. Carbon*</i>	6.19	2.72	7.3	3.9	7.0	4.5	4.8	4.6	6.8	7.4	3.6	3.9	14.7	4.9	6.2	5.9	4.2	10.5	5.0	6.30
<i>Iron*</i>	0.78	0.53	0.66	0.50	0.86	0.69	2.43	1.00	1.64	0.47	0.52	0.70	0.51	0.47	0.62	1.00	0.66	1.06	0.13	0.27
<i>US (%)</i>	0.91	0.10	97	100	93	93	86	92	91	99	69	98	100	80	68	100	97	100	98	77
<i>SS (%)</i>	9	0.10	3	0	7	7	14	8	9	1	32	2	0	20	32	0	3	0	2	23
<i>Width (m)</i>	3.7	1.96	4.08	9.94	4.70	1.86	1.51	4.40	1.54	2.63	3.03	2.21	3.81	4.02	2.98	2.88	3.21	5.31	3.17	5.69
<i>Depth(m)</i>	0.33	0.079	40.29	49.51	20.29	15.73	17.30	23.93	13.42	26.56	28.67	40.24	32.16	31.49	31.51	27.27	27.20	46.18	22.11	45.00
<i>Flow (rps)</i>	216.53	126.12	184.11	307.22	307.89	20.00	258.89	333.67	162.92	248.67	338.11	322.33	340.78	252.00	408.89	64.22	217.67	27.44	79.67	23.11
<i>Riparian FW(m)</i>	33.22	19.56	30	0	15	30	30	20	10	30	30	10	15	10	15	15	10	10	12	10

\* = mg L-1; # = µg L-1

S2 Table – Abundance (fish) and density (phytoplankton, periphyton and zooplankton) of species measured in the 18 streams of Piracanjuba, Ribeirão Vermelho, and River dos Bois, in the municipality of Silvânia, State of Goiás, Brazil.

	Total	P1	P2	P3	P4	P5	P6	P7	P8	P9	P10	P11	P12	P13	P14	P15	P16	P17	P18
<b>Fish</b>																			
<i>Aspidoras fuscoguttatus</i>	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
<i>Astyanax bockmanni</i>	3	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	1	0
<i>Astyanax fasciatus</i>	78	0	0	21	25	1	0	0	1	0	6	5	12	0	2	4	1	0	0
<i>Astyanax lacustris</i>	76	0	0	0	0	17	2	0	0	2	7	18	20	0	4	0	4	2	0
<i>Bryconamericus stramineus</i>	31	0	0	0	0	0	0	0	0	1	2	0	0	6	0	21	1	0	0
<i>Bryconamericus turiuba</i>	199	2	10	83	0	26	13	0	1	3	5	2	34	2	0	6	3	9	0
<i>Cetopsis gobioides</i>	2	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
<i>Cetopsorhamdia iheringi</i>	14	0	4	0	0	0	6	0	0	0	1	0	0	2	0	1	0	0	0
<i>Characidium gomesi</i>	66	0	0	0	0	0	7	0	2	6	4	17	6	13	0	9	1	0	1
<i>Characidium zebra</i>	27	0	0	0	0	0	0	0	0	0	2	9	14	0	0	0	2	0	0
<i>Cichlasoma paranaense</i>	3	0	2	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
<i>Eigenmannia virescens</i>	1	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0
<i>Gymnotus carapo</i>	39	3	1	0	6	4	1	1	2	5	3	4	3	0	2	0	1	2	1
<i>Hasemania hanseni</i>	11	0	0	0	0	0	0	0	0	3	0	8	0	0	0	0	0	0	0
<i>Hisonotus insperatus</i>	3	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0
<i>Hisonotus sp.</i>	4	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Hoplias malabaricus</i>	2	0	0	0	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0
<i>Hypostomus ancistroides</i>	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
<i>Hypostomus sp.</i>	24	1	2	0	0	0	2	0	0	0	2	8	3	3	0	0	3	0	0
<i>Imparfinis schubarti</i>	99	0	0	0	0	0	1	0	0	0	1	66	6	17	0	7	1	0	0
<i>Leporinus sp.</i>	4	1	1	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0
<i>Leporinus sp.1</i>	3	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0
<i>Parodon nasus</i>	3	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0
<i>Phenacorhamdia tenebrosa</i>	24	2	2	0	0	0	2	0	0	1	2	5	0	1	0	9	0	0	0
<i>Piabina argentea</i>	132	0	2	9	2	0	16	0	10	0	7	0	1	3	9	52	0	21	0
<i>Pimelodella gracilis</i>	104	0	0	0	0	0	0	0	0	0	0	71	23	1	1	5	3	0	0
<i>Pimelodus sp.</i>	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
<i>Poecilia reticulata</i>	110	0	0	0	5	21	0	62	0	0	0	0	0	0	0	0	0	22	0
<i>Prochilodus lineatus</i>	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
<i>Pseudopimelodus pulcher</i>	13	0	0	0	0	0	0	0	0	0	0	0	0	3	0	3	7	0	0
<i>Rhamdia quelen</i>	15	0	0	1	1	2	0	0	3	5	0	1	1	1	0	0	0	0	0
<i>Steindachnerina insculpta</i>	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Synbranchus marmoratus</i>	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

<i>Aspidoras fuscoguttatus</i>	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
Zooplankton	Total Density	P1	P2	P3	P4	P5	P6	P7	P8	P9	P10	P11	P12	P13	P14	P15	P16	P17	P18
<i>Alona affinis</i>	5	0	0	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Alona guttata</i>	2	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Alona ossiani</i>	26	4	0	19	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0
<i>Alona verrucosa</i>	3	0	0	0	2	1	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Alona yara</i>	11	3	3	2	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
<i>Alonella dadayi</i>	3	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0
<i>Arcella conica</i>	21	4	0	1	5	0	2	1	3	2	1	2	0	0	0	0	0	0	0
<i>Arcella costata</i>	5	1	0	0	0	0	0	0	0	2	2	0	0	0	0	0	0	0	0
<i>Arcella crenulata</i>	5	0	0	0	0	0	0	1	0	0	2	0	0	0	0	0	0	2	0
<i>Arcella dentata</i>	8	2	0	0	2	0	0	2	2	0	0	0	0	0	0	0	0	0	0
<i>Arcella discoides</i>	39	7	4	0	0	2	0	0	2	4	3	0	2	0	2	6	4	0	3
<i>Arcella gibbosa</i>	19	4	0	1	4	0	0	0	2	4	2	0	0	0	2	0	0	0	0
<i>Arcella gibbosa mitriformis</i>	5	0	0	0	0	0	1	1	0	1	0	2	0	0	0	0	0	0	0
<i>Arcella hemisphaerica</i>	8	4	0	0	0	0	0	1	1	2	0	0	0	0	0	0	0	0	0
<i>Arcella hemisphaerica undulata</i>	7	0	0	0	1	0	0	0	0	0	0	0	3	2	0	0	0	1	0
<i>Arcella megastoma</i>	2	1	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
<i>Arcella mitrata</i>	8	1	0	0	0	0	0	2	0	2	0	0	0	2	1	0	0	0	0
<i>Arcella vulgaris</i>	50	5	3	4	4	3	0	4	6	2	3	4	0	0	0	5	4	0	3
<i>Arcella vulgaris undulata</i>	7	0	0	0	2	0	0	0	0	1	0	0	0	1	0	0	0	3	0
<i>Bosmina hagmanni</i>	53	2	1	3	9	8	2	2	1	3	0	3	0	0	0	9	10	0	0
<i>Bosminopsis deitersi</i>	67	0	0	0	12	14	6	4	2	3	0	4	0	0	0	10	12	0	0
<i>Brachionus falcatus</i>	19	2	2	2	8	0	0	5	0	0	0	0	0	0	0	0	0	0	0
<i>Brachionus sp.</i>	18	2	3	6	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Centropyxis aculeata</i>	24	0	3	2	6	0	1	3	2	0	2	2	2	0	0	0	1	0	0
<i>Centropyxis aculeata var.</i>	5	1	0	0	0	1	0	0	0	2	0	0	0	0	1	0	0	0	0
<i>Centropyxis aerophila</i>	5	2	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0
<i>Centropyxis cassis</i>	9	0	0	0	1	0	1	2	1	3	1	0	0	0	0	0	0	0	0
<i>Centropyxis constricta</i>	19	1	0	0	5	0	0	0	3	0	1	3	1	5	0	0	0	0	0
<i>Centropyxis discoides</i>	21	4	2	2	0	0	0	0	3	3	3	3	0	0	0	0	0	1	0
<i>Centropyxis ecornis</i>	27	3	0	3	3	0	1	3	4	0	2	2	6	0	0	0	0	0	0
<i>Centropyxis gibba</i>	34	6	0	3	2	0	0	0	4	2	2	2	0	5	1	0	2	5	0
<i>Centropyxis minuta</i>	4	0	0	0	1	2	0	0	1	0	0	0	0	0	0	0	0	0	0
<i>Centropyxis platystoma</i>	8	2	0	0	0	0	0	2	1	1	0	0	1	0	0	0	0	0	1
<i>Cephalodella sp.</i>	9	0	0	2	0	0	2	2	0	0	0	0	0	0	3	0	0	0	0
<i>Ceriodaphnia cornuta</i>	20	0	0	2	0	1	3	0	0	4	0	0	5	0	3	0	0	2	0
<i>Chydorus eurynotus</i>	9	2	4	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Chydorus pubescens</i>	7	0	4	0	0	1	0	0	0	0	0	0	0	2	0	0	0	0	0

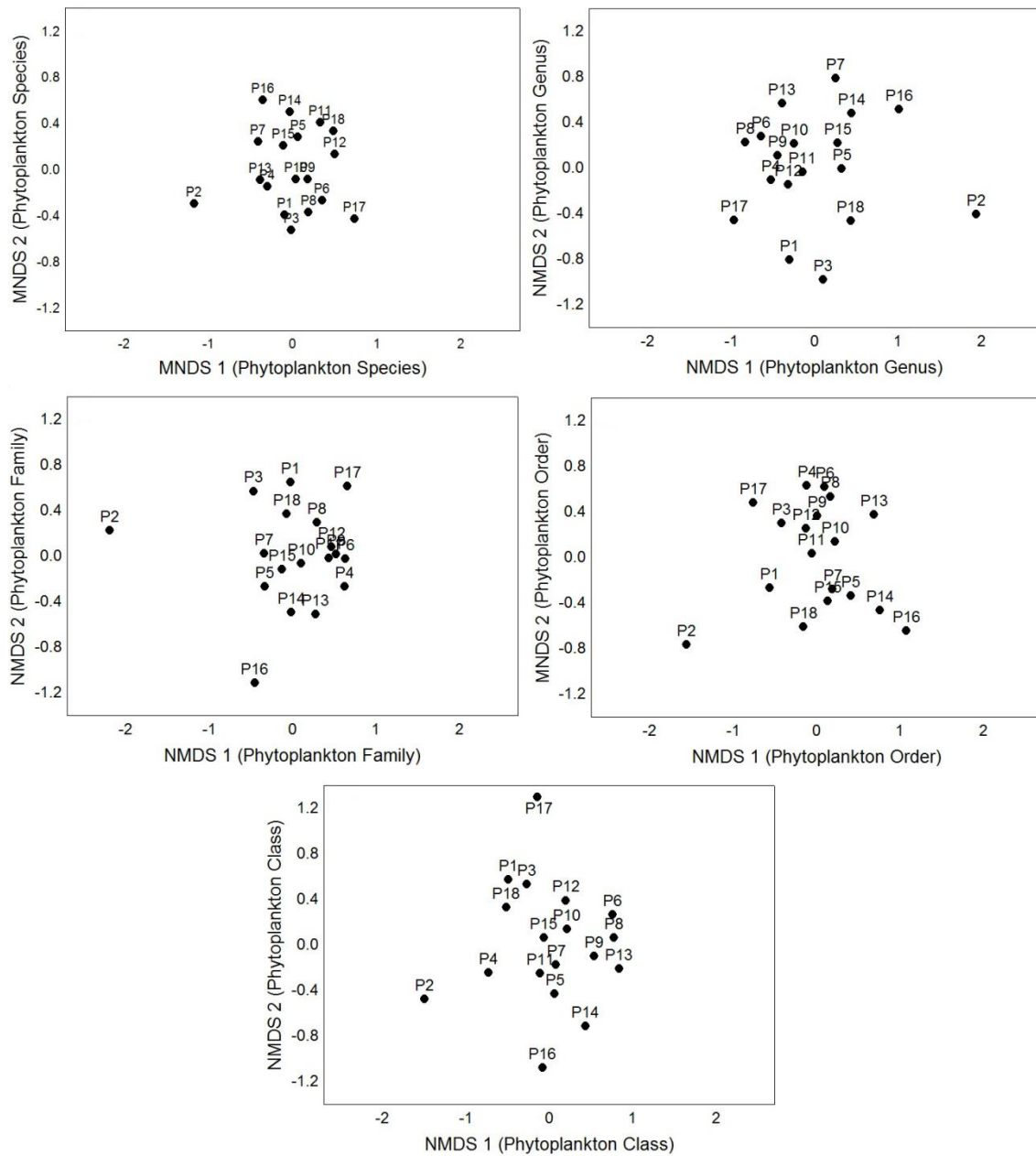
<i>Coronatella poppei</i>	9	4	0	2	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Cyclopyxis eurystoma</i>	7	0	0	0	1	0	0	2	1	0	3	0	0	0	0	0	0	0	0
<i>Cyclopyxis kahli</i>	12	0	0	0	1	0	0	0	0	0	0	0	4	6	0	0	0	1	0
<i>Diaphanosoma spinulosum</i>	3	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Diffugia achlora</i>	11	1	0	0	0	0	0	1	0	2	0	0	0	7	0	0	0	0	0
<i>Diffugia corona</i>	8	0	0	0	0	0	0	0	0	2	0	0	3	0	0	1	0	2	0
<i>Diffugia cylindrus</i>	8	0	0	0	0	1	0	1	1	2	0	0	0	0	0	0	0	3	0
<i>Diffugia elegans</i>	14	6	0	0	3	0	0	0	0	0	3	0	1	0	1	0	0	0	0
<i>Diffugia gramen</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Diffugia lobostoma</i>	13	4	0	0	2	0	0	0	2	1	0	2	0	2	0	0	0	0	0
<i>Diffugia oblonga</i>	21	0	2	0	0	0	1	2	0	0	0	4	5	0	0	0	2	5	0
<i>Euglypha acanthophora</i>	22	0	0	0	0	1	0	1	3	0	1	4	0	4	3	0	0	4	1
<i>Euglypha denticulata</i>	7	2	0	0	0	0	0	0	0	1	0	4	0	0	0	0	0	0	0
<i>Euglypha filifera</i>	4	0	0	0	1	0	0	1	0	0	0	0	2	0	0	0	0	0	0
<i>Euglypha laevis</i>	12	2	0	0	0	0	0	3	1	3	2	0	0	0	0	0	0	1	0
<i>Euglypha rotunda</i>	11	0	0	0	2	0	0	0	0	0	0	2	1	3	0	2	0	1	0
<i>Euglypha sp.</i>	6	2	0	0	0	2	0	0	1	0	0	0	0	0	0	0	0	1	0
<i>Euglypha tuberculata</i>	16	0	0	0	3	0	0	2	0	0	1	0	4	3	3	0	0	0	0
<i>Euryalona . brasiliensis</i>	5	0	3	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Heleopera petricola</i>	21	5	0	2	2	4	0	0	1	2	0	0	0	1	0	1	0	3	0
<i>Keratella americana</i>	24	4	3	6	0	0	0	5	0	0	0	0	4	2	0	0	0	0	0
<i>Keratella cochlearis</i>	11	0	0	5	6	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Keratella cochlearis var.</i>	14	3	0	0	5	0	0	6	0	0	0	0	0	0	0	0	0	0	0
<i>Keratella lenzi</i>	15	0	2	5	0	0	0	6	0	0	0	0	0	2	0	0	0	0	0
<i>Lecane bulla</i>	22	0	2	0	4	0	4	0	0	0	0	2	0	1	4	0	0	0	5
<i>Lecane curvicornis</i>	8	4	0	2	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
<i>Lecane papuana</i>	14	4	0	0	2	0	0	1	0	0	0	0	2	0	0	0	0	2	3
<i>Lecane quadridentata</i>	7	0	2	2	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0
<i>Lecane signifera</i>	13	0	2	0	0	0	4	0	0	0	0	3	0	0	0	0	0	0	4
<i>Lepadella sp.</i>	20	3	0	0	3	0	2	0	0	0	0	3	3	2	0	0	0	0	4
<i>Lesquereusia modesta</i>	15	2	0	0	0	3	0	0	0	0	2	1	3	0	2	0	0	2	0
<i>Lesquereusia spiralis</i>	11	4	0	0	2	0	2	0	0	3	0	0	0	0	0	0	0	0	0
<i>Limnocalanus sp.</i>	28	0	2	2	6	0	0	0	2	1	0	1	0	0	2	0	4	6	2
<i>Macrothrix sp.</i>	7	3	2	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0
<i>Moina micrura</i>	77	2	0	73	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Moina minuta</i>	6	3	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Nebela sp.</i>	4	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0	0	0	0
<i>Netzelia oviformis</i>	9	0	0	0	0	0	0	3	2	0	0	0	1	0	0	0	0	3	0
<i>Netzelia tuberculata</i>	12	7	0	0	0	0	0	0	0	0	0	1	0	3	1	0	0	0	0

<i>Netzelia wailesi</i>	9	0	0	0	2	0	0	0	0	0	1	0	6	0	0	0	0	0	0
<i>Nicsmirnovius paggii</i>	5	0	0	3	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0
<i>Notodiptomus sp. 1</i>	23	0	0	0	3	3	1	2	1	0	0	0	2	0	4	0	3	4	0
<i>Notodiptomus sp. 2</i>	20	0	2	2	0	2	0	1	0	1	0	1	0	0	0	0	7	4	0
<i>Protocucurbitella coroniformes</i>	6	3	0	0	1	0	0	0	0	1	0	0	1	0	0	0	0	0	0
<i>Quadrullella symmetrica</i>	14	0	0	0	4	0	0	0	3	0	0	0	0	2	0	0	3	2	0
<i>Thermocyclops minutus</i>	52	2	0	3	7	7	2	0	0	4	0	0	3	0	5	0	8	9	2
<i>Thermocyclops sp.</i>	35	1	0	0	3	6	1	3	4	0	0	0	2	1	2	0	5	7	0
<i>Trichocerca bicristata</i>	11	4	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3
<i>Trichocerca similis</i>	7	0	3	0	2	0	2	0	0	0	0	0	0	0	0	0	0	0	0
<i>Trichocerca sp.</i>	16	2	0	2	0	0	0	0	0	0	0	2	6	1	2	0	0	0	1
<i>Trinema enchelys</i>	18	7	0	0	0	0	0	2	1	2	0	2	0	0	3	0	0	0	1
<b>Periphyton</b>	<b>Total Density</b>	<b>P1</b>	<b>P2</b>	<b>P3</b>	<b>P4</b>	<b>P5</b>	<b>P6</b>	<b>P7</b>	<b>P8</b>	<b>P9</b>	<b>P10</b>	<b>P11</b>	<b>P12</b>	<b>P13</b>	<b>P14</b>	<b>P15</b>	<b>P16</b>	<b>P17</b>	<b>P18</b>
<i>Amphipleura sp.1</i>	16	0	0	0	0	0	0	0	0	0	0	16	0	0	0	0	0	0	0
<i>Aulacoseira sp.1</i>	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Aulacoseira sp.2</i>	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
<i>Chridella crystiformis</i>	30	0	0	20	0	1	9	0	0	0	0	0	0	0	0	0	0	0	0
<i>Closterium leibleinii</i>	2	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Coelastrum reticulatum</i>	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0
<i>Cosmarium sp.1</i>	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Cosmarium sp.2</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Cosmarium sp.3</i>	2	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	0	0
<i>Cyclotella sp.1</i>	101	0	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Desconhecido sp.1</i>	106	0	0	13	0	0	30	0	0	0	62	0	0	0	1	0	0	0	0
<i>Eremosphaera sp.1</i>	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Eunotia sp.1</i>	76	0	4	0	0	0	0	1	0	14	0	38	7	0	0	0	0	10	2
<i>Eunotia sp.3</i>	96	0	0	0	0	1	1	20	0	0	0	36	5	4	1	4	1	23	0
<i>Eunotia sp.4</i>	4	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	2	0	0
<i>Eunotia sp.6</i>	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
<i>Fragilaria sp.1</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Frustulia sp.1</i>	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
<i>Geitlerinema sp.2</i>	23	0	8	15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Gloeocapsopsis sp.1</i>	116	0	0	16	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Gokenkinia radiata</i>	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Gyrosigma sp.1</i>	2	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0
<i>Homoeothrix sp.1</i>	100	0	100	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Monoraphidium contortum</i>	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
<i>Monoraphidiummarcuatum</i>	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0
<i>Monoraphidiumgriffithii</i>	3	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0

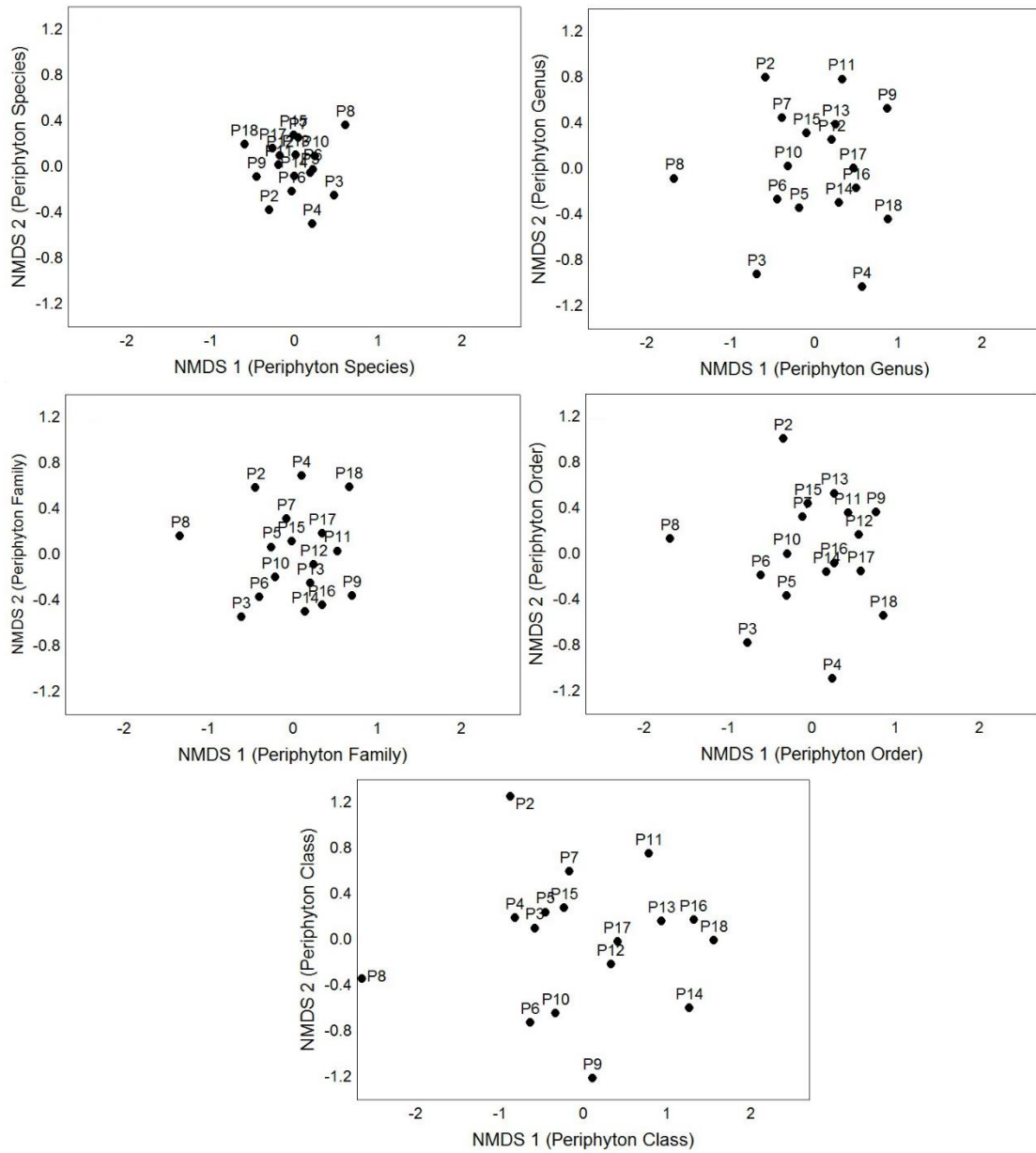
<i>Navicula 1</i>	165	0	2	0	1	10	2	0	0	1	6	100	9	21	3	4	2	4	0
<i>Nitzschia sp.1</i>	4	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0	0	0
<i>Peridinium sp.2</i>	3	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0
<i>Phormidium sp.1</i>	85	0	85	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Pinnularia latarea</i>	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Pinnularia saprophila</i>	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
<i>Pinnularia sp.1</i>	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Pseudonabaena limnetica</i>	140	0	0	60	0	55	13	6	1	0	4	0	0	0	0	1	0	0	0
<i>Rhizoclonium sp.1</i>	3	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Scenedesmus opoliensis</i>	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Sellaphora sp.2</i>	197	0	0	0	0	0	0	100	0	0	0	42	22	2	0	14	0	17	0
<i>Sellaphora sp.3</i>	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	7	0
<i>Sellaphorasp.1</i>	9	0	0	0	0	1	0	3	0	0	4	0	0	1	0	0	0	0	0
<i>Spirogyra sp.1</i>	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Taxon sp.1</i>	106	0	0	13	0	0	30	0	0	0	62	0	0	0	1	0	0	0	0
<i>Unaria una</i>	4	0	0	0	0	0	0	0	0	0	0	0	0	3	0	1	0	0	0
<b>Phytoplankton</b>	<b>Total Density</b>	<b>P1</b>	<b>P2</b>	<b>P3</b>	<b>P4</b>	<b>P5</b>	<b>P6</b>	<b>P7</b>	<b>P8</b>	<b>P9</b>	<b>P10</b>	<b>P11</b>	<b>P12</b>	<b>P13</b>	<b>P14</b>	<b>P15</b>	<b>P16</b>	<b>P17</b>	<b>P18</b>
<i>Amphipleura sp.1</i>	5.59	0	0	0	0	0	0	0	0	0	0	5.59	0	0	0	0	0	0	0
<i>Aulacoseira sp.1</i>	11.18	0	0	0	0	5.59	0	0	0	0	0	0	0	0	0	0	0	0	5.59
<i>Chlamydomonas sp.1</i>	33.55	0	0	0	0	5.59	0	0	0	0	0	5.59	0	0	0	0	0	0	22.36
<i>Chlamydomonas sp.2</i>	11.18	0	0	0	0	0	0	0	0	0	0	0	11.18	0	0	0	0	0	0
<i>Chroococcus minimus</i>	352.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	352.2
<i>Chroococcus minutus</i>	83.87	67.09	0	5.59	0	5.59	0	0	0	0	0	5.59	0	0	0	0	0	0	0
<i>Closterium leibleinii</i>	5.59	0	0	0	0	0	0	0	0	0	0	5.59	0	0	0	0	0	0	0
<i>Coelastrum reticulatum</i>	5.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.59
<i>Cosmarium sp.1</i>	5.59	0	0	0	0	0	0	5.59	0	0	0	0	0	0	0	0	0	0	0
<i>Cosmarium sp.2</i>	11.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	11.1	0	0	0
<i>Crucigenia quatrata</i>	5.59	0	0	0	0	0	0	0	0	0	0	0	5.59	0	0	0	0	0	0
<i>Crucigenia tetrapedia</i>	11.18	11.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Cryptomonas erosa</i>	33.55	0	0	0	0	5.59	0	0	0	5.59	0	0	0	0	11.1	11.1	0	0	0
<i>Cryptomonas marsonii</i>	67.09	0	0	0	0	0	0	0	0	0	5.59	0	0	61.5	0	0	0	0	0
<i>Cryptomonas obovata</i>	33.55	0	0	0	0	0	0	16.7	5.59	0	5.59	5.59	0	0	0	0	0	0	0
<i>Cryptomonas pierenoidifera</i>	5.59	0	0	0	0	0	5.5	0	0	0	0	0	0	0	0	0	0	0	0
<i>Dictyosphaerium pulchellum</i>	5.59	0	0	5.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Dinobryon elegantissimum</i>	5.59	0	0	0	0	0	0	0	0	0	5.59	0	0	0	0	0	0	0	0
<i>Eremosphaera sp.1</i>	301.92	268.3	0	5.59	0	5.59	0	0	0	0	5.59	0	0	0	0	5.59	0	0	11.18
<i>Euglena limnophila</i>	5.59	0	0	0	0	5.59	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Eunotia sp.1</i>	33.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	16.7	0	0	16.77
<i>Eunotia sp.2</i>	11.18	0	0	0	0	0	0	0	0	0	0	5.59	0	0	0	0	0	0	5.59

<i>Eunotia sp.3</i>	123.00	11.18	0	0	5.59	5.59	0	5.59	0	0	5.59	0	0	5.59	5.59	55.9	22.3	0	0
<i>Eunotia sp.4</i>	33.55	0	0	0	0	16.77	0	0	0	0	0	5.59	5.59	0	5.59	0	0	0	0
<i>Eunotia sp.5</i>	11.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	11.1	0	0	0
<i>Franceia droescheri</i>	5.59	0	0	0	0	0	0	5.59	0	0	0	0	0	0	0	0	0	0	0
<i>Frustulia sp.1</i>	39.14	0	0	0	0	5.59	0	0	0	0	0	5.59	0	0	0	27.9	0	0	0
<i>Geitlerinema sp.1</i>	16.77	0	0	11.18	5.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Gokenkinia radiata</i>	16.77	0	0	11.18	0	5.59	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Golenkinia sp.1</i>	5.59	0	0	0	0	5.59	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Kirchneriella sp.1</i>	27.96	22.36	0	0	0	0	0	5.59	0	0	0	0	0	0	0	0	0	0	0
<i>Merismopedia sp.1</i>	44.73	0	0	39.14	0	0	0	0	0	0	0	5.59	0	0	0	0	0	0	0
<i>Monoraphidium arcuatum</i>	251.60	44.73	0	27.96	22.3	5.59	5.5	0	5.59	33.5	55.9	0	0	11.1	0	27.9	0	0	11.18
<i>Monoraphidium caribeum</i>	5.59	0	0	0	0	5.59	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Monoraphidium contortum</i>	212.46	67.09	0	16.77	0	0	5.5	0	22.3	50.3	27.9	5.59	5.59	0	0	0	0	5.59	5.59
<i>Monoraphidium griffithii</i>	1375.40	0	0	0	0	0	5.5	0	0	0	0	967.2	380.1	0	0	0	0	0	22.36
<i>Monoraphidium irregulare</i>	5.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.59
<i>Monoraphidium komarkovae</i>	111.82	0	0	0	0	33.55	0	0	0	0	33.5	0	22.36	0	0	0	0	22.3	0
<i>Navicula sp.1</i>	357.83	5.59	0	0	0	123.0	0	11.1	0	5.59	0	167.7	16.77	0	11.1	16.7	0	0	0
<i>Nitzschia sp.1</i>	251.60	0	0	0	0	173.3	0	0	0	0	33.5	22.36	0	0	5.59	5.59	5.59	0	5.59
<i>Parvodinium umbonatum</i>	16.77	0	0	0	0	0	5.5	11.1	0	0	0	0	0	0	0	0	0	0	0
<i>Pediastrum gracillimum</i>	22.36	22.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Pedinomonas minutissima</i>	5.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5.59	0
<i>Peridinium sp.1</i>	150.96	0	0	5.59	0	0	0	22.3	0	0	11.1	83.87	27.96	0	0	0	0	0	0
<i>Peridinium sp.2</i>	11.18	0	0	0	0	0	0	11.1	0	0	0	0	0	0	0	0	0	0	0
<i>Phacus sp.1</i>	22.36	0	0	0	0	0	0	0	0	0	0	16.77	0	0	0	0	5.59	0	0
<i>Pinnularia sp.1</i>	22.36	0	0	0	0	0	0	11.1	0	0	0	5.59	0	0	0	5.59	0	0	0
<i>Pleurotaenium minutum</i>	11.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	11.18
<i>Pleurotaenium tenuissimum</i>	5.59	0	0	0	0	0	0	0	0	0	5.59	0	0	0	0	0	0	0	0
<i>Pseudokephryon ovum</i>	167.73	0	0	0	0	106.2	0	5.59	5.59	0	33.5	0	5.59	11.1	0	0	0	0	0
<i>Pseudonabaena limnetica</i>	21.68	0	4.9	5.59	0	0	0	5.59	0	0	0	0	0	0	0	5.59	0	0	0
<i>Scenedesmus denticulatus</i>	234.82	5.59	0	223.6	0	0	0	0	0	0	0	0	5.59	0	0	0	0	0	0
<i>Scenedesmus opoliensis</i>	33.55	0	0	11.18	0	16.77	0	0	5.59	0	0	0	0	0	0	0	0	0	0
<i>Sellaphora sp.1</i>	50.32	0	0	0	0	0	0	0	0	0	0	22.36	11.18	0	0	11.1	0	0	5.59
<i>Sellaphora sp.2</i>	273.96	0	0	0	0	0	0	0	0	5.59	0	123.0	39.14	0	5.59	16.7	0	0	83.87
<i>Staurastrum sp.1</i>	67.09	67.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Staurastrum sp.2</i>	5.59	5.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Staurastrum sp.3</i>	5.59	5.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Staurastrum sp.4</i>	5.59	5.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Staurastrum sp.5</i>	5.59	0	0	5.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Staurastrum sp.6</i>	5.59	0	0	5.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

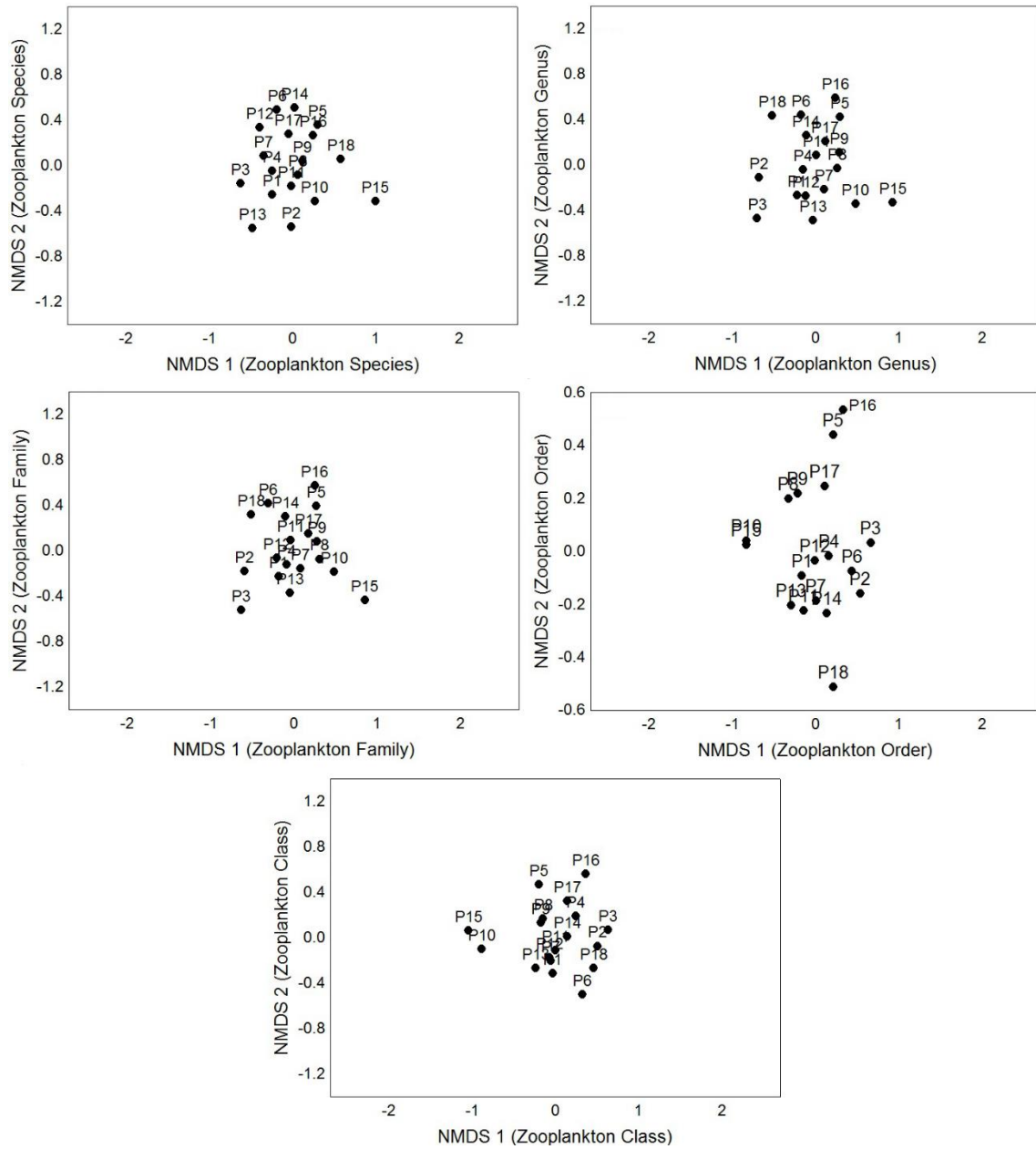
<i>Staurastrum sp.7</i>	39.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	39.1	0
<i>Surirella sp.1</i>	5.59	0	0	0	0	0	0	0	0	0	0	5.59	0	0	0	0	0	0	0	0
<i>Tetraedrum trigonum</i>	11.18	11.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Trachelomonas sp.1</i>	5.59	0	0	0	0	5.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Trachelomonas sp.2</i>	11.18	0	0	0	0	0	0	5.59	0	0	0	0	0	0	5.59	0	0	0	0	0
<i>Urosolenia sp.1</i>	11.18	11.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
<i>Westella botryoides</i>	44.73	0	0	0	0	0	0	0	39.1	0	5.59	0	0	0	0	0	0	0	0	0



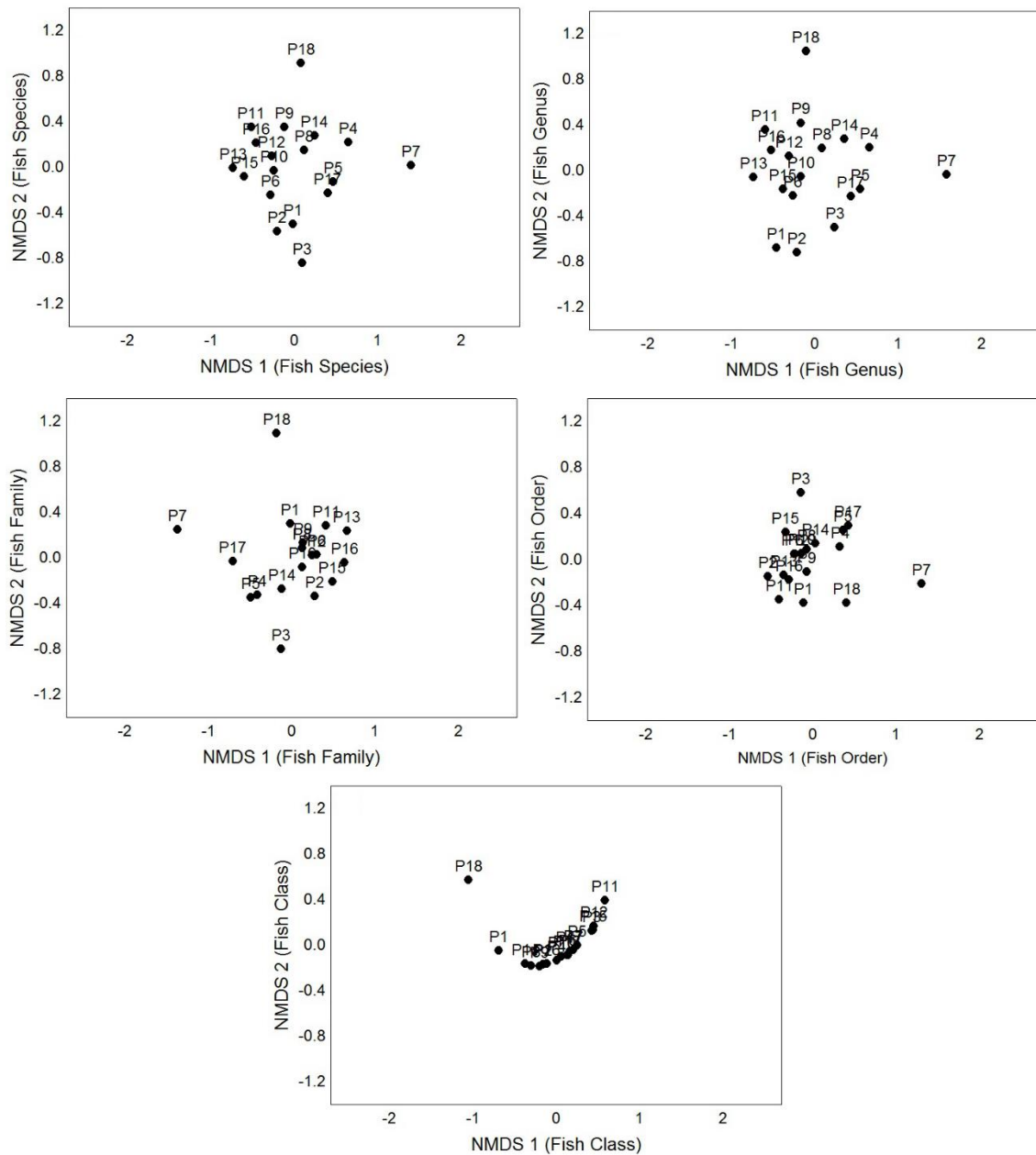
S1 Fig. - First and second axes obtained in the Non-Metric Multidimensional Scaling analysis (NMDS) for phytoplankton.



S2 Fig. - First and second axes obtained in the Non-Metric Multidimensional Scaling analysis (NMDS) for periphyton.



S3 Fig. - First and second axes obtained in the Non-Metric Multidimensional Scaling analysis (NMDS) for zooplankton.



S4 Fig. - First and second axes obtained in the Non-Metric Multidimensional Scaling analysis (NMDS) for fish.

## R PROGRAM SCRIPTS

### 1. Taxonomic Resolution

#### For phytoplankton, periphyton, zooplankton and fish data

```
install.packages("vegan")
library(vegan)

# importing files and standardization
sp<-read.table("sp.txt",header=TRUE)
sp<-t(sp) # Sampling points must be on the lines
sp<-decostand(sp, method = "hellinger")

genus<-read.table("genus.txt",header=TRUE)
genus<-t(genus) # Sampling points must be on the lines
genus<-decostand(genus, method = "hellinger")

family<-read.table("family.txt",header=TRUE)
family<-t(family) # Sampling points must be on the lines
family<-decostand(family, method = "hellinger")

order<-read.table("order.txt",header=TRUE)
order<-t(order) #Sampling points must be on the lines
order<-decostand(order, method = "hellinger")

class<-read.table("class.txt",header=TRUE)
class<-t(class) # Sampling points must be on the lines
class<-decostand(class, method = "hellinger")

# MANTEL

# Building a Bray Curtis distance matrix
braysp<-vegdist(sp, "bray")
braygenus<-vegdist(genus, "bray")
brayfamily<-vegdist(family, "bray")
brayorder<-vegdist(order, "bray")
brayclass<-vegdist(class, "bray")

# correlate the matrices
species_genus<-mantel(braysp, braygenus, method="pearson", permutations=10000)
species_family<-mantel(braysp, brayfamily, method="pearson", permutations=10000)
species_order<-mantel(braysp, brayorder, method="pearson", permutations=10000)
species_class<-mantel(braysp, brayclass, method="pearson", permutations=10000)

# MNDS

sp.nmnds <- metaMDS(sp, distance="bray", k=2)
summary(sp.nmnds)
axis.sp<-sp.nmnds$points
```

```
genus.nmds <- metaMDS(genus, distance="bray", k=2)
summary(genus.nmds)
axis.genus<-genus.nmds$points
```

```
family.nmds <- metaMDS(family, distance="bray", k=2)
summary(family.nmds)
axis.family<-family.nmds$points
```

```
order.nmds <- metaMDS(order, distance="bray", k=2)
summary(order.nmds)
axis.order<-order.nmds$points
```

```
class.nmds <- metaMDS(class, distance="bray", k=2)
summary(class.nmds)
axis.class<-class.nmds$points
```

```
#PROCRUSTES
```

```
sp_genus<-protest(axis.sp, axis.genus, scores = "sites", permutations = 1000)
sp_family<-protest(axis.sp,axis.family, scores = "sites", permutations = 1000)
sp_order<-protest(axis.sp, axis.order, scores = "sites", permutations = 1000)
sp_class<-protest(axis.sp, axis.class, scores = "sites", permutations = 1000)
```

```
#####
```

## 2. Numerical Resolution

### For phytoplankton, periphyton, zooplankton and fish data

```
library(vegan)
```

```
# importing files and standardization
```

```
sp.abundance<-read.table("sp.abundance.txt", header = TRUE) #data of the species abundance
```

```
sp.abundance<-decostand(sp.abundance, method = "hellinger")
```

```
sp.occurrence<-read.table("sp.occurrence.txt", header = TRUE) # data of the species occurrence
```

```
#MANTEL
```

```
# Building a Bray Curtis distance matrix
```

```
sp.abundance.matrix<-vegdist(sp.abundance, "bray")
```

```
sp.occurrence.matrix<-vegdist(sp.occurrence, "jaccard")
```

```
# correlate the matrices
```

```
abundance_occurrence<-mantel(sp.abundance.matrix, sp.occurrence.matrix, method="pearson", permutations=10000)
```

```
#NMDS
```

```

sp.abundance.nmds <- metaMDS(sp.abundance, distance="bray", k=2)
summary(sp.abundance.nmds)
axis.sp.abundance<-sp.abundance.nmds$points

sp.occurrence.nmds <- metaMDS(sp.occurrence, distance="jaccard", k=2)
summary(sp.occurrence.nmds)
axis.sp.occurrence<-sp.occurrence.nmds$points

#PROCRUSTES

abundance_occurrence<-protest(axis.sp.abundance, axis.sp.occurrence, scores = "sites",
permutations = 1000)

```

```
#####
```

### 3. Cross Taxa

#### Biological Groups

```

library(vegan)

# importing files and standardization
fish<-read.table("fish.txt",header = TRUE) # data of the abundance of fish species
fish<-t(fish) # Sampling points must be on the lines
fish<-decostand(fish, method = "hellinger")

phytoplankton<-read.table("phytoplankton.txt",header = TRUE) # data of the
abundance of phytoplankton species
phytoplankton<-t(phytoplankton) # Sampling points must be on the lines
phytoplankton<-decostand(phytoplankton, method = "hellinger")

periphyton<-read.table("periphyton.txt",header = TRUE) # data of the abundance of
periphyton species
periphyton<-t(periphyton) # Sampling points must be on the lines
periphyton<-decostand(periphyton, method = "hellinger")

zooplankton<-read.table("zooplankton.txt",header = TRUE) # data of the abundance of
zooplankton species
zooplankton<-t(zooplankton) # Sampling points must be on the lines
zooplankton<-decostand(zooplankton, method = "hellinger")

# MANTEL

# Building a Bray Curtis distance matrix
brayfish<-vegdist(fish, "bray")
brayphytoplankton<-vegdist(phytoplankton, "bray")
brayperiphyton<-vegdist(periphyton, "bray")
brayzooplankton<-vegdist(zooplankton, "bray")

```

```
# correlate the matrices
fish_phytoplankton<-mantel(brayfish, brayphytoplankton, method="pearson",
permutations=10000)
fish_periphyton<-mantel(brayfish, brayperiphyton, method="pearson",
permutations=10000)
fish_zooplankton<-mantel(brayfish, brayzooplankton, method="pearson",
permutations=10000)
phytoplankton_periphyton<-mantel(brayphytoplankton, brayperiphyton,
method="pearson", permutations=10000)
phytoplankton_zooplankton<-mantel(brayphytoplankton, brayzooplankton,
method="pearson", permutations=10000)
zooplankton_periphyton<-mantel(brayzooplankton, brayperiphyton, method="pearson",
permutations=10000)
```

```
# MNDS
```

```
fish.nmds <- metaMDS(fish, distance="bray", k=2)
summary(fish.nmds)
axis.fish<-fish.nmds$points
```

```
phytoplankton.nmds <- metaMDS(phytoplankton, distance="bray", k=2)
summary(phytoplankton.nmds)
axis.phytoplankton<-phytoplankton.nmds$points
```

```
periphyton.nmds <- metaMDS(periphyton, distance="bray", k=2)
summary(periphyton.nmds)
axis.periphyton<-periphyton.nmds$points
```

```
zooplankton.nmds <- metaMDS(zooplankton, distance="bray", k=2)
summary(zooplankton.nmds)
axis.zooplankton<-zooplankton.nmds$points
```

```
#PROCRUSTES
```

```
fish_phytoplankton<-protest(axis.fish, axis.phytoplankton, scores = "sites",
permutations = 1000)
fish_periphyton<-protest(axis.fish,axis.periphyton, scores = "sites", permutations =
1000)
fish_zooplankton<-protest(axis.fish, axis.zooplankton, scores = "sites", permutations =
1000)
phytoplankton_periphyton<-protest(axis.phytoplankton, axis. periphyton, scores =
"sites", permutations = 1000)
phytoplankton_zooplankton<-protest(axis.phytoplankton, axis. zooplankton, scores =
"sites", permutations = 1000)
zooplankton_periphyton<-protest(axis.zooplankton, axis. periphyton, scores = "sites",
permutations = 1000)
```

## **Trophic Groups**

```
library(vegan)
```

```

# importing files and standardization
fish<-read.table("fish.txt",header = TRUE) # data of the abundance of fish species
fish<-t(fish) # Sampling points must be on the lines
fish<-decostand(fish, method = "hellinger")

phytoplankton<-read.table("phytoplankton.txt",header = TRUE) # data of the
abundance of phytoplankton species
phytoplankton<-t(phytoplankton) # Sampling points must be on the lines
phytoplankton<-decostand(phytoplankton, method = "hellinger")

periphyton<-read.table("periphyton.txt",header = TRUE) # data of the abundance of
periphyton species
periphyton<-t(periphyton) # Sampling points must be on the lines
periphyton<-decostand(periphyton, method = "hellinger")

zooplankton<-read.table("zooplankton.txt",header = TRUE) # data of the abundance of
zooplankton species
zooplankton<-t(zooplankton) # Sampling points must be on the lines
zooplankton<-decostand(zooplankton, method = "hellinger")

carnivorous.fish<-read.table("carnivorous_fish.txt",header = TRUE)
carnivorous.fish <-t(carnivorous.fish) # Sampling points must be on the lines
carnivorous.fish <-decostand(carnivorous.fish, method = "hellinger")

herbivorous.fish<-read.table("herbivorous_fish.txt",header = TRUE)
herbivorous.fish <-t(herbivorous.fish) # Sampling points must be on the lines
herbivorous.fish <-decostand(herbivorous.fish, method = "hellinger")

herbivorous.zooplankton <-read.table("herbivorous_zooplankton.txt",header = TRUE)
herbivorous.zooplankton<-t(herbivorous.zooplankton) # Sampling points must be on the
lines
herbivorous.zooplankton <-decostand(herbivorous.zooplankton, method = "hellinger")

# MANTEL

# Building a Bray Curtis distance matrix
brayphytoplankton<-vegdist(phytoplankton, "bray")
brayperiphyton<-vegdist(periphyton, "bray")
brayzooplankton<-vegdist(zooplankton, "bray")
brayfishC<-vegdist(carnivorous.fish, "bray")
brayfishH<-vegdist(herbivorous.fish, "bray")
brayzooplanktonH<-vegdist(herbivorous.zooplankton, "bray")

# correlate the matrices
herbivorous.fish_phytoplankton<-mantel(brayfishH, brayphytoplankton,
method="pearson", permutations=10000)
herbivorous.fish_periphyton<-mantel(brayfishH, brayperiphyton, method="pearson",
permutations=10000)

```

```

carnivorous.fish_zooplankton<-mantel(brayfishC, brayzooplankton, method="pearson",
permutations=10000)
phytoplankton_zooplankton.herbivorous<-mantel(brayphytoplankton,
brayzooplanktonH, method="pearson", permutations=10000)
periphyton_zooplankton.herbivorous<-mantel(brayperiphyton, brayzooplanktonH,
method="pearson", permutations=10000)
phytoplankton_periphyton<-mantel(brayphytoplankton, brayperiphyton,
method="pearson", permutations=10000)

```

#### **4. Relationship with the environment and spatial distances**

**#Repeat the analysis separately for each taxonomic level of phytoplankton, periphyton, zooplankton and fish data**

```

library(vegan)
library(usdm)
library(spdep)
library(ncf)
library(adespatial)

```

#### **#SPATIAL FILTERS CONSTRUCTION**

```

coordinates<-read.table("coordinates.txt",header=TRUE) # file with the latitude and
longitude of the sampling points
distance.matrix<-vegdist(coordinates,method="euclid")
filters<-pcnm(distance.matrix)
filters.pcnm<-filters$vector

```

#### **# SPATIAL FILTERS SELECTION**

```

global.model<-rda(data, filters.pcnm)
p.global.model<-anova(global.model, step=10000)
R2.global.model<-RsquareAdj(global.model)

```

filters.sel<-forward.sel(data, filters.pcnm, nperm = 1000, adjR2thresh = R<sup>2</sup>.global.model, alpha = 0.05)# spatial filters selection. Data represents abundance each taxonomic level (species, genus, family, order and class) of phytoplankton, periphyton, zooplankton and fish. During the selection process, the selection stops if (1) the next selected variables is not significant (> 0.05), and (2) if the R<sup>2</sup>adj of the model including this variable exceeds the R<sup>2</sup>adj of the global model.

#### **# ENVIRONMENTAL VARIABLES SELECTION**

```

environment<-read.table("environment.txt",header=TRUE)
environment.VIF.sel<-vifcor(environment, th=0.5)

```

```
global.model<-rda(data, environment.VIF.sel)
p.global.model<-anova(global.model, step=10000)
R2.global.model <-RsquareAdj(global.model)
```

environment.sel<-forward.sel(data, environment, nperm = 1000, adjR2thresh = R<sup>2</sup>.global.model, alpha = 0.05) )# environmental variables selection. Data represents abundance each taxonomic level (species, genus, family, order and class) of phytoplankton, periphyton, zooplankton and fish. During the selection process, the selection stops if (1) the next selected variables is not significant (> 0.05), and (2) if the R<sup>2</sup>adj of the model including this variable exceeds the R<sup>2</sup>adj of the global model.

## RDA

```
data<-read.table("data.txt",header=FALSE)# data represents abundance each taxonomic level (species, genus, family, order and class) of phytoplankton, periphyton, zooplankton and fish.
```

```
data<-decostand(data, "hellinger")
RDA<-varpart(data, environment.sel, filters.sel, data=a)
plot(RDA)
```

```
# Anova
siga<-rda(data, environment.sel, filters.sel)
sigb<-rda(data, filters.sel, environment.sel)
```

```
plot(siga)
plot(sigb)
```

```
A<-anova(siga, step=10000)
B<-anova(sigb, step=10000)
```

## OR

```
analysis<-rda(data, environment.sel)
p<-anova(analysis, step=10000)
R2adj<-RsquareAdj(analysis)
```

## OR

```
analysis<-rda(data, filters.sel)
p<-anova(analysis, step=10000)
R2adj<-RsquareAdj(analysis)
```

## **CAPÍTULO II**

**Efeitos diretos e indiretos do uso do solo, variáveis internas e produtividade na diversidade de peixes de riachos**

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Teresa, João Carlos Nabout.**

**Anápolis**

**2021**

## Resumo:

Ecosistemas aquáticos dulcícolas indicam às influências externas de maneira importante, o que faz com que exista respostas importantes na ecologia sobre a compreensão das metacomunidades aquáticas. Para pequenos corpos d'água, existe uma maior sensibilidade das comunidades aquáticas, tanto para poluição, quanto para desmatamento das áreas ripícolas destes riachos, o que afeta diretamente a diversidade de vários grupos aquáticos. Assim, o objetivo deste trabalho foi compreender de forma integrada os efeitos dos ecossistemas periféricos sobre a biodiversidade aquática em riachos tropicais. As amostragens dos peixes, das variáveis internas dos riachos, produtividade e do uso do solo foram realizadas entre agosto e setembro de 2017, durante a estação seca do Bioma Cerrado. A partir dos dados da metacomunidade foram estimadas a riqueza das espécies, assim como suas contribuições locais para diversidade beta (LCBD) e diversidade funcional (entropia quadrática de Rao). Os dados de uso de solo e ambientais foram submetidos a uma Análise de Componentes Principais (PCA) para agrupar os dados em eixos de importância, posteriormente foi realizada uma análise de caminhos (*Pathway* análise) com os dois eixos principais em relação a riqueza e o Rao. Nós encontramos a partir das amostragens um total 1.098 indivíduos de 33 espécies, pertencentes a seis ordens e 18 famílias, os padrões de riqueza e Rao foram distintos entre os pontos amostrais. Os resultados indicaram uma relação positiva entre variáveis de paisagem com a riqueza de espécies, indicando que áreas mais preservadas e com pastagem apresentaram maior número de espécies, para ambiente de riacho no Cerrado. Além disso, a paisagem demonstrou relação negativa com primeiro eixo das variáveis ambientais, indicando que riachos mais preservados, e com áreas de pastagem, apresentaram mais quantidade de tronco, clorofila e riqueza de fitoplâncton. Encontramos também, que os riachos com maior riqueza de perifíton e folhiços apresentaram maior riqueza de espécies. Assim, corroboramos diversos outros trabalhos que indicam que a paisagem é importante para comunidade ictíica local, mesmo que indiretamente, demonstrando que a preservação das áreas ripárias está ligada a manutenção da comunidade ictíica e que estes ambientes devem ser considerados alvos para ações urgentes de preservação.

Palavras-chave: metacomunidade, *Pathway* análise, cerrado, peixes, riacho

## **Introdução**

Impactos causados por ecossistemas terrestres sobre ecossistemas aquáticos, principalmente dulcícolas, respondem às influências externas de maneira importante, o que faz com que exista um paradigma importante na ecologia sobre a compreensão das metacomunidades aquáticas (Ward, 1998). Sabe-se que os impactos causados pelas mudanças nos ambientes externos causam efeitos cumulativos em ambientes de riachos e se estendem em múltiplas escalas espaciais (Ward 1989, Teresa & Casatti 2012, Teresa et al. 2015, Leal et al., 2018; Leitão et al. 2018, Dala-Corte et al. 2020), tornando se um dos fatores que mais impactam a qualidade, distribuição e os fluxos das águas superficiais em diversas escalas (Rodell et al. 2018).

Os riachos geralmente passam por impactos na forma de gradientes (Cilleros et al. 2017), o que muitas vezes impede a compreensão dos padrões históricos das comunidades de peixes locais (Terra et al., 2016). Dentre os diferentes tipos de conversão de área natural as mais comuns são as formações de áreas de agricultura e pastagens para criação de gado, promovem diferentes alterações na paisagem (Terra et al., 2016). A agricultura, por exemplo, tem deixado um impacto grave no mundo, ocupando áreas maiores do que muitos dos biomas naturais (Foley et al., 2005). Além disso, a agropecuária é cada vez mais estimulada por conta do aumento da população humana e das atividades socioeconômicas, levando a um aumento das cargas de poluentes e nutrientes (esgoto, agrotóxicos e fertilizantes), causando redução da qualidade da água (Moss et al., 2011, Destouni e Jarsjo 2018, Levi et al. 2018). Nutrientes como nitrogênio e fósforo são as substâncias mais encontradas nos ambientes aquáticos afetados, o que pode gerar eutrofização local (Miranda *et al.*, 2014). Além disso, mudanças na cobertura do solo levam a processos como maior lixiviação e conseqüentemente assoreamento dos corpos d'água, causando mudanças no fluxo e na

configuração da paisagem, conseqüentemente na capacidade de dispersão das espécies (Liu et al., 2013). As transformações no ambiente entorno dos corpos d'água causam redução na qualidade do habitat e impactos mais intensos para ambientes dulcícolas, como riachos, rios e lagos (Riseng *et al.*, 2011), causados pela interferência direta no ciclo de nutrientes e produção de alimentos local.

Para pequenos corpos d'água, no entanto, numerosos estudos mostram uma maior sensibilidade das comunidades aquáticas, tanto para poluição, quanto para desmatamento das áreas ripícolas destes riachos (Waters, 1995), o que afeta diretamente a diversidade de vários grupos aquáticos (Casatti *et al.*, 2009). As zonas ripárias tem função de reter sedimentos e contaminantes das áreas adjacentes, atuando como um amortecedor contra os impactos do desmatamento (Dudgeon, 2008), além de manter a heterogeneidade do habitat aquático (Naiman e Décamps, 1997). Portanto, a vegetação ripária tem influência em várias escalas em comunidades aquáticas, atingindo inclusive a dinâmica trófica entre os grupos (Allan e Castillo 2007; Lorion e Kennedy, 2009). As mudanças causadas pelas alterações externas podem ser de efeitos diretos ou indiretos nas comunidades aquáticas (Dala-Corte et al., 2016; Ceballos et al., 2017; Crist et al., 2017), mas ambas podem levar a alterações na variabilidade dos serviços e funções ecossistêmicas a ela associados (Wang et al., 2017; Yang et al., 2018). Estes impactos, em sua maioria, são graves e muitas vezes irreversíveis para os ecossistemas aquáticos (Miranda et al., 2014).

Para peixes de riacho, por exemplo, a vegetação ripária determina condições hidrológicas fundamentais como a temperatura, oxigênio dissolvido, contribuição do material alóctone para alimentação, refúgio e sítios de reprodução para as espécies de peixes (Schneider e Winemiller, 2008), além da alteração da composição e função da comunidade ao longo do gradiente fluvial (Vannote et al., 1980). As relações indiretas

são consideradas a partir dos diferentes tipos de uso do solo sobre a riqueza e diversidade, pois a cobertura florestal tem efeito sobre diversidade funcional para as comunidades de peixes (Teresa *et al.*, 2012) sendo a peça-chave para maior abundância e diversidade das espécies de maneira geral (Pickett e Cadenasso 1995, Harborne *et al.*, 2011; Rees *et al.*, 2014). Já as relações diretas são compreendidas em dois momentos, primeiro pelo tipo de uso do solo e sua interferência direta sobre as variáveis internas e de produtividade, e segundo a interferências das variáveis internas e de produtividade diretamente sobre a comunidade local (Pandit *et al.*, 2009), que se mostram mais dependentes da qualidade do habitat (Casatti et al. 2009). Um exemplo é a utilização de agrotóxicos, fertilizantes ou esgoto, que resulta no aumento de nutrientes na água, causando o aumento de algas e consequentemente clorofila-a (Barros, 2008; Miranda et al., 2014), o que leva a uma interferência direta especificamente no excesso de nutrientes especificamente o nitrogênio e o fósforo, interferindo no ciclo de nutrientes e produção de alimentos local e consequentemente na diversidade de vários grupos aquáticos (Casatti et al., 2009). A eutrofização leva a efeitos diretos sobre oxigênio dissolvido na água (OD), floração de cianobactérias e alterações na turbidez, levando a morte de peixes e outros animais (Von Sperling, 1994; Motta, 2006).

Por estes motivos, neste trabalho nós investigamos os efeitos diretos e indiretos do uso do solo (ambientes naturais, de agricultura e pastagem), e das variáveis ambientais (tronco, areia e lama, fluxo, temperatura, clorofila, nitrato e folhiço) sobre a diversidade taxonômica e funcional de peixes de riacho no Bioma Cerrado inseridas em diferentes níveis de ambientes impactados pela ação humana. A partir desse objetivo, nós testamos as seguintes hipóteses:(I) Os diferentes tipos de uso de solo (natural, agricultura e pastagens) causam efeitos diretos sobre variáveis ambientais locais específicas (Bryce et al., 1999; Pinto et al. 2006; Leal et al., 2016) de forma que ambientes com menos

vegetações remanescentes tenham mudanças nas condições hidrológicas fundamentais como a temperatura, oxigênio dissolvido, contribuição do material alóctone para alimentação, refúgio e sítios de reprodução para as espécies de peixes (Schneider & Winemiller, 2008).

A retirada ou redução da vegetação natural levam a alterações da composição e função da comunidade ao longo do gradiente fluvial (Vannote et al., 1980) e influência em vários grupos da comunidade aquática, como algas, fitoplâncton, zooplâncton e invertebrados, além da dinâmica trófica entre os grupos (Allan & Castillo 2007; Lorion & Kennedy, 2009). Hipotetizamos também que, de forma independente, (II) as variáveis ambientais estarão relacionadas diretamente aos padrões de riqueza funcional e taxonômica da comunidade ictífica local (Casatti et al. 2006; Hoeinghaus et al. 2007; Macedo et al. 2014). Esta relação está registrada em diversos artigos que identificaram as condições internas do riacho (e.g.: temperatura, clorofila, fluxo etc.) como determinantes diretos para comunidade de peixes local. As alterações no fluxo por exemplo causam modificações na complexidade de habitat, profundidade e composição dos substratos (Brejão et al., 2018; Zeni et al., 2019), alterações na temperatura por sua vez podem levar a mudança na composição das espécies locais por espécies invasoras, principalmente aquelas mais tolerantes a mudanças na estrutura do habitat e espécies detritívoras, presentes em sua maioria em rios mais largos (Scott e Helfman, 2001; Lorion e Kennedy, 2009). Nossa terceira hipótese é de que (III) cada tipo de cobertura do solo estará relacionado de forma direta a qualidade da água e ambiente interno do riacho e como consequência afetará a comunidade peixes fazendo com que assim possamos encontrar efeitos indiretos das mudanças da cobertura do solo sobre a diversidade taxonômica e funcional da comunidade de peixes (Pittman et al. 2004; Dudgeon 2019; Grill et al. 2019). Essas relações serão avaliadas usando um modelo de

equação estrutural, no qual serão testados os efeitos diretos e indiretos das variáveis de paisagem, internas e produtividade sobre a riqueza taxonômica e funcional da comunidade peixes, dessa forma compreender de forma integrada os efeitos dos ecossistemas periféricos sobre a biodiversidade aquática em riachos tropicais.

## **Material e Métodos**

### **Área de estudo e amostragem dos peixes**

As coletas foram realizadas em 18 riachos da Bacia do Alto Rio Paraná em Goiás (Figura 1). Os riachos estão inseridos no Bioma Cerrado em um local com grande heterogeneidade de paisagem, com área de preservação nativa (Floresta Nacional de Silvânia) e diferentes tipos de uso do solo, como agrícola e pastagem. O trabalho foi realizado em 18 riachos situadas no alto da Bacia do Rio Paraná, contemplando três sub-bacias: sub-bacia do Piracanjuba (5 riachos), Ribeirão Vermelho (9 riachos) e Rio dos Bois (4 riachos).

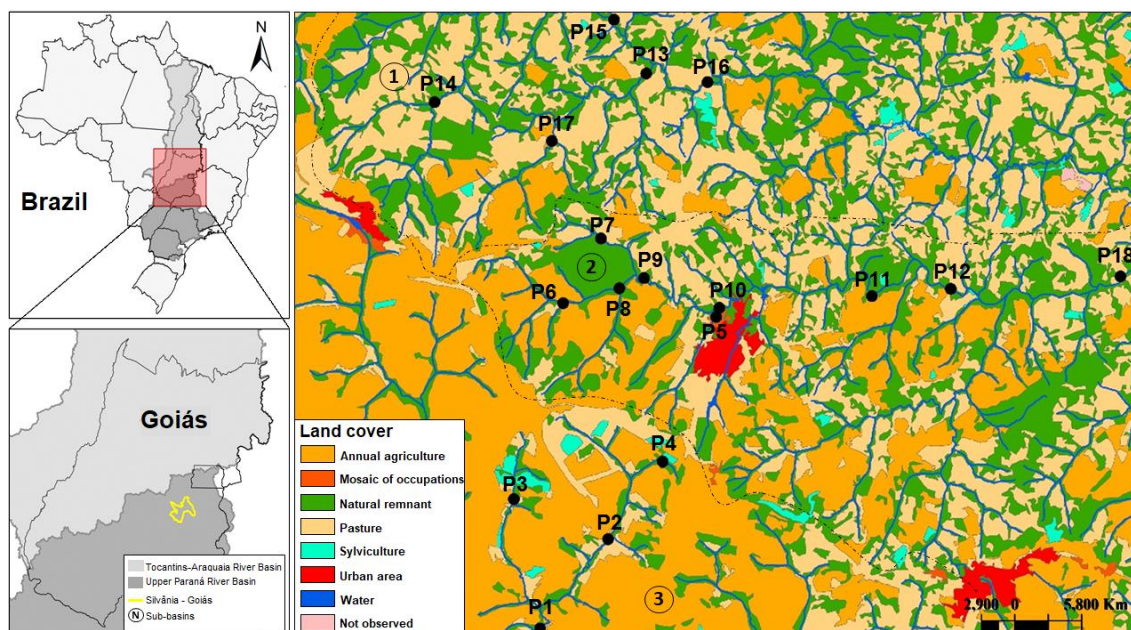


Figura 1. Localização dos 18 pontos de coleta na Alta Bacia do Rio Paraná, divididas em três sub-bacias inseridas no Bioma Cerrado na cidade Silvânia - Goiás, Brasil.

As amostragens dos peixes foram realizadas entre agosto e setembro de 2017, durante a estação seca (maio a setembro) do Bioma Cerrado. Os peixes foram capturados pelo método de pesca elétrica, com auxílio de um gerador de corrente alternada (1.000 W, 300–500 V, 1–3 A) que contava com dois puçás ligados a corrente elétrica, e mais um puçá adicional, sem eletricidade. A pesca elétrica foi realizada de jusante a montante, seguindo uma trajetória que explorava todos os tipos de microhabitats ao longo de 80 metros (Mazzoni et al., 2000). Após a captura, os peixes foram anestesiados em solução de água e Eugenol e logo depois transferidos para formalina 10%, e após 72 horas depositados em álcool 70% para melhor preservação dos indivíduos (Claro-García e Shibatta, 2013; Lima e Caires, 2011; Miranda e Mazzoni, 2003; Mazzoni et al., 2000). Os indivíduos foram identificados por meio de chaves de identificação não publicadas fornecidas por taxonomista (FR Carvalho, UFMS).

## **Uso do solo, variáveis internas e produtividade**

As variáveis preditoras da diversidade de peixes foram divididas em uso do solo e variáveis internas. As variáveis internas foram amostradas dentro dos riachos incluindo a temperatura, profundidade, turbidez, fluxo, nitrato, areia, rochas, troncos, folhiço e clorofila-a. As variáveis de uso de solo foram representadas pela porcentagem de pastagem, agricultura e área natural para cada ponto amostral. A produtividade local foi medida a partir da quantidade de clorofila e

As variáveis internas dos riachos de temperatura da água e clorofila-a foram medidas utilizando a sonda Eureka Manta 2 Amphibian, enquanto as concentrações de nitrato foram estimadas em laboratório seguindo padrão de avaliação de água e esgoto (Apha, 1998). As características internas de habitat foram medidas a partir de 9 transectos equidistantes (10m) dentro do trecho amostral de 80 metros, dos quais calculados os valores médios das variáveis ambientais de cada local amostral. Para cada ponto amostral foram obtidas as seguintes variáveis: fluxo, medido por meio do fluxômetro General Oceanics ®, modelo 2030); composição do substrato estável (rochas e troncos) e instável (areia/lama e folhiços), estimado visualmente como a proporção de cada componente do substrato (Cummins, 1962).

As variáveis de uso do solo foram construídas a partir da avaliação da porcentagem dos diferentes tipos de uso do solo, como agricultura, pastagem ou vegetação natural, a partir da avaliação de imagem de satélites TerraClass (Miranda 2018) para o Bioma Cerrado (<http://www.dpi.inpe.br/tccerrado/>). As porcentagens foram produzidas a partir da construção e avaliação do tipo da ocupação de solo a montante do ponto amostral até a área de nascente. Esse processo foi feito considerando

as classificações das vegetações (natural, pastagem e agricultura) de cada lado dos riachos em um buffer de 50 metros (Brasil, 2015).

### **Diversidade taxonômica e funcional**

A riqueza das espécies foi organizada a partir do número de espécies por cada ponto amostral. Os peixes amostrados foram classificados de acordo com sua categoria funcional, baseadas em 20 atributos funcionais distintos pré-determinados, agrupados nas características de comportamento alimentar (piscívoros, detritívoros, insetos terrestres, inseto aquáticos, zooplâncton, perifíton e vegetais), uso do habitat (bentônicos, margem, nectobentônicos, nectônicos e superfície), preferência de fluxo (rápido, intermediário e lento), tamanho (pequeno, médio e grande) e tolerância (tolerante e intolerante) as modificações ambientais (Tabela 1). Os peixes foram ainda organizados quanto a sua categoria trófica em herbívoros ou carnívoros (Teresa e Casatti, 2012). Para medida de diversidade funcional das comunidades peixes, nós utilizamos a entropia quadrática de Rao (Q de Rao). Este índice de diversidade funcional considera a abundância das espécies e calcula a distância funcional par a par (baseada na matriz de características funcionais) entre todas as espécies da comunidade (Botta-Dukat, 2005). Os atributos funcionais mensurados neste estudo apresentavam diferentes características matemáticas, como variáveis *fuzzy* (alimentar, habitat, fluxo) e variáveis nominais (tamanho e tolerância). Por essa razão, foram convertidos em uma matriz de distância de Gower, usando o método proposto por Pavoine et al. (2009).

Portanto, as comunidades com espécies que têm características muito diferentes terão valores de Q de Rao maiores do que aquelas que compreendem um número maior de espécies com características muito semelhantes. O Q de Rao não aumenta

monotonicamente com a riqueza de espécies (Botta-Duk at, 2005), garantindo assim que um alto valor de diversidade funcional não é apenas um artefato de um alto valor de riqueza de espécies. Usamos o pacote FD (Laliberte et al. 2014) no *R Statistical Environment* (R Core Team, 2015) para calcular os valores Q de Rao.

Table 1: Biological traits used in deconstructing the stream fish metacommunity.

Trait Group	Single Traits	Descriptions and interpretations
Habitat use	Benthic	Organisms living or associated with the stream bottom, species with dorsoventrally flattened bodies <sup>a</sup>
	Marginal	Species that prefer swimming close to the banks or amongst the marginal vegetation of water bodies <sup>a,b</sup>
	Nektobenthic	Species typically associated with river or stream bottoms but actively swim in the lower portion of the water column <sup>c</sup>
	Nektonic	Classified as species that swim or move freely in all layers of the water column <sup>c</sup>
	Surface	Surface or pelagic fish that have the body compressed laterally and are found in more structured and productive lentic environments <sup>a</sup>
Flow Preference	Fast water	Represented by species that prefer areas of fast water. These areas may represent more restricted environmental conditions, limiting the occurrence of several species, which results in highly similar fish communities <sup>d,e</sup>
	Intermediate water	Represented by low flow velocity and, consequently, places that are richer in food resources and formation of different mesohabitats <sup>f,g,h</sup>
	Slow water	Represented by areas of low water flow, indicating habitats composed of fine sediments and organic materials. In these habitats, pool formations are common as sites of substrate particle deposition zones <sup>e,i</sup>
Size	Large	Individuals larger than 150 mm <sup>e</sup> .
	Medium	Individuals between 50–150 mm <sup>e</sup> .
	Small	Individuals smaller than 50 mm <sup>e</sup> .

<sup>a</sup>Oliveira *et al.*, (2010), <sup>b</sup>Brejão *et al.*, (2013), <sup>c</sup>Lincoln *et al.*, (1995), <sup>d</sup>Angermeier e Schlosser (1989), <sup>e</sup>Teresa e Casatti (2012), <sup>f</sup>Burhnheim (2002), <sup>g</sup>Angermeier and Karr (1983), <sup>h</sup>Langeani *et al.*, (2005), <sup>i</sup>Moon, (1939).

## **Análise de dados**

As variáveis ambientais (exceto pH) foram transformadas em logaritmo ( $X+1$ ) e variáveis de uso de solo (porcentagem) foram transformadas usando transformação de raiz quadrada de arco seno.

Para avaliação dos dados, nós agrupamos as variáveis em preditoras e respostas de acordo com as hipóteses testada. Para hipótese I projetamos as variáveis de cobertura de solo como preditoras diretas causando efeitos sobre as variáveis ambientais. Para hipótese II consideramos que as variáveis ambientais são as preditoras sobre a riqueza e diversidade funcional da comunidade de peixes local, as quais são consideradas variáveis respostas. Em nossa terceira hipótese nós consideramos um efeito indireto em que as variáveis no uso do solo são consideráveis preditoras sobre as variáveis respostas riqueza e diversidade funcional.

A partir dos dados da metacomunidade foram estimadas a riqueza das espécies, assim como suas contribuições locais para diversidade beta (LCBD), diversidade funcional (entropia quadrática de Rao) e contribuição local para os 18 riachos amostrados.

### *Pathway* análises

A partir destes conceitos, desenvolvemos dois modelos teóricos para compreender quais os efeitos diretos e indiretos dos diferentes tipos de coberturas vegetais (paisagem natural, agricultura e pastagem) sobre a as características internas dos ambientes e em seguida a diversidade de peixes (riqueza de espécies e RAO) em regiões de riachos no Cerrado (Figura 2).

Baseados nos 18 pontos amostrais e nas sete variáveis ambientais selecionadas, foi realizada uma Análise de Componentes Principais (PCA) com intuito de simplificar o

modelo, tornando-o mais confiável. A partir da PCA foram selecionados os dois primeiros eixos, que tem maior explicabilidade sobre os efeitos entre as variáveis e sua resposta a riqueza e ao RAO.

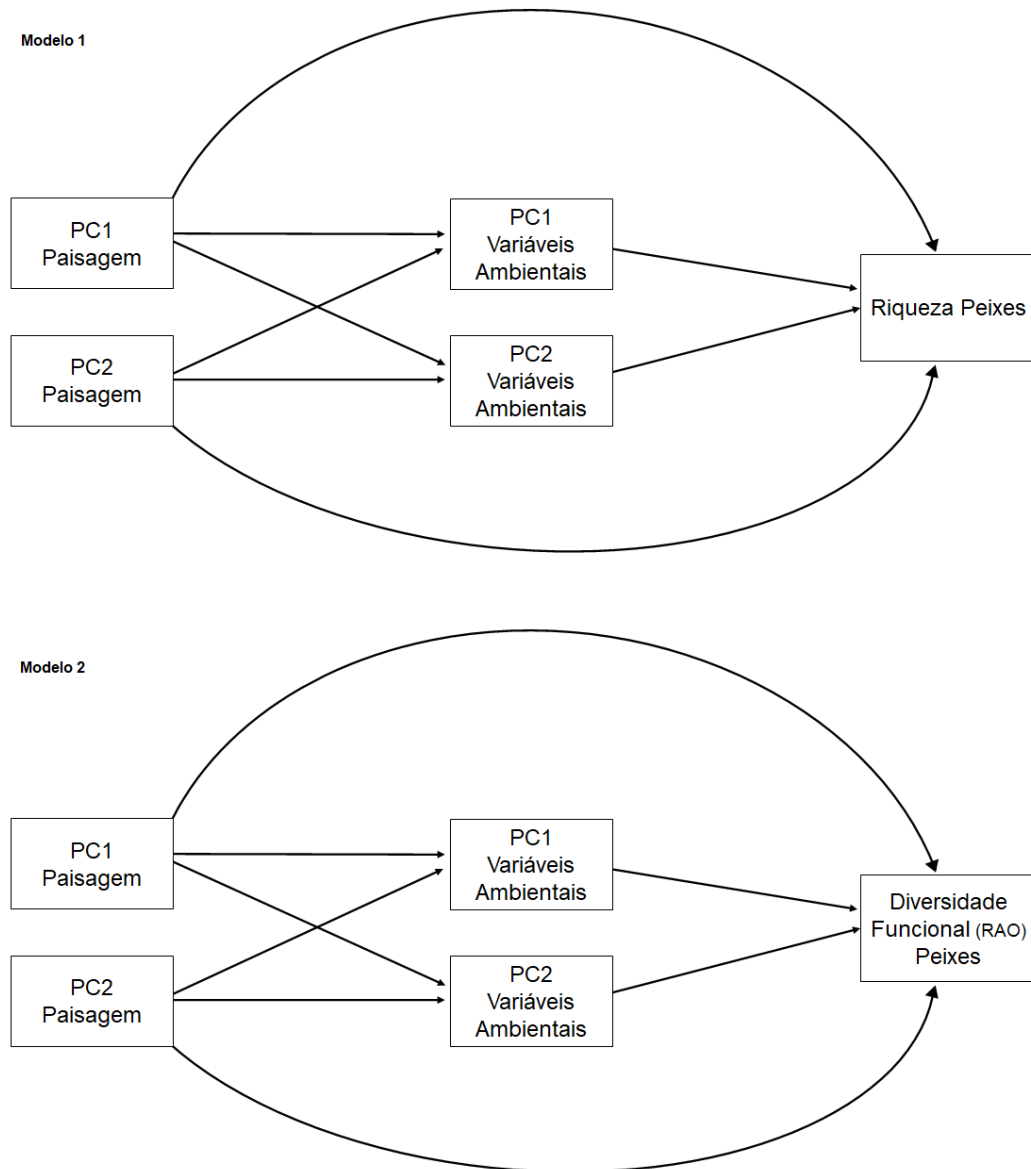


Figura 2. Modelos teóricos globais desenvolvidos para prever os efeitos diretos e indiretos sobre a diversidade funcional (entropia quadrática de Rao) e a riqueza de espécies matéria.

As análises foram feitas com utilização da modelagem de equações estruturais (SEM; Fox, 2010) para examinar o suporte do modelo, com uso do pacote lavaan (Rosseel, 2017) e para elaboração da imagem foi utilizado o pacote semPlot versão 1.1.2 (Epskamp, 2014), todos processos no software R (R Core Team, 2019).

Os dois modelos propostos foram baseados na literatura atual, na qual encontramos estudos que relatam que alterações no clima e tipo de cobertura do solo causam modificações na complexidade de habitat, profundidade e composição dos substratos (Brejão et al., 2018; Zeni et al., 2019). A perda da mata riparia causam diminuição da abundância e substituição de espécies (Jones et al., 1999), alterações na composição da comunidade e mudanças na diversidade funcional (Teresa et al., 2012; Heino, et al., 2018; Harvey & Altermatt, 2019; Henriques-Silva et al., 2019).

As mudanças nas variáveis internas do habita, como introdução de nutrientes alóctones causam aumento de algas e consequentemente clorofila-a (Barros, 2008; Miranda et al., 2014), o que interfere no ciclo de nutrientes (Casatti et al., 2009) e causa efeitos sobre a concentração de oxigênio dissolvido, floração de cianobactérias alteração na ocorrência de grupos aquáticos (Von Sperling, 1994; Motta, 2006). As mudanças das variáveis internas de habitat causam diversas seleções dos grupos de peixes locais, pois alguns atributos funcionais de habitat ou ocupação do espaço (bentônicos, nectobentônicos, nectônicos, de margens e de superfície) estão fortemente relacionados com a capacidade de dispersão (Costello et al., 2015; Kulbicki et al., 2015; Luiz et al., 2012), que por sua vez estão associadas com a velocidade da água (Blake, 2004), complexidade interna do habitat (Ferrari 2017) e alimentação (Casatti *et al.*, 2015; Henriques et al., 2017).

## Resultados

### *Fish Communities and Landscape use*

Nós encontramos a partir das amostragens um total 1.098 indivíduos de 33 espécies, pertencentes a seis ordens e 18 famílias: Characiformes (7 famílias), Siluriformes (6), Gymnotiformes (2), Cyprinodontiformes (1), Cichliformes (1) e Synbranchiformes (1). Dentre as espécies amostradas as mais abundantes foram *Bryconamericus turiuba*, *Piabina argentea* e *Poecilia reticulata*, compreendendo 40% da abundância total (Tabela S1). A riqueza total apresentou uma pequena variação entre os riachos, com no mínimo duas espécies em P7 e P18; e no máximo 15 em P10 (Figura 3a). Para a classificação da diversidade funcional dos grupos de peixes encontramos que os grupos com maior número de espécies foram as bentônicas (15 espécies), de fluxo rápido (13 espécies) e de médio porte (20 espécies). Para os habitats, o grupo com maior abundância foi o de peixes nectônicos (48% ou 530 indivíduos), composto por duas espécies muito abundantes, como *Bryconamericus turiuba* (18%) e *Piabina argentea* (12%).

A diversidade funcional baseada no índice Q de Rao, também apresentou variação ao longo dos pontos amostrais, embora com um padrão diferente do observado para riqueza de espécies. Os menores valores de Q de Rao foram observados nos riachos (P7 e P11), enquanto os maiores valores nos riachos P1, P2, P5 e P9 (Figura 3b). Os valores de contribuições locais baseados em LCDB são encontrados nos pontos P1, P4, P5, P7 e P18 (Figura 3c).

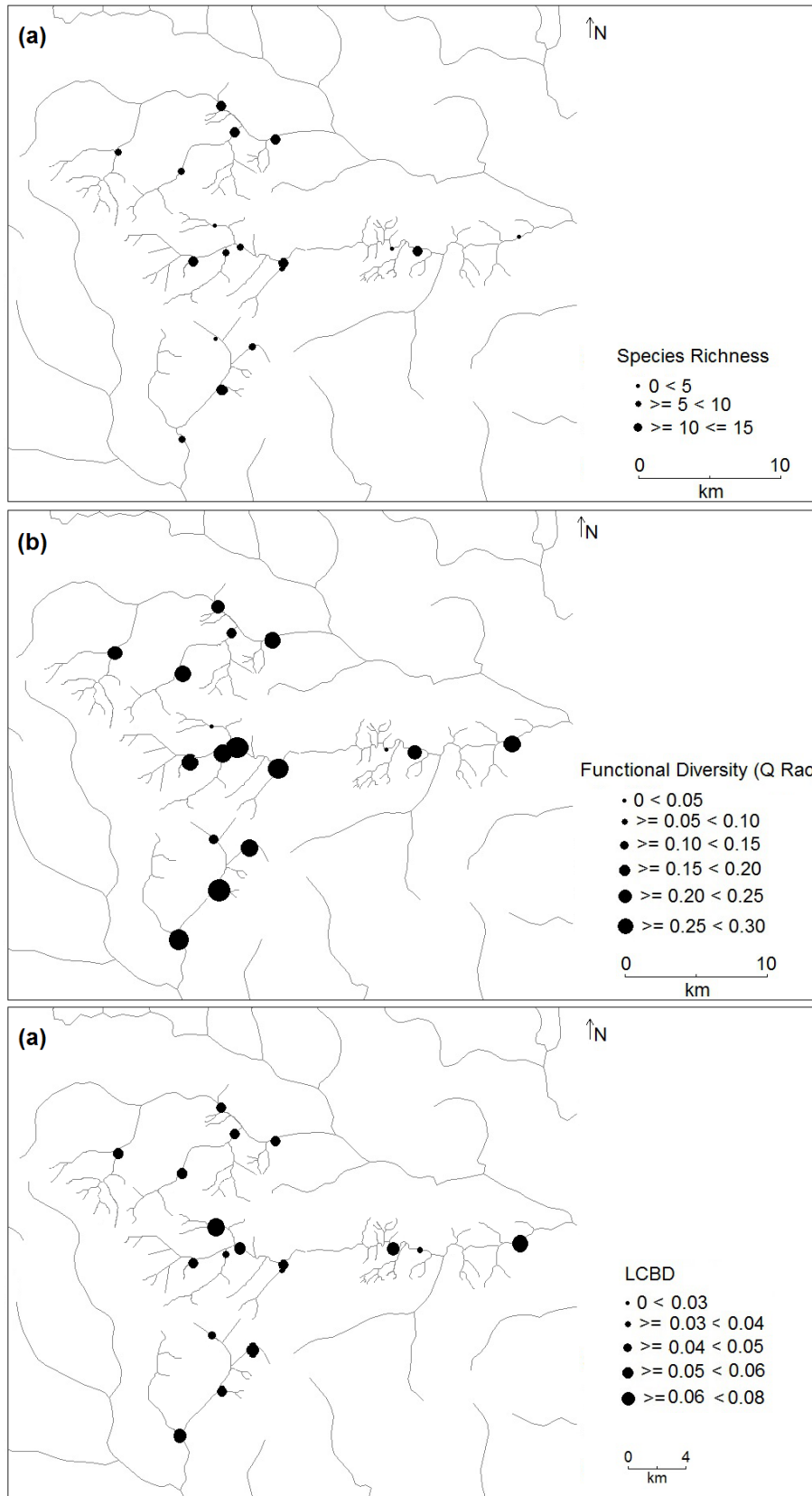


Figura 3 – Variação na riqueza de espécies, diversidade funcional (entropia quadrática de Rao) e Contribuição local para diversidade beta (LCBD) nos 18 riachos amostrados.

As análises da região apresentaram um grande mosaico de vegetação, com área natural de 39,66%, área urbana de 4,45%, pastagem de 33,76%, agricultura de 21,03% e silvicultura de 1,08%. Os riachos amostrados variam em relação ao tipo de cobertura do solo, sendo representados principalmente pelo uso para agricultura (Tabela 2). Os riachos também apresentaram variação em relação às variáveis ambientais internas, como turbidez, fluxo e tipo de substrato (Tabela 2). Todos os riachos apresentaram uma pequena profundidade.

Tabela 2 – Média de Desvio Padrão (DP) para as variáveis internas e uso de solo mensuradas nos 18 riachos em três sub-bacias inseridas no Bioma Cerrado na cidade Silvânia - Goiás, Brasil.

	Média	DP
Pastagem (%)	29	16.6
Natural (%)	30.4	12.4
Agricoltura (%)	37.1	23.6
Temperatura (°C)	18.3	1.88
Profundidade (cm)	29.2	10.4
Turbidez (NTU)	69.6	165.8
Fluxo (rps)	200.6	130
Nitrogênio Total (mg/L)	0.98	1.15
Subs. Instavel (areia e lama) %	91.1	10.7
Subs. Consolidado (rochas)%	8.9	10.8
Tronco (%)	33.2	18.6
Folhiço (%)	58.1	20.3

#### *Análise de Componentes Principais (PCA)*

As análises de componentes principais para as variáveis de uso de solo e de variáveis ambientais indicaram que os dois primeiros eixos apresentaram forte explicabilidade para organização das variáveis, tanto para uso do solo quanto variáveis (Figura 4). Para paisagem, observamos que os três eixos são opostos entre si, e que os pontos amostrais relacionados ao eixo 1 (PC1) estão ligados ao ambiente natural e que as culturas anuais estão relacionadas ao

eixo 2 (PC2). As áreas de pastagem estão opostas aos pontos com áreas de cultura anual, dentre os quais os pontos 15 e 16 são os pontos mais marcantes para este tipo de cobertura do solo.

Para as variáveis locais observou-se que 11 dos 18 pontos se relacionaram ao eixo 1 e com as características ambientais de riqueza e densidade de fitoplâncton e perifíton, fluxo, folhicho e presença de rochas (Figura 4). Enquanto os pontos 11 e 1 ligados ao eixo 2, com destaque a presença de clorofila, tronco, nitrogênio e turbidez e opostos a características como densidade e riqueza de perifíton e folhicho.

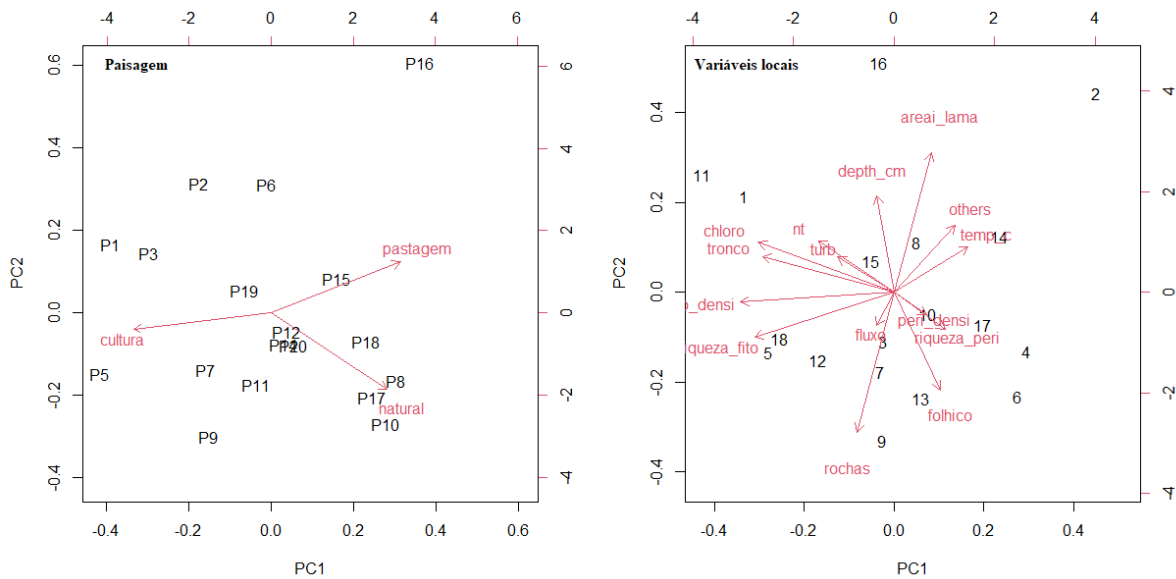


Figura 5. Representação das Análises de Componentes Principais baseadas nos tipos de uso de solo local (pastagem, culturas anuais e ambiente natural) e variáveis ambientais locais para 18 pontos amostrais em riachos do Cerrado.

As análises de caminho indicaram relações positivas e negativas entre as variáveis de cobertura de solo e ambientais em relação as riquezas e RAO. Os dois modelos apresentaram as mesmas relações positivas, das quais o eixo ambiental 1 (PC1 Paisagem) influencia negativamente o eixo 1 das variáveis ambientais (PC1 Variáveis Ambientais). Além disso, o eixo 2 ambiental, mais relacionado as culturas anuais, apresentaram relação e direta, tanto com riqueza quanto com RAO. As demais interações foram positivas, no entanto, nenhuma delas apresentou resultado significativo, indicando que nossas relações não são claras ou diretamente relacionadas (Figura 5). No entanto, é necessário considerar que essas duas métricas de diversidade da comunidade ictífica local podem ser direta e indiretamente sustentadas por variáveis de cobertura de solo, produtividade e variáveis internas.

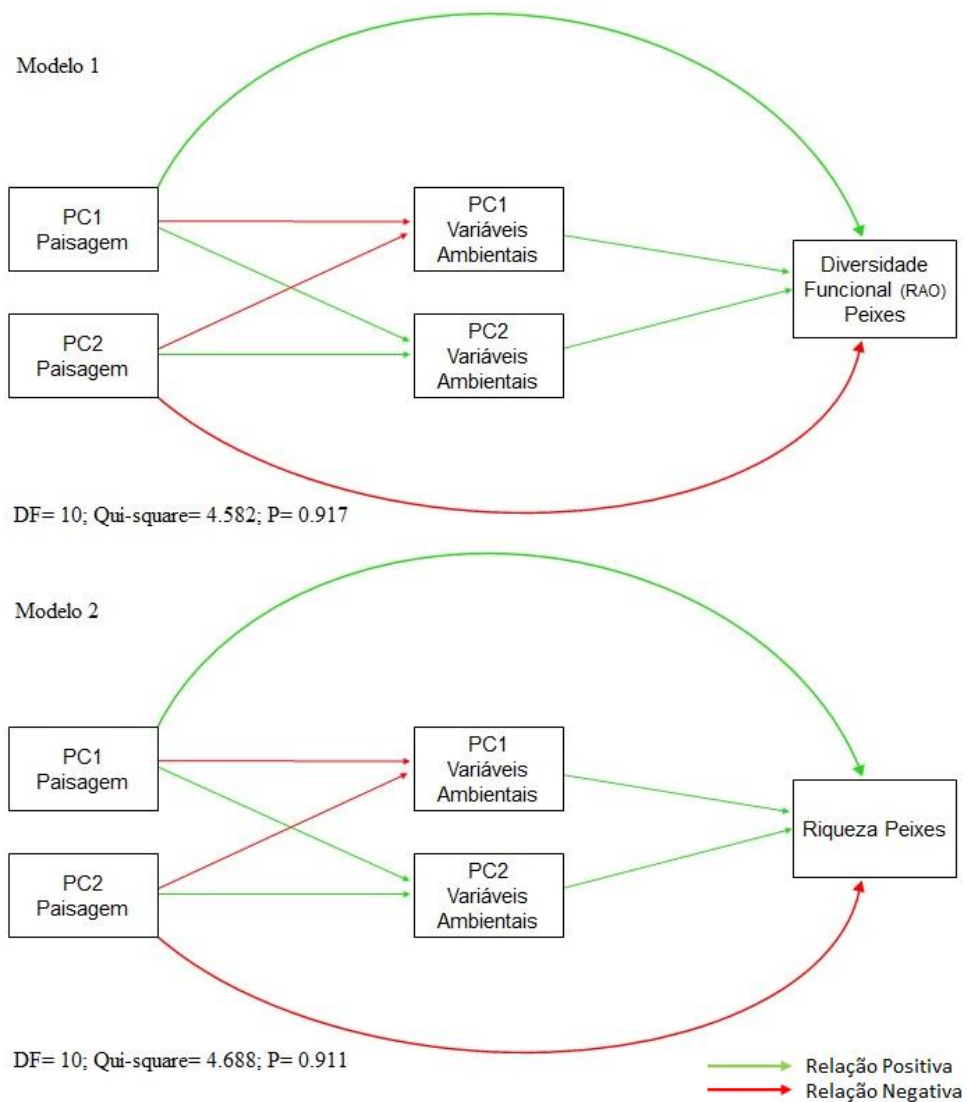


Figura 5. Modelos de equações estruturais indicando os caminhos pelos quais os diferentes tipos de uso do solo afetam a riqueza de espécies e a diversidade funcional (entropia quadrática de Rao). Setas contínuas são relações significativas e pontilhadas são não significativas, a espessura da seta é proporcional ao tamanho do efeito padronizado estimado, enquanto a cor verde significa relação positiva e a vermelha correlação negativa, para relações significativas os valores são indicados sobre as setas.

## Discussão

Neste trabalho não encontramos claramente evidências de que a comunidade ictíca de riachos do Cerrado são afetadas em sua maioria por variáveis internas, ou seja, influências dos efeitos diretos das variáveis ambientais locais, estruturais e produtividade sobre a riqueza e diversidade funcional. O efeito da conversão do ambiente sobre as comunidades aquáticas de peixes de riachos terá diferentes impactos a depender da escala a que estão submetidos (Dala-Corte et al., 2016; Gonçalves et al., 2020). Além disso, as comunidades de peixes podem ser influenciadas por múltiplos mecanismos que causem variações nas taxas biogeoquímicas demandadas pelos peixes (Trentman et al. 2020), causando uma variação local.

Nossos resultados mostram que as variáveis ambientais (estrutura do habitat e química da água) correlacionadas com a riqueza e diversidade funcional, corroborando com outros trabalhos que indicam que a organização de peixes em áreas de cabeceira é organizada pelas variáveis ambientais (Carvalho e Tejerina-Garro 2015; Vitorino et al. 2016). Essa relação é direcionada pela relação direta das variáveis locais como fluxo, temperatura e clorofila (produtividade).

### *Efeitos diretos das variáveis internas e produtividade sobre a diversidade*

As relações negativas entre tronco, nitrato, clorofila e turbidez com a maior parte dos pontos amostrais, provavelmente esta relacionada a ausência de tronco em vários dos riachos avaliados, o que está relacionada com o desmatamento e retirada da mata ripária, fazendo com que exista a redução no número de galhos e troncos no riacho (Dala-Corte et al. 2016), auxiliando na homogeneização do ambiente. Já os nitratos podem estar relacionados a fontes externas e carregadas pela chuva, material orgânico e inorgânico de origem externa e a fixação biológica é feita por bactérias e algas cianofíceas (Esteves 1998; King et al. 2005; Abell et al.,

2007; Dala-Corte et al. 2016). No entanto, nosso estudo foi realizado em período de seca, o que faz com que exista redução da lixiviação de componentes presentes no solo e ao entorno, o que pode ter mascarado interações indiretas do uso do solo sobre a riqueza e diversidade funcional das espécies.

Variáveis internas são conhecidas cada vez mais por interferirem diretamente na assembleia de peixes de riachos (Tejerina-Garro et al. 2005; Jackson et al. 2001; Oberdorff et al. 2001; Väliverronen 1998; Monroe et al. 2009) podendo apresentar variações entre as relação de acordo com a mudança entre períodos de chuva e seca no Cerrado, isso porque em épocas de chuvas existe uma maior descarga na drenagem, seguido pela redução do fluxo no final do verão (Horowitz 1978), o que interfere diretamente no número de espécies, indivíduos e suas funções no habitat (Giam et al. 2015). Além disso, nosso estudo corrobora com outros estudos que indicam que o uso do solo na escala de microbacia influencia diretamente na qualidade da água (Mello et al. 2017, 2018) e na estrutura do riacho (Freitas et al. 2018; Leitão et al. 2018; Macedo et al. 2014; Montag et al., 2019) e indiretamente nas assembleias de peixes (Dala-Corte et al. 2016; Leitão et al. 2018). No geral encontramos que as variáveis ambientais foram positivamente relacionadas a riqueza e diversidade funcional do que os diferentes tipos de uso do solo (Leal et al. 2018; Macedo et al. 2014).

#### *Efeitos diretos do uso do solo*

A relação positiva do eixo 1, mais relacionado a ambientes naturais, foi o único efeito direto do uso do solo observado neste trabalho, no entanto efeitos como este já foram relatados em diversos outros estudos, inclusive em diferentes biomas, como para zona ribeirinha das assembleias de peixes na Amazônia (Leitão et al. 2018), e Cerrado (de Carvalho et al. 2017). A manutenção de uma mata riparia é compreendida cada vez mais

como uma porção fundamental para vida em riachos, porque além de servir como amortecedor para os impactos da mudança de estrutura do meio ambiente ao entorno dos riachos, serve como regulados da qualidade do ambiente para sobrevivência, alimentação e reprodução da comunidade de peixes.

É necessário destacar que este trabalho foi desenvolvido em comunidades presentes riachos pequenos de primeira à quarta ordem, isso faz com que esses indivíduos dependam ainda mais das condições de preservação do ambiente externo, por se tratar de peixes de corpo pequeno e na maioria das vezes alimentação especializada. Isso faz com que qualquer mudança ou intervenção no ambiente externo afete os peixes da comunidade local, corroborando com nosso resultado de que a diversidade funcional também é afetada positivamente pelo ambiente natural. Diversos trabalhos indicam que a riqueza de espécies aumenta ao longo do rio, da cabeceira até a foz, seguindo um padrão de biodiversidade (Vannote et al., 1980). Isso por que os riachos possuem maior heterogeneidade de habitat, como corredeiras rasas de fluxo rápido, poças profundas de fluxo lento, manchas de detritos lenhosos e folhagem (Forman, 1995) o que faz com que apresente uma população mais especializada referentes as condições ambientais.

A agricultura (eixo 2) tiveram uma relação positiva, mas não significativa, com riqueza dos peixes locais e RAO. No entanto isso pode ser explicado por que o aumento do impacto antropogênico pode causar um efeito positivo sobre riqueza de espécies, principalmente aquelas não nativas, como *Poecilia reticulata*, classificada como espécies detritívoras e mais tolerantes as mudanças na qualidade da água (Lorion & Kennedy 2009; Alexandre et al. 2010; Schulz et al. 2001).

## **Conclusão**

Os nossos modelos foram desenvolvidos para acessar informações sobre os caminhos que interferem nas comunidades de peixes em ambientes de riacho. Os resultados indicaram uma relação positiva entre o primeiro eixo das variáveis de paisagem (PC1) com a riqueza de espécies, indicando que áreas mais preservadas e com pastagem apresentaram maior número de espécies, para ambiente de riacho no Cerrado. Além disso, o eixo 1 da paisagem (PC1 paisagem) demonstrou relação negativa com primeiro eixo das variáveis ambientais (PC1 variáveis ambientais), indicando que riachos mais preservados e com áreas de pastagem, apresentaram mais quantidade de tronco, clorofila e riqueza de fitoplâncton. Encontramos também, que os riachos com maior riqueza de perifíton e folhiços (PC1 variáveis ambientais) apresentaram maior riqueza de espécies. Desta forma, corroboramos diversos outros trabalhos que indicam que a paisagem é importante para comunidade ictíca local, mesmo que indiretamente, demonstrando que a preservação das áreas ripárias está ligada a manutenção da comunidade ictíca e que estes ambientes devem ser considerados alvos para ações urgentes de preservação.

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Table S1: Fish species found in streams with the functional traits of habitat type, dispersal, and size.

<b>Species</b>	<b>Habitat use</b>	<b>Velocity preference</b>	<b>Size</b>	<b>Order</b>	<b>Family</b>	<b>Genus</b>
<i>Aspidoras fuscoguttatus</i>	Benthic	Fast	Small	Siluriformes	Callichthyidae	Aspidoras
<i>Astyanax bockmanni</i>	Nektonic	Slow	Medium	Characiformes	Characidae	Astyanax
<i>Astyanax fasciatus</i>	Nektonic	Slow	Medium	Characiformes	Characidae	Astyanax
<i>Astyanax lacustris</i>	Nektonic	Slow	Medium	Characiformes	Characidae	Astyanax
<i>Bryconamericus turiuba</i>	Nektonic	Intermediate	Medium	Characiformes	Characidae	Bryconamericu
<i>Cetopsis gobioides</i>	Benthic	Fast	Medium	Siluriformes	Cetopsidae	Cetopsis
<i>Cetopsorhamdia iheringi</i>	Benthic	Fast	Medium	Siluriformes	Heptapteridae	Cetopsorhamdia
<i>Characidium zebra</i>	Benthic	Intermediate	Medium	Characiformes	Crenuchidae	Characidium
<i>Characidium gomesi</i>	Benthic	Fast	Medium	Characiformes	Crenuchidae	Characidium
<i>Cichlasoma paranaense</i>	Nektobenthic	Slow	Medium	Cichliformes	Cichlidae	Cichlasoma
<i>Curculionichthy sp</i>	Marginal	Intermediate	Small	Siluriformes	Loricariidae	Curculionichthys
<i>Curculionichthys insperatus</i>	Marginal	Intermediate	Small	Siluriformes	Loricariidae	Curculionichthys
<i>Eigenmannia virescens</i>	Marginal	Intermediate	Large	Gymnotiformes	Sternopygidae	Eigenmannia
<i>Gymnotus carapo australis</i>	Marginal	Slow	Large	Gymnotiformes	Gymnotidae	Gymnotus
<i>Hasemania hanseni</i>	Nektonic	Slow	Small	Characiformes	Characidae	Hasemania
<i>Hoplias malabaricus</i>	Margins	Slow	Large	Characiformes	Erythrynidae	Hoplias
<i>Hypostomus ancistroides</i>	Benthic	Intermediate	Medium	Siluriformes	Loricariidae	Hypostomus
<i>Hypostomus sp</i>	Benthic	Fast	Medium	Siluriformes	Loricariidae	Hypostomus
<i>Imparfinis schubarti</i>	Benthic	Fast	Medium	Siluriformes	Heptapteridae	Imparfinis
<i>Leporinus sp</i>	Nektobenthic	Slow	Medium	Characiformes	Anostomidae	Leporinus
<i>Leporinus sp1</i>	Nektobenthic	Slow	Medium	Characiformes	Anostomidae	Leporins
<i>Parodon nasus</i>	Benthic	Fast	Medium	Characiformes	Parodontidae	Parodon
<i>Phenacorhamdia tenebrosa</i>	Benthic	Fast	Medium	Siluriformes	Heptapteridae	Phenacorhamdia
<i>Piabarchus stramineus</i>	Nektonic	Intermediate	Small	Characiformes	Characidae	Piabarchus
<i>Piabina argentea</i>	Nektonic	Intermediate	Small	Characiformes	Characidae	Piabina
<i>Pimelodella gracilis</i>	Benthic	Slow	Medium	Siluriformes	Heptapteridae	Pimelodella
<i>Pimelodus sp</i>	Benthic	Fast	Large	Siluriformes	Pimelodidae	Pimelodus
<i>Poecilia reticulata</i>	Surface	Slow	Small	Cyprinodontiformes	Poeciliidae	Poecilia

<i>Prochilodus lineatus</i>	Nektobenthic	Slow	Large	Characiformes	Prochilodontidae	Prochilodus
<i>Rhamdia quelen</i>	Benthic	Slow	Medium	Siluriformes	Heptapteridae	Rhamdia
<i>Rhyacoglanis paranensis</i>	Benthic	Fast	Medium	Siluriformes	Pseudopimelodidae	Rhyacoglanis
<i>Steindachnerina insculpta</i>	Nektobenthic	Slow	Medium	Characiformes	Curimatidae	Steindachnerina
<i>Synbranchus marmoratus</i>	Marginal	Slow	Large	Synbranchiformes	Synbranchidae	Synbranchus

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