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A Conceptual Framework and Methods for Studying the Connectivity of Fishes

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ABSTRACT

Connectivity is a multifaceted concept that has important implications for the management and conservation of marine and freshwater fishes. We developed a conceptual framework that encompasses multiple, interrelated categories of connectedness, including landscape (e.g., structural, functional) connectivity and ecological (e.g., trophic, genetic, demographic) connectivity, that together shape the flow of organisms, energy and information across ecosystems. We also synthesised six key methods that can be used to study connectivity of fishes: (1) telemetry, including satellite, acoustic, radio and passive integrated transponders (PIT), (2) mark-recapture, (3) environmental tracers, including stable isotopes and otolith-microchemistry, (4) genetics, (5) community structure analysis and (6) emerging technologies and tools (e.g., remote sensing and artificial intelligence). For each method, we describe the categories of connectivity it can assess and provide real-world examples where they have been effectively used. We also identify limitations of each method. This article highlights the diverse and evolving toolbox of methods used to assess fish connectivity, underscoring the need for continued collaboration, innovation and integration of new approaches to refine our understanding and address remaining challenges in this critical area of aquatic ecology and fisheries management.

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1 | Introduction

Effective management of fish populations necessitates a comprehensive understanding and consideration of connectivity (Gibson et al. 2011), which is a complex concept that links ecosystem elements to spatial and temporal dimensions (Lapointe et al. 2014). Connectivity includes the spatial movement of individuals as well as the flow of genetic materials, energetic resources and nutrients (Calabrese and Fagan 2004). In aquatic ecosystems, interconnectedness across habitats influences the distribution and abundance of fishes, along with their evolutionary trajectories (Arthington et al. 2016). Additionally, fish often undertake movements across habitat types to access different resources (e.g., spawning and overwintering habitat, refugia, food) or may transition to new habitats during ontogenetic shifts (Lucas and Baras 2008; Brönmark et al. 2014; Secor 2015; Cooke et al. 2022). Fish face a suite of anthropogenic stressors, including habitat deterioration and loss, river engineering and damming of rivers, river flow regulation and overfishing, that fragment connectivity and impair species movements and ecosystem function (Rolls et al. 2014; Crook et al. 2015; Arthington et al. 2016; Lennox, Birnie-Gauvin, et al. 2025). Reduced connectivity can profoundly affect fish by minimising or eliminating access to critical habitats, decreasing gene flow and altering nutrient and energy pathways (Jeffrey et al. 2015). As the panoply of stressors that threaten the persistence of wild fish populations increases, it is essential that we better understand, and expand upon, the pros, cons and limitations of the methods in our connectivity toolbox to conserve biodiversity, fish populations, and the ecosystem services they provide (Lapointe et al. 2014).

While fish connectivity research and the tools used to evaluate connectivity have advanced, there is currently no comprehensive summary of those tools along with their benefits and limitations. Accordingly, we undertake a review to detail contemporary field and analytical methods to study fish connectivity, first providing an in-depth overview of connectivity and defining the hierarchical elements that contribute to this multifaceted concept. Next, we identify six key methods to assess connectivity including telemetry, mark–recapture, environmental tracers, genetics, community structure analysis and emerging tools and technologies to help us better understand how fishes, and the energy and information they bring with them, move across landscapes. For each method, we provide examples of successful implementation to highlight real-world scenarios that supported the management of fishes. We also consider limitations for each method. We conclude by identifying and discussing knowledge gaps in the evidence base that may hinder the management of fishes in relation to connectivity.

2 | What Is Connectivity?

Connectivity is the flow of materials, energy and organisms across space and time (Ward 1989; Beger et al. 2022). In aquatic ecosystems, connectivity is a hierarchical process that links elements within ecosystems and can be divided into landscape and ecological connectivity (Lapointe et al. 2014). First, landscape connectivity refers to the degree to which a landscape facilitates or impedes the movement of organisms among spatially distinct entities or resource patches, emphasising the physical structure of the landscape and an organism's response to structure. Landscape connectivity can be further refined to structural and functional connectivity (Tischendorf and Fahrig 2000). Structural connectivity is defined by the quantity and spatial arrangement of landscape features serving as habitat patches and potential movement routes (corridors) between habitat patches, focusing on the physical characteristics of aquatic environments such as the presence and arrangement of different habitats. Importantly, structural connectivity includes ecohydraulic attributes, such as flow velocity, discharge patterns and water-level fluctuations, which directly affect habitat continuity (Katopodis 2012; Cooke et al. 2025). The analysis of structural connectivity has been well established in landscape ecology and is largely dependent on foundational metrics like patch size, geometry, corridor patterns, and the study of extinction-colonisation dynamics (i.e., Metapopulation Theory, Theory of Island Biogeography) which can be integrated into aquatic ecosystems (MacArthur and Wilson 1967; Levins 1969). Next, functional connectivity describes an organism's behavioural response to these landscape features and the outcome of those responses in terms of survival and reproduction (Taylor et al. 1993, 2007; Tischendorf and Fahrig 2000). Functional connectivity reflects how organisms actually use space, capturing their ability to navigate, survive and reproduce across habitats based on their behaviour and interactions with landscape/seascape features (e.g., Turgeon et al. 2010; Roy and Le Pichon 2017).

Second, ecological connectivity encompasses trophic, genetic and demographic connectivity (Soulé et al. 2004; Bryan-Brown et al. 2017). Trophic connectivity describes the movement and transfer of energy and nutrients through different levels of the food web, linking primary producers to top predators and capturing how different trophic levels are linked through migration, subsidy flows and consumption (Polis et al. 1997; Talley et al. 2006). The trophic connection can be formed through the movement of either consumers or resources between habitats and affects ecosystem structure, stability and function (Talley et al. 2006). This includes vertical linkages between different trophic levels, such as primary producers, herbivores and predators, and horizontal exchanges across habitats and within trophic levels. Second, genetic connectivity refers to the movement of genetic material between nearby or distant habitat regions over multiple generations and can occur through processes such as dispersal and reproduction, facilitating gene flow across the landscape (Carr et al. 2017; Xuereb et al. 2021). Finally, demographic connectivity emerges from variation in organismal movement through space and time, shaping food web structure at both the population and community levels. At the population scale, the movement of individuals among sites drives immigration and emigration, colonisation of new habitats, and source-sink dynamics, ultimately influencing persistence, abundance and population dynamics (Pulliam 1988). At the community scale, these dispersal processes govern differences in species composition and interaction networks, manifesting as variations in alpha, beta and gamma diversity (Tonkin et al. 2016). Moreover, sites that are highly disconnected will be more strongly constrained by dispersal limitations, leading to reduced population resilience and altered community assembly relative to more connected systems (Sale 2004; Brown and Swan 2010; Heino et al. 2015). Variations in scale, ranging from

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TABLE 1 | Glossary of connectivity terms. References are provided in-text.

<table>
<tr><td colspan="5">**Connectivity**</td></tr>
<tr><td colspan="5">The flow of materials, energy and organisms across space and time</td></tr>
<tr><td colspan="2">**Landscape connectivity**</td><td colspan="3">**Ecological connectivity**</td></tr>
<tr><td colspan="2">The degree to which the landscape facilitates or impedes movement among resource patches, emphasising the physical structure of the landscape with an organism's response to that structure</td><td colspan="3">Includes propagule dispersal, adult movement, species migrations, species interactions and ontogenetic linkages, with the associated flows of energy and matter</td></tr>
<tr><td>**Structural connectivity**</td><td>**Functional connectivity**</td><td>**Trophic connectivity**</td><td>**Genetic connectivity**</td><td>**Demographic connectivity**</td></tr>
<tr><td>The quantity and spatial arrangement of landscape features serving as habitat patches and potential movement routes (corridors) between habitat patches</td><td>The behavioural responses of animals to landscape features and the outcome of those responses in terms of survival and reproduction</td><td>The flow of energy and nutrients through different levels of the food web, linking various organisms from primary producers to top predators</td><td>The movement of genetic material between nearby or distant habitat regions over multiple generations</td><td>The movement of individuals, through immigration and emigration, that shapes population dynamics and community diversity</td></tr>
</table>

an individual's genetic composition to a global landscape, across the five subcategories of connectivity (structural, functional, trophic, genetic, demographic) dictates which methods are most appropriate to define connectivity relationships. A glossary of connectivity terms is provided in Table 1.

While each subcategory of connectivity is distinct, they are inherently interrelated and interdependent. For example, trophic, genetic and demographic connectivity rely on functional connectivity. Functional connectivity is particularly relevant in terms of the persistence of fish populations as it facilitates essential life processes such as migration, breeding and dispersal (Flecker et al. 2010; Lake 2011) and is particularly important in systems subject to environmental disturbances or human modifications. Functional connectivity enhances ecological connectivity on trophic, genetic and demographic scales by enabling fish movement and the subsequent transfer of nutrients and energy across disparate habitats. These movements facilitate survival and reproduction, supporting gene flow, enhancing genetic diversity and ultimately contributing to population and community stability (Bruckerhoff et al. 2019).

Connectivity is highly contextual, varying by species, geography, life stage and environmental conditions, as fishes differ in their ability to navigate obstacles separating habitats (Gido et al. 2015). Within open ecosystems (e.g., pelagic areas in oceans, lentic systems in freshwaters), connectivity can be affected by hydrological features like currents and upwelling (i.e., structural and trophic connectivity; O'Dwyer et al. 2021), reducing available habitat and creating barriers between fish populations and communities (i.e., functional and demographic connectivity; Franklin et al. 2024; Heino et al. 2015). Marine connectivity can be altered by energy (tidal and wind turbines) and transportation (bridges, causeways, harbours, docks) infrastructure (Bice et al. 2023; Lennox, Birnie-Gauvin, et al. 2025). Loss of natural habitats, like coral reefs, through natural disturbance events or climate-induced mortality events can also alter connectivity, particularly for smaller reef-associated species (Syms and Jones 2000). Additionally, changes in freshwater discharges that empty into marine environments can alter salinity levels or lead to droughts in low-lying aquatic environments, ultimately disrupting connections between important nearshore and estuarine foraging and nursery habitats (Gillanders and Kingsford 2002; Danylchuk et al. 2023).

In lotic ecosystems, especially river corridors, water flows play a key role in connecting landscape patches where structural connectivity operates across four dimensions, including longitudinal, lateral, vertical and temporal, collectively forming a 'riverscape' (Amoros and Bornette 2002; Fagan 2002). The term riverscape was coined by Leopold and O'Brien Marchand (1968) as a contraction of the terms 'river' and 'landscape', and has been broadly adopted to describe the complex mosaic of perennially interacting river and floodplain conditions (Erős and Campbell Grant 2015; Torgersen et al. 2022; Garvey and Whiles 2023). It extends to 'coastal riverscapes' influenced by downstream factors like tidal intrusion and coastal wetlands (Garvey and Whiles 2023). The branching structure of river networks plays a key role in shaping demographic connectivity; for example, Campbell Grant et al. (2007) demonstrate how dendritic network geometry influences structural, functional, genetic and demographic connectivity among fish populations by affecting movement pathways, dispersal limitations and population dynamics. Seasonal reductions in structural connectivity can isolate fish in suboptimal habitats (e.g., dry periods can strand fish in shrinking pools, limiting movement to refugia; Sedell et al. 1990) and restrict access to essential energy resources, limiting trophic connectivity (Chessman 2013). Anthropogenic modifications like dams, road crossings and water withdrawals can further disrupt connectivity and remain among the greatest threats to freshwater fishes (Gido et al. 2015). Conversely, dynamic discharge events like floods or spring freshets can enhance structural connectivity in fragmented systems, promoting recolonisation and genetic exchange (i.e., functional and genetic connectivity, respectively; Pringle 2003). Floods may also form or restore lateral connections between rivers and floodplains,

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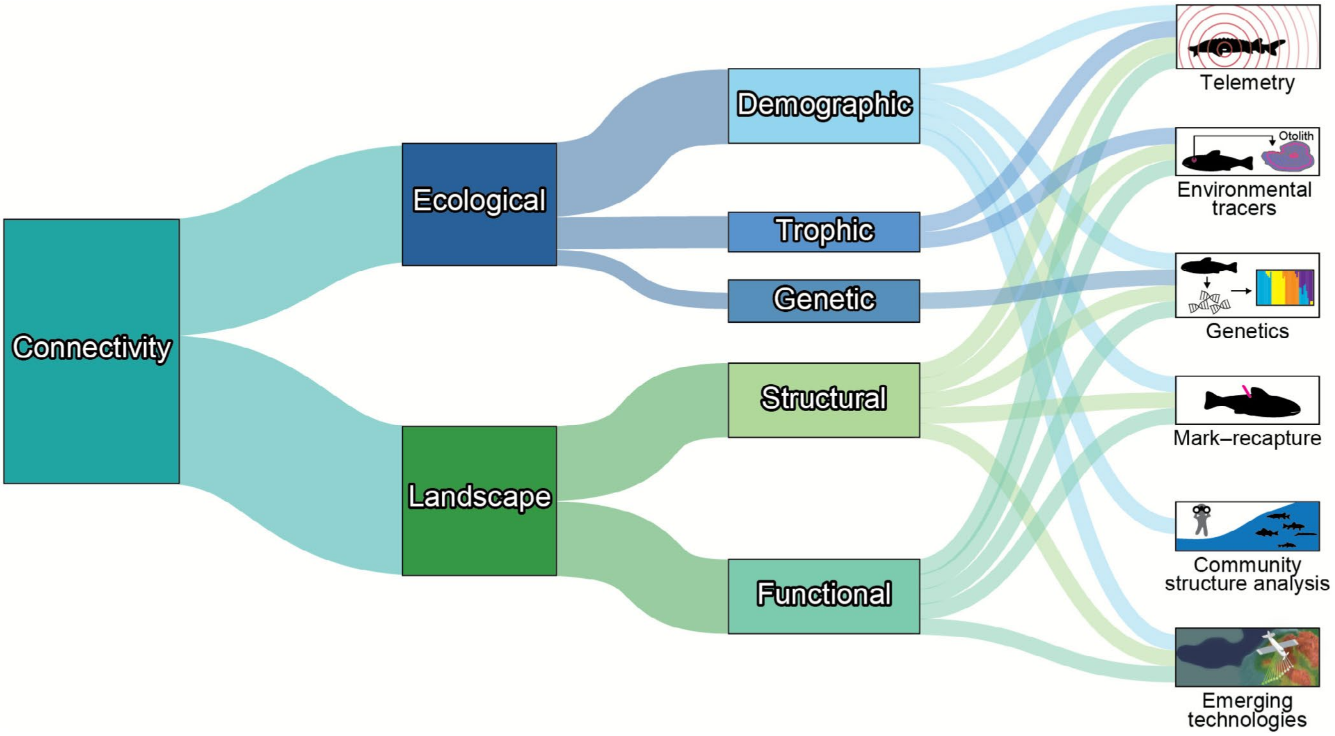

FIGURE 1 | Conceptual diagram of connectivity categories linked with methods for evaluating fish connectivity. Researchers often separate connectivity into ecological and landscape, focusing on demographic-level differences among fish communities, trophic linkages or genetics when studying ecological connectivity, and structural or functional movements when evaluating landscape connectivity. In most cases, there are several methods (icon boxes) to study each form of connectivity. Details of linkages between methods and connectivity subcategories are as follows: Telemetry can evaluate demographic, trophic, structural and functional connectivity; environmental tracers can help elucidate trophic, structural and functional connectivity; genetics may offer insights into demographic, genetic, structural and functional connectivity; mark–recapture and emerging technologies can provide information on demographic, structural and functional connectivity; community structure analysis can contribute to the understanding of demographic connectivity; the emerging tools and technologies we discuss can provide information on demographic, structural and functional connectivity. A glossary of connectivity terms is provided in Table 1 and examples of research that evaluated each category of connectivity are presented in Table 2.

facilitating nutrient and organism movement and providing nursery habitat for juvenile fish, though such flood dynamics are increasingly influenced by both human modifications to river systems and climate change-driven shifts in flow regimes and precipitation (Tockner et al. 2000; Jacobson et al. 2022).

In cases where a permeable in-river barrier (e.g., navigation locks) provides a new movement corridor in a system where fish movements were historically restricted by waterfalls or rapids, the functional connectivity of native species may instead be elevated, or their ranges expanded (Rahel 2007; Bergman et al. 2024). Note, however, that these in-river barriers have also inadvertently facilitated the dispersal of nonnative species by altering natural flow patterns and creating new aquatic connections between previously isolated ecosystems (Rahel 2007). For example, the Welland Canal resulted in the infamous sea lamprey (*Petromyzon marinus*) and alewife (*Alosa pseudoharengus*) invasions across the Laurentian Great Lakes (Smith 1968; Hartman 1972), and to date, 45 non-Indigenous macroinvertebrates have been introduced to the river Rhine via the large-scale Eurasian network of inland waterways (Leuven et al. 2009). Today, rivers and waterways with semi-permeable dams and navigation locks are considered an ‘ecological paradox’ (Bergman et al. 2021) or ‘connectivity conundrum’ (Zielinski et al. 2020) because they may both limit and promote connectivity depending on structural aspects and species capabilities (Piczak, Bzonek, et al. 2023; Piczak, Theÿsmeÿer, et al. 2023). Given the complexity and potential conflicts among riverine landscape management goals, practitioners must evaluate tradeoffs and prioritise strategies that balance wildlife and ecosystem conservation with human use (Fullerton et al. 2010; Rahel and McLaughlin 2018).

The resilience of aquatic populations to environmental disturbances is tightly coupled with the degree of connectivity within and between ecosystems (Timpane-Padgham et al. 2017; Young et al. 2018; Thieme et al. 2023). Understanding, maintaining and restoring connectivity is essential to enhance the resilience of aquatic species and reverse biodiversity loss trends (Beger et al. 2022; Tickner et al. 2020; Thieme et al. 2023). Effective conservation depends on a clear understanding and integration of connectivity into management frameworks (Crooks and Sanjayan 2006). Below, we describe methods for studying fish connectivity for each of the five subcategories of connectivity (functional, structural, trophic, genetic, demographic). See Figure 1 for a conceptual diagram of connectivity categories linked with methods for evaluating fish connectivity.

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TABLE 2 | Examples of methods used to study fish connectivity. A '/' denotes that there is no submethod to evaluate connectivity.

Method	Connectivity type	Submethod	Example	References
Telemetry	Demographic; trophic; functional; structural	Satellite	Satellite tagging, combined with photo identification, revealed that reef manta rays (*M. alfredi*) exhibit long-distance, directional movements between two World Heritage Areas (Ningaloo and Shark Bay) in Western Australia, with individuals travelling up to 700 km, demonstrating previously unknown connectivity across these protected areas	Armstrong et al. (2020)
		Acoustic	Acoustic telemetry was used to examine the movements of grey reef (*C. amblyrhynchos*), silvertip (*C. albimarginatus*) and bull (*C. leucas*) sharks in Australia's Great Barrier Reef Marine Park. While grey reef sharks showed high site fidelity to specific areas, silvertip and bull sharks moved between reefs and across long distances, suggesting they require networks of connected reserves or broader spatial management tools to maintain protections across their ranges	Espinoza et al. (2015)
		Radio	In the Savannah River (USA), American shad (*A. sapidissima*) were tracked using radio telemetry to determine connectivity pathways across the New Savannah Bluff Lock and Dam. Researchers discovered an average of 30% of fish moving upstream via the navigation lock, suggesting that locks may be an effective movement corridor	Bailey et al. (2004)
		Passive Integrated Transponder (PIT)	Mountain whitefish (*P. williamsoni*) are native salmonids distributed throughout the Columbia River Basin, USA, with little known of their tributary-specific life history traits. Researchers used PIT tags to assess movements, discovering previously unknown resident and migratory populations, and suggested that connectivity between tributaries be maintained to support different populations when considering watershed-scale management plans	Snow and Goodman (2021)
Mark–recapture	Demographic; functional; structural	/	Using a long-term (1995–2008) mark–recapture data set, researchers demonstrated that paddlefish (*P. spathula*) maintain unidirectional upstream-to-downstream movement through Missouri River dams, with dam discharge acting as a key driver of connectivity, especially during high-flow events	Pracheil et al. (2015)
Genetics	Demographic; genetic; structural; functional	/	Genetic analysis of Lahontan cutthroat trout (*O. clarkii henshawi*) revealed distinct spatial genetic structure among tributary populations in Nevada's Humboldt River. Gene flow was reduced due to physical barriers and geographic distance, and indicated that migratory individuals could facilitate recolonization of extirpated streams	Neville et al. (2006)
		eDNA	In bays near Hainan Island, China, eDNA revealed that fish communities in natural seaweed and seagrass beds versus cultivated seaweed (*Eucheuma*) areas were significantly different, whereas fish species' compositions in the natural beds were similar. The researchers suggest managing natural beds as single protected units and offer a 'cultivation-protection hybrid model' with recommendations to retain portions of natural *Eucheuma* beds for fish shelter and to limit cultivation to ensure natural habitat persistence	Wu et al. (2025)

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TABLE 2 | (Continued)

Method	Connectivity type	Submethod	Example	References
Environmental tracers	Trophic; functional; trophic	Stable isotopes	In New Zealand, researchers used $\delta^{13}C$ and $\delta^{15}N$ stable isotopes to show that marine-derived amphidromous fish serve as key prey items for longfin eels (*A. dieffenbachii*), demonstrating trophic connectivity between coastal lagoons and inland rivers	Stewart et al. (2022)
		Otoliths	In the Netherlands, European smelt (*O. eperlanus*) connectivity between the (marine) migratory Wadden Sea population and (freshwater) landlocked Ijsselmeer and Markermeer Lakes populations—regions separated by a large dam—was evaluated using otolith microchemistry, revealing no evidence of mixing. Because the lake populations are isolated, researchers suggest adjusting dam operations during spawning periods to improve connectivity	Tulp et al. (2013)
Community structure analysis	Demographic	/	In the Great Plains, USA, researchers evaluated stream fish communities in dendritic ecological networks (DENs) using a Dendritic Connectivity Index (DCI) to quantify connectivity within DENs and assess fragmentation effects. By combining field sampling with DCI modelling, they found that fragmented stream sections had lower species richness and greater community composition variation, indicating that fragmentation disrupts connectivity and homogenises fish communities	Perkin and Gido (2012)
Emerging tools and technology	Demographic; structural; functional	Remote sensing	Researchers used remote Google Earth Imagery and machine learning to identify river barriers globally, providing a comprehensive inventory to guide targeted, on-the-ground efforts to assess and mitigate barriers that may affect fish connectivity	Parks et al. (2024)
		Biological monitoring	The ‘Riverwatcher’ is an automatic, passive and contactless counting device that can support long-term monitoring projects in a low-cost way. Fish are guided through a chute where infrared scanners can provide information on size and species (based on silhouette shape). The Riverwatcher can validate fish passage structure functionality and determine migratory characteristics and abundances of species and populations	Haas et al. (2024)
		Data integration and analytics	Conducted in Buck Island Reef National Monument (USA), researchers applied resource selection functions (RSFs) using machine learning to an acoustic telemetry dataset to model habitat use by four shark species. Unlike traditional methods (raw detection counts, kernel density estimates), RSFs accounted for habitat availability and environmental drivers, revealing species-specific preferences, movement corridors and predator–prey hotspots	Griffin et al. (2021)

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3 | Methods to Study Fish Connectivity

3.1 | Telemetry

3.1.1 | Satellite Telemetry

Over the past four decades, satellite telemetry has emerged as a powerful tool for tracking broad-scale and long-distance movements of oceanic fishes, especially large-bodied pelagic species whose migrations extend beyond the detection range of coastal acoustic telemetry networks (Hammerschlag et al. 2011; Hussey et al. 2015; Renshaw et al. 2023; Robichaud et al. 2025). First applied to fish in the 1980s, satellite telemetry leveraged earlier advancements in terrestrial wildlife tracking that led to the development of miniaturised, waterproof tags (Hockersmith and Beeman 2012). These tags are affixed to each animal externally and can transmit positioning data through the ARGOS satellite system in real time or archive data over the course of a set deployment for batch transmission, depending on the tag type. The first iteration of the modern 'Smart Position or Temperature Transmitting' (SPOT) tag was used to track a basking shark (*Cetorhinus maximus*) off the coast of Scotland for 17 days using ARGOS satellites in 1982 (Priede 1984). Since then, the use of SPOT tags (which transmit real-time position data when the animal surfaces) has expanded significantly, aided by advances in towed and fin-attached designs that enable tracking of individuals for months to years depending on the tag model and programming (Patterson and Hartmann 2011; Hays et al. 2021). A second type of satellite tag, the 'pop-up satellite archival tag' (PSAT), was developed in the 1990s to allow tracking of species that rarely surface, such as Atlantic bluefin tuna (*Thunnus thynnus thynnus*) (Block et al. 1998). In PSAT tags, a battery-powered electrolysis process causes a pin to dissolve at a preprogrammed time to release the tag from the animal and 'pop up' to the surface to transmit light level, temperature and depth data to satellites. Satellite telemetry can provide insights into connectivity across spatially disparate habitats, capturing broad horizontal movements (e.g., structural and functional connectivity; Weng et al. 2007; Lea et al. 2015) and/or vertical dynamics (e.g., depth changes; Andrzejaczek et al. 2019, 2022).

Satellite telemetry is best used to answer broad spatial questions. Both SPOT and PSAT tags have positioning errors, with SPOT errors ranging from under 250 m to unbounded estimates depending on the number of messages transferred between the tag and satellite (i.e., more messages result in increasing spatial accuracy, but require more time at the surface for the tag) (ARGOSweb 2017). PSAT tags generate a position estimate, influenced by movement, light levels, and temperature, making them unsuitable for finer-scale movement studies. Fast GPS-integrated tags, first used on ocean sunfish (*Mola mola*; Sims et al. 2009), offer more accurate positioning (< 100 m; ARGOSweb 2017) by deriving locations through Fastloc-GPS and relaying those locations through the ARGOS system (Thomson et al. 2017). Similar to SPOT tags, these tags require surfacing to transmit, limiting their use to large-bodied, surfacing fishes (Meyer et al. 2018), although one study used a floating towed tag on benthic stingrays in shallow water (Martins et al. 2019). In recent decades, the proliferation of satellite tagging in marine environments (Renshaw et al. 2023) has substantially improved our ability to delineate fish stocks (Gatti et al. 2020; Arostegui et al. 2024), identify species overlap with fishing effort (Queiroz et al. 2019), and explore the spatial ecology of highly mobile fish species for which other forms of telemetry were not feasible (Hussey et al. 2015). For example, PSAT tagging of Atlantic halibut (*Hippoglossus hippoglossus*) in the Gulf of St. Lawrence revealed convergence of all individuals during the spawning season despite being tagged in disparate locations during the nonspawning season, suggesting a single stock management structure in the Canadian Northwestern Atlantic (Gatti et al. 2020). Satellite tags can also provide information on Marine Protected Area (MPA) use by highly mobile species. Satellite telemetry and photo-ID data revealed that reef manta rays (*Mobula alfredi*) regularly moved between two of Australia's UNESCO World Heritage Areas, the Ningaloo Reef and Shark Bay, demonstrating long-range movements of up to 700 km in addition to smaller-scale movements more associated with site fidelity (Armstrong et al. 2020—Table 2). These findings highlighted the role of satellite tracking in identifying movement corridors and informing the effective design and management of MPAs to ensure they encompass the full spatial range of migratory species like manta rays.

Despite expanding our ability to study highly mobile fishes, satellite telemetry has several limitations. While PSAT tags store data, allowing for continuous archiving until the preprogrammed pop-off date, they do not allow for real-time tracking like SPOT and Fastloc-GPS tags can. Researchers must then balance the benefits of long-term deployment duration with the cons of battery drain, since the tag must have enough energy left to transmit its data at the deployment end (battery failures can result in all data being lost). In contrast, the PSAT's strength is the SPOT and Fastloc-GPS tags' weakness; they do not archive time series data. Unlike marine mammals and sea turtles, which are commonly tracked with this tagging technology, fish are not obligated to surface for any length of time. Differences in individual level and overall species behaviours can lead to no transmissions from SPOT tags or transmissions that are too brief to generate a geolocation. Location error is also a challenge for PSAT tags, whose geolocation calculations are based on light level, which can be quite coarse especially in deep or turbid waters (Nielsen et al. 2023). Satellite tags are also large compared to other tagging methods, so researchers must consider tag burden, battery life and the regional scale of their research questions when selecting a tag model and applying this technology to study the movements of large marine (Block et al. 2011; Matley et al. 2025) and anadromous fishes (e.g., sturgeon; Erickson et al. 2011).

3.1.2 | Acoustic Telemetry

Like satellite telemetry, the use of acoustic telemetry has expanded over the last few decades and is primarily used to examine functional connectivity (Cooke et al. 2013; Hussey et al. 2015). Acoustic tags emit a sonic pulse, sending unique identification codes and time-stamped data from tagged fish that is detected and logged by underwater receivers (hydrophones) for later retrieval and analysis of animal presence

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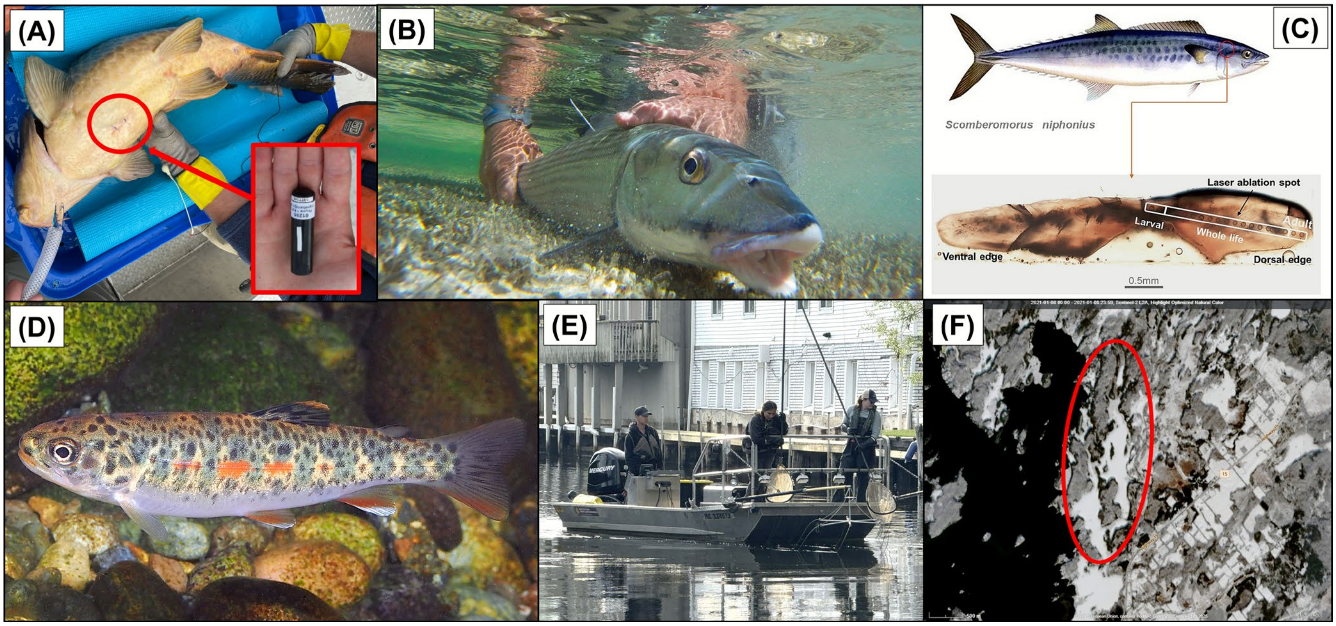

FIGURE 2 | Photo mosaic representing examples of methods for evaluating fish connectivity. (A) Acoustic telemetry: A nonnative common carp (*Cyprinus carpio*) being surgically implanted with an acoustic tag in the Great Lakes to study movement patterns and effectiveness of an exclusion barrier (Piczak, Brooks, et al. 2023); (B) Mark–recapture: A bonefish (*Albula vulpes*) study in the Bahamas Archipelago assessing site fidelity and connectivity between homesites and prespawning sites to inform protected area designation (Boucek et al. 2019); (C) Environmental tracers: Otolith biogeochemistry elucidated effects of a climate event on population connectivity of Spanish mackerel (*Scomberomorus niphonius*) along China's coast (Pan et al. 2024); (D) Genetics: Spatial patterns of allelic variation showed that coastal cutthroat trout (*Oncorhynchus clarkii clarkii*) in western North America found above natural waterfall barriers were highly differentiated from populations below (Whiteley et al. 2010); (E) Boat electrofishing in the Lower Boardman (Ottaway) River, USA was used to sample fish community structure and support assessments of species likely to encounter an in-development fish passage structure ('FishPass'; www.glfc.org/fishpass.php), contributing to understanding demographic connectivity and seasonal patterns of fish movements (Swanson et al. 2023); (F) Sentinel-2 satellite imagery was used to identify the onset of the ice-on period within a Freshwater Protected Area ('FPA'; outlined in red), after which fish appeared unable to move in to, or out of, FPA boundaries (Bergman et al. 2025). Photo credits: (A) Morgan Piczak; (B) Aaron J. Adams; (C) Pan et al. (2024); (D) USFWS—Pacific Region, Wikimedia Commons; (E) Reid Swanson; (F) The Copernicus Data Space Ecosystem Browser. All photos used with permission.

(Heupel et al. 2006; Crossin et al. 2017). Tracking can be conducted manually, using a vessel to locate or follow an acoustic tag, or by positioning autonomous receivers at fixed locations in configurations (e.g., arrays, gates, curtains; overlapping detection zones for 2D or 3D position analysis) that allow researchers to answer specific questions related to regional connectivity, residency and boundary crossing (reviewed in Crossin et al. 2017). In recent years, advances in acoustic tag technology have enabled researchers to collect additional data on variables such as temperature, depth and locomotor activity (Cooke et al. 2013; Matley et al. 2022; Jacoby and Piper 2023). Technological improvements have also made acoustic telemetry more affordable and accessible, broadening its application across various disciplines (Hussey et al. 2015). With respect to studying fish connectivity, acoustic telemetry has been successfully applied in studies on migration (Aarestrup et al. 2014; Larocque et al. 2020), habitat use (Piczak, Brooks, et al. 2023—Figure 2A), Marine (Lédée et al. 2021) and Freshwater Protected Areas (Bergman et al. 2025), and demographic connectivity (Faulks et al. 2011; Espinoza et al. 2015—Table 2). It is a valuable tool for identifying barriers to functional connectivity caused by anthropogenic structures like hydro-dams and navigation locks (Fritts et al. 2021; Bergman et al. 2022, 2024) and assessing restoration efforts after barriers are removed (Roday et al. 2024). The use of predation-style acoustic tags (Halfyard et al. 2017), which transmit a predation code when consumed by a predator, can provide details on trophic and demographic connectivity.

The typical stationary receiver array used for acoustic telemetry (Figure 3A) offers a less-time intensive alternative compared to active tracking methods, like radio telemetry, or traditional sampling methods, such as in-person observations (e.g., snorkelling, SCUBA diving) or fish collection techniques (e.g., netting, trapping, electrofishing), which may be limited by the time and effort researchers can dedicate and the spatial area they can physically cover (Kraus et al. 2018). Once an acoustic telemetry array is deployed and maintained, it will continuously store data without requiring the presence of researchers. This capability makes acoustic telemetry a powerful tool for studying animal movement patterns on scales previously unattainable with traditional fisheries techniques (Lennox et al. 2017).

Acoustic telemetry is primarily limited by the spatial coverage of receiver arrays and the challenges associated with maintenance. These limitations are partially addressed through large-scale telemetry data-sharing networks such as the Riverine Acoustic Fish Telemetry Network (RAFT), Great Lakes Acoustic Telemetry Observation System (GLATOS),

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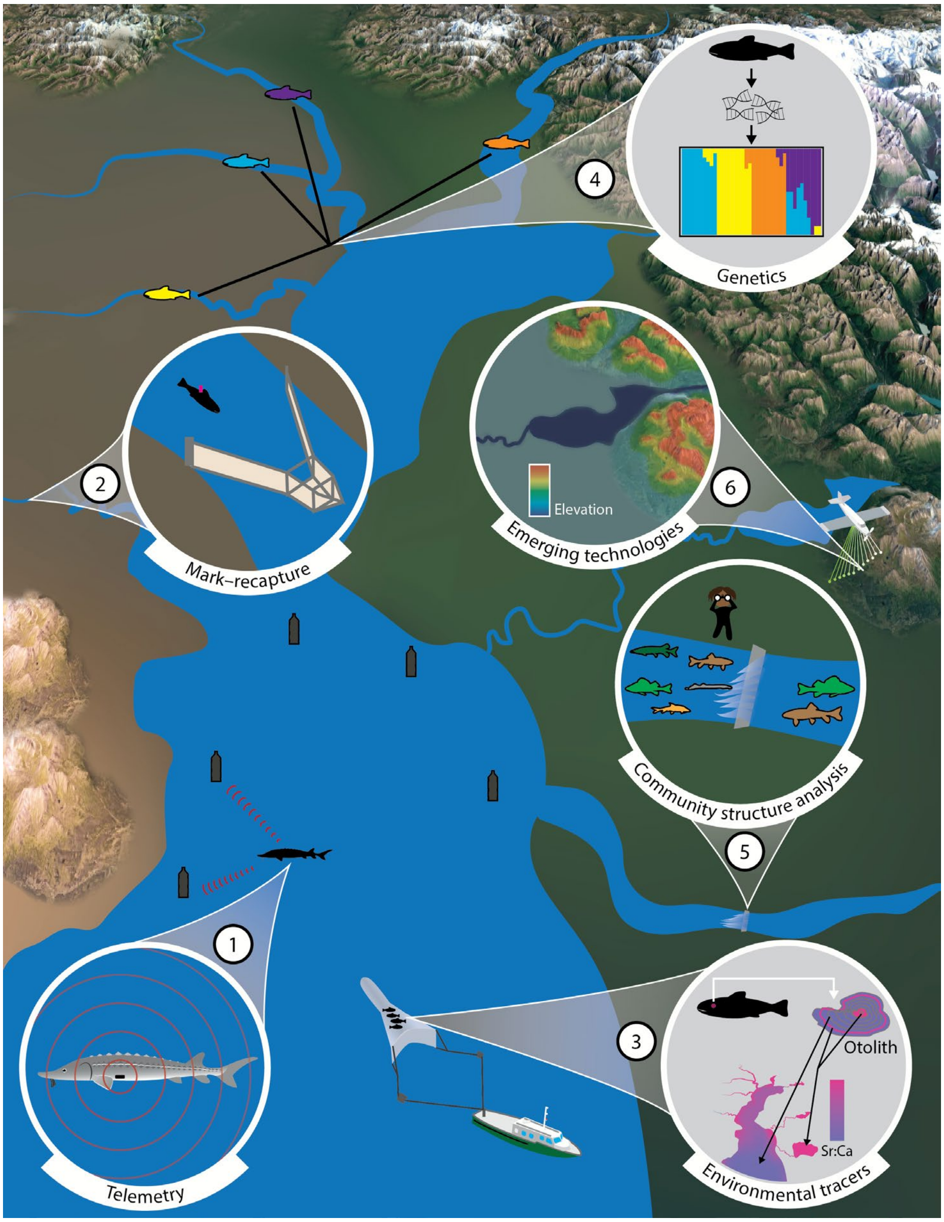

FIGURE 3 | Depiction of methods used to study connectivity of fishes: (1) telemetry (example shown is acoustic telemetry, where an active acoustic transponder is implanted in the fish and a coded acoustic signal is received by submerged hydrophones); (2) mark–recapture (example shown is a downstream migrant trap where tagged or marked individuals are physically recaptured); (3) environmental tracers (example shown is otolith microchemistry, where the otolith of a fish is extracted and individual growth rings are analysed for isotopic content like Sr.:Ca; fish movement is determined by comparing isotopic ratios found in the environment to those in the otolith); (4) genetics (example shown is genetic tissue extracted from fish and sequenced; sequence data are then used to assign individuals to particular groups); (5) community structure analysis (example shown is an evaluation of fish community composition above and below a barrier to determine upstream and downstream connectedness); (6) emerging tools and technologies (example shown is airborne Light Detection and Ranging [lidar] used to create digital elevation maps with high resolution topography and shallow water bathymetry).

Ocean Tracking Network (OTN), the European Tracking Network (ETN) and the Integrated Marine Observing System (IMOS). These networks foster collaboration and enable researchers to extend their studies across larger, shared arrays maintained by multiple users (e.g., Griffin et al. 2018; Piczak, Brooks, et al. 2023). Acoustic detection data are also affected by environmental noise, high tag densities, habitat complexity and/or other environmental factors, reducing detection accuracy (Payne et al. 2010; Selby et al. 2016). As with any study attempting to implant tags to monitor fish movements (especially small individuals), there can be physiological stress associated with tag implantation (Sandford et al. 2020; Vollset et al. 2020), including cortisol responses (Zakęś et al. 2022) and tag shedding (by tag size and species—Kimball and Mace III 2020; by procedure—Moore and Brewer 2021). For both satellite and acoustic telemetry transmitters, there is an unavoidable trade-off among tag size, sampling capacity and battery life, such that the smallest tags do not have a long battery life even when sampling (detection) rates are less frequent. New technological developments and further miniaturisation

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have offered the chance to successfully tag very small and laterally and vertically compressed individuals, though these tags typically have a short battery life (at most a few months) (Lennox, Mastrodimitropoulos, et al. 2025). As such, data cannot be collected on connectivity across life stages. Advances in positioning systems have improved detection precision (Guzzo et al. 2018), which is particularly important for understanding movement barriers; however, the effectiveness of these systems remains limited to areas with sufficiently dense receiver arrays.

3.1.3 | Radio Telemetry

Radio transmitters have long been used to assess functional connectivity of aquatic animals and to track migratory species over long distances in freshwater systems. These devices transmit radio signals (uniquely coded transmissions, or over frequencies unique to an individual) to a receiver with an antenna that is either stationary (Östergren and Rivinoja 2008; Sullivan et al. 2020) or mobile, including actively held by a human (Gilroy et al. 2010) or mounted to a plane, boat, vehicle, or aerial drone (McCleave et al. 1978; Koehn et al. 2009; Munakata et al. 2021). Radio signals travel well in the air and can emit signals across the air–water interface (Kuechle and Kuechle 2012), but limited transmitting capacity occurs as depth increases (> 10 m). Further, radio transmission is almost completely inhibited in saltwater and is best used in freshwater environments (Kuechle and Kuechle 2012). Other important factors that can influence radio signal strength include vegetation density, rock walls, mountains, buildings and electronics (e.g., sonar, hand-held radios). Unlike acoustic telemetry, radio transmitters perform well in 'noisy' environments such as turbulent waters of streams or near dams. Radio tags can be surgically implanted into the body cavity, gastrically inserted or attached externally (Jepsen et al. 2015) for a range of fish body sizes given that the weights of these tags range between 1 to 30 g. Overall, radio telemetry is an excellent tool to elucidate landscape connectivity in freshwater systems in cases where aquatic animals primarily occupy shallow streams, littoral areas or limnetic zones allowing for the unidirectional radio signal to be registered by the receiver antenna (Lucas and Baras 2000).

Radio telemetry can identify functional connectivity of aquatic animals including movement corridors, habitat use and behaviour. For example, radio telemetry has been used to assess diadromous fish migrations in riverine systems (Knight et al. 1977; Gelder et al. 2024) or to learn about home ranges of fishes (Ebner et al. 2011) and habitats used within aquatic systems (Ebner et al. 2011; Hahn et al. 2011). Importantly, radio tracking can assess structural connectedness between spawning tributaries and a main river (Tummers et al. 2016), or between canals and wetlands (Parkos III and Trexler 2014), and has helped identify important spawning habitat locations (Weller et al. 2016) and nursery habitats (Weller and Chow-Frazer 2019). This technology can also be used to assess interactions of fish with anthropogenic barriers in rivers that hinder functional connectivity (e.g., dams, Monan and Liscom 1973; hydropower stations, Grimardias et al. 2022), providing vital data to improve management of fishes that may be blocked by such in-river barriers. For example, in the Savannah River (USA), radio telemetry was used to track American shad (*Alosa sapidissima*) as they interacted with and navigated past a lock-and-dam structure. Although previous studies on fish passage through navigation locks often concluded that locks are poor movement corridors (see Fritts et al. 2021), Bailey et al. (2004) discovered that approximately 30% of tagged American shad used a navigation lock to successfully move upstream during conservation locking operations (i.e., the strategic use and operation of navigation locks to facilitate fish movements), suggesting that conservation locking may offer a viable solution for enhancing fish connectivity in regulated rivers (Table 2).

Manual radio tracking does have limitations and can require considerable labour and a consistent schedule, unlike acoustic or satellite telemetry, which are typically passive. Similar to acoustic and satellite transmitters, there is a size limitation of tags that can be used in small individuals. In addition, while stationary antenna stations may require less effort overall, they still require routine maintenance for data retrieval and battery replacement, much like acoustic receiver networks. However, radio telemetry systems can be deployed as fixed monitoring networks, with some configurations allowing for permanent power and remote data transmission. Finally, radio telemetry is most feasible in freshwater due to the attenuation of radio signals to practically zero in brackish and sea water (due to dissolved salts; Kuechle and Kuechle 2012) and, in addition, is only applicable to monitoring fish residing near the surface of rivers, streams and/or shallow lakes given depth limitations (Lucas and Baras 2000).

3.1.4 | Passive Integrated Transponders

Passive integrated transponders (PIT) are biocompatible, plastic- or glass-encased, microchip-based tags that are implanted internally into individual fish and have been used to track fish movements (i.e., functional connectivity) since 1983 (Prentice and Park 1983; Gibbons and Andrews 2004). Modern PIT tags are relatively small, ranging in sizes from 8 to 32 mm long and 1–4 mm in diameter, are inexpensive (< 10 USD/tag) compared to other telemetry tag types, and are not limited by battery life because they only transmit when energised by a receiver (Smyth and Nebel 2013). PIT tags are detected using Radio Frequency Identification (RFID) which detects an individualised identification code from a tag (typically at a frequency of 134.2 kHz; Bégout et al. 2016) when within range of a receiver to specify individuals (Zentner et al. 2021). PIT tags come in two varieties, full-duplex (FDX) and half-duplex (HDX), each having different benefits. First, FDX tags can receive and send signals simultaneously, allowing for a more efficient tag reading. These devices lack a capacitor, and thus can be smaller than HDX, allowing for use on smaller species and/or juvenile fishes (Watson et al. 2019), though they have a shorter transmission range than HDX tags. HDX tags contain a capacitor that allows it to alternate between reading and receiving transmissions, providing a stronger signal in both directions, and increasing the transmission range at the expense of a larger size and lower read efficiency (Hill et al. 2006).

Functional connectivity is often studied using PIT tags and arrays to track movements of key species between interconnected lotic habitats. These types of data analyses require networks of

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antennae that can be fixed (Booth et al. 2013) or mobile (Booth et al. 2014; Curtis et al. 2024) and offer meter-scale resolution which works well in narrow, shallow systems and in proximity to structures, though they are more limited in open, marine environments. In boreal river systems, where resource availability varies seasonally and spatially, a transponder antenna array was used to track kilometre-scale movements of arctic grayling (*Thymallus arcticus*) and rainbow trout (*Oncorhynchus mykiss*) across a network of connected tributaries to target favourable foraging grounds and elucidate aspects of trophic and functional connectivity (Bentley et al. 2015). Researchers have also used PIT to uncover hidden patterns of population-specific life histories and demographic connectivity across freshwater networks; Snow and Goodman (2021) discovered two distinct populations of mountain whitefish (*Prosopium williamsoni*) with differing life histories—one migratory and one resident—an important finding for managers intending to target or protect specific populations (Table 2). Across smaller spatial ranges, PIT arrays can be strategically used to determine passage success for tagged species to evaluate engineering efforts that support structural connectivity (Weibel and Peter 2013; Jensen et al. 2024). PIT tags are also commonly used to compare the timing of migration events across multiple age classes of wild and hatchery-reared diadromous fishes, especially salmonids (Achord et al. 1996). PIT tagging methods can be used in tandem with mark–recapture frameworks or model simulations (Sabal et al. 2020) to support additional research objectives like estimating abundance, analysing behavioural responses, tracking growth through time or understanding apparent survival (Rudershausen et al. 2019; Kimball and Mace III 2020). In addition, since PIT tags are not limited by battery power, they are often used in parallel with other telemetry methods to efficiently identify individuals during a recapture event in situ and allow for the tracking of animals tagged with other telemetry devices following battery death.

Broadly, there are two main types of limitations associated with PIT tags to study fish connectivity related to performance and welfare. First, there can be issues stemming from feasibility and efficacy associated with detectability, including the need to install and maintain antennas (Brännäs et al. 1994), recapturing individuals (Gibbons and Andrews 2004), variable detection probabilities (Zentner et al. 2021) and environmental fluctuations (e.g., flow rate, O'Donnell et al. 2010). Although PIT is generally considered a less invasive tagging method compared to acoustic and radio telemetry, there has been effort to account for the survival and tag shedding issues that stress can cause by creating predictive models that adjust for tag loss and fish mortality over time (McCutcheon et al. 2025). Despite these drawbacks, PIT tags are still highly successful if appropriately implemented in experimental studies and continue to be widely used in freshwater (Ficke et al. 2012), estuarine (Kimball and Mace III 2020) and marine ecosystems (Calò et al. 2013) because of the relative risk-to-benefit ratio (e.g., no surgery needed) when compared to other tagging technologies.

3.2 | Mark–Recapture

Collecting fish movement data can be challenging and expensive due to difficulties in accessing (often remote) fish habitats, expensive technologies and time and cost commitments from personnel and capture success (Metcalfe and Craig 2012; Ogburn et al. 2017). Researchers have long turned to the capture–mark–recapture method (dating back to 1886; Walton 1886), a widely used technique for estimating movements and migrations among other parameters (e.g., population sizes, survival rates), to mitigate these challenges. Capture–mark–recapture, or simply 'mark-recapture', involves capturing a sample of individuals from a population, marking them in a minimally invasive manner and releasing them back into their environment (Figure 3B). A second sample is then taken to recapture marked individuals, noting information like recapture location to assess distances travelled over time or biometric data like fish size for growth estimates. Usually, a small external tag, labelled with a unique ID and contact information, is attached to the fish so that if a member of the public recaptures a tagged individual, they can report their catch to the respective researchers. Indeed, many studies have reported participatory science (sometimes referred to as 'community' or 'citizen' science), a form of collaboration between professional scientists and amateur volunteers or interested participants (Fan and Chen 2019), to be a low-cost method of collecting high-quality data to support research (Støttrup et al. 2018; Fulton et al. 2019). Today, tagging programmes have been implemented globally, engaging the public in movement data collection on an array of marine (Ortiz et al. 2003; Maggs et al. 2019) and freshwater (Howe et al. 2006; Garrone Neto et al. 2014; Keplinger 2021) species.

In cases where the study species may not be suitable for participatory science (e.g., if the species is not recreationally important and therefore may not be captured by anglers; too small for external tags), researchers may carry out both mark and recapture (e.g., Midwood and Chow-Fraser 2015). In these cases, researchers may use conventional external tags, Visible Implant Elastomer (VIE) tags or coded-wire tags (CWTs) to name a few. VIE tags are biocompatible, coloured marks injected subdermally but visible externally and may be more appropriate for tracking small species or individuals that cannot handle the burden of external tags (Leblanc and Noakes 2012). By using unique colour(s) and injection positions, individuals can be coded to provide unique identifiers (Booth and Shipley 2012). A CWT is a small piece of stainless-steel wire approximately 1 mm long that contains a specific alphanumeric code, identifying an individual or group (containing up to thousands of individuals) of fish released at the same place and time. CWTs have become the cornerstone of one of the world's largest fish tagging programs to monitor Pacific salmonid migrations, survival and hatchery contributions, with millions of individuals tagged since the 1970s (Jensen et al. 2023). This program is managed by a network of US and Canadian federal, state and Tribal/Indigenous agencies, offering an example of a network for understanding the functional and demographic connectivity of salmon across oceans, rivers and international boundaries. CWTs (in conjunction with other methods) have also been used to quantify salmon straying, a phenomenon in which individuals migrate and attempt reproduction at non-natal sites (Quinn 1993). In the context of hatcheries or other anthropogenic interventions, straying may be considered negative as a 'failure to home' (Keefer and Caudill 2014). However, in wild populations, it is a critical evolutionary feature of salmonids that buffers against spatial and temporal variation in habitat

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quality and can allow for the colonisation of new habitats and recolonisation after local extinction (reviewed in Keefer and Caudill 2014). For example, Westley et al. (2025) used long-term (23 years) CWT data from the Columbia River basin, USA to reveal that Chinook salmon straying rates are generally low but can vary among sites and years, with elevated straying linked to warmer water temperatures, fewer returning local fish and local dynamics between specific hatcheries and tributaries. Note that CWTs are not limited to salmonid species and have been used to track functional and structural connectivity of other species like paddlefish (*Polyodon spathula*; Pracheil et al. 2015—Table 2) and pumpkinseed sunfish (*Lepomis gibbosus*; Jarvis et al. 2020).

Regardless of the tag type, mark–recapture can provide the evidence needed to develop new, or refine current, conservation policies. For example, a bonefish (*Albula vulpes*) mark–recapture study in the Bahamas Archipelago assessed site fidelity and functional connectivity between homesites and prespawning sites, informing the designation of six National Parks to protect bonefish habitats (Boucek et al. 2019; Figure 2B). Mark–recapture can also help assess the functional and structural connectivity of anthropogenic barriers (e.g., navigation locks, hydropower dams) to determine species-specific passability (Klinge 1994; Marson et al. 2006; Garrone Neto et al. 2014) and has been valuable in evaluating the effectiveness of invasive species barriers, like electrical barriers (Verrill and Berry Jr. 1995). Interestingly, mark–recapture data can also be compounded or related to telemetry data. For example, telemetry data (including detections from PIT) can serve a dual purpose by functioning as pseudo mark–recapture data, where detections at fixed receivers also act as recapture events (Perry et al. 2012). Similarly, Close-Kin Mark–Recapture (CKMR) approaches use genetic samples that can provide information on functional, demographic and genetic connectivity from the spatial distribution of close relatives (Casas and Saborido-Rey 2023).

Despite the benefits, mark–recapture has limitations, such as low recapture probabilities (Lees et al. 2021) and assumptions that can be difficult to control: a closed population, equal catchability, lasting marks, no impact on behaviour or survival and random recapture (Dennis et al. 2024). Thus, while mark-recapture offers valuable spatial–temporal data on connectivity, it may not be suitable for studies requiring information on mechanisms or specific timing of movements.

3.3 | Environmental Tracers

3.3.1 | Stable Isotopes

Stable isotope analysis (SIA) is an increasingly important tool for understanding connectivity within and across aquatic systems (Hobson 2023). Stable isotopes are intrinsic, biogeochemical chemical markers found in fish tissues that can reflect what individual fish have been consuming, and where, and therefore reflect local trophic patterns (Boecklen et al. 2011). In addition, these markers provide time-integrated information, offering a record of individual geographical use (Hobson 1999). Naturally occurring stable isotopes, such as carbon (δ13C), nitrogen (δ15N), sulfur (δ34S) and oxygen (δ18O), can be measured in the tissues of animals (e.g., scales, muscle, liver, eye lenses, otoliths, etc.) or the environment. Among the commonly used isotopes in fisheries research, carbon, nitrogen and sulfur provide insights on functional, structural and trophic connectivity both individually and collectively when analysed together (Shipley and Matich 2020; Raoult et al. 2024). These isotopes vary predictably across habitats because environmental conditions, such as primary production sources, nutrient regimes, salinity and benthic–pelagic coupling, shape distinct baseline isotope signatures. When consumers feed in those habitats, the spatially structured environmental isotopic baselines are incorporated into their tissues. Thus, comparing fish tissue to these baselines allows researchers to infer structural connectivity by identifying which habitats or regions individuals have occupied and how they move among isotopically distinct environments. Carbon isotopes can trace primary production in marine systems (e.g., nearshore seagrass and mangrove-based production versus offshore phytoplankton sources), nitrogen isotopes can indicate the relative trophic position of consumers within food webs, and sulfur isotopes can help differentiate ecosystems based on their sulfur sources, such as pelagic versus benthic environments or marine versus freshwater systems (Hobson 2023; Raoult et al. 2024). Because different prey sources, habitats, and trophic pathways (e.g., benthic, littoral, pelagic) often have distinct stable isotope signatures, these isotopic differences can act as natural biomarkers, allowing researchers to trace the movements of consumers in response to seasonal migrations, ontogenetic shifts and habitat disturbances (Fry 2006). Indeed, SIA has been widely applied to trophic connectivity studies in fishes across estuaries (Herzka 2005; Reis-Santos et al. 2015), lakes and rivers (Hesslein et al. 1991; Shibata et al. 2011; O'Mara et al. 2021) and marine environments (Rooker et al. 2008; Logan et al. 2020). Moreover, SIA may be more efficient or appropriate in some cases because it does not require marking and recapture (or detecting) of individuals, and it requires only a small amount of animal material, making it an effective method for small individuals (Durbec et al. 2010).

Fundamentally, SIA can help determine the energy pathways and the habitats animals rely on (Boecklen et al. 2011) and answer applied questions related to stock structure and the timing and locations of ontogenetic shifts and migrations (Hobson 1999; Rubenstein and Hobson 2004; Shipley et al. 2021). Stable isotope mixing models have traditionally been used for trophic connectivity when quantifying dietary contributions in foodscapes (Fry 2006; Farly et al. 2019; Stewart et al. 2022). At larger spatial scales, 'isoscapes' (i.e., gradients of isotopic baselines) allow the probabilistic determination of origins based on geographic isotope variability (Bowen et al. 2005; Bowen 2010). By comparing tissue samples from fish to the isotopic composition of an isoscape, its migration or origin can be estimated and, thus, provide a means to also examine structural and functional connectivity (Hobson et al. 2010). For example, within the marine environment, isotopic variation influenced structural connectivity; including oceanographic processes, such as temperature and productivity gradients, has informed the geographic origins and movement patterns in migratory teleosts and elasmobranchs (Trueman et al. 2012). Integrating SIA with complementary approaches is also expanding its utility to understand other types of connectivity. In the Florida Keys, USA, Brownscombe et al. (2023) used a telemetry-based regional isoscape to examine structural and functional connectivity of permit (*Trachinotus*

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falcatus), resulting in a median reliance of 70% on seagrass-based prey (range: 29%–100%). Despite frequent and extensive movements to and from the Florida Reef Tract, permit primarily relied on seagrass flats as their main energy channel. In contrast, permit associated with artificial reefs exhibited higher residence periods and reliance on pelagic and offshore energy channels, such as planktonic sources. As advances continue, the integration of SIA and complementary methodologies will play an increasingly important role in determining fish habitat and trophic connectivity with greater precision and broader applicability, enabling more advanced spatial ecological paradigms.

Foodscapes, which encompass the spatial and trophic connections between habitats, play a critical part in shaping consumer–resource interactions across ecosystems (Rossi et al. 2024). While there is considerable historical literature on predator (consumer) movements facilitating cross-system trophic connectivity, prey (or resource) movements across ecosystem boundaries represent a 'second axis' of trophic connectivity, which can affect demographic connectivity. For example, recent research highlighted the importance of small amphidromous fishes in transporting marine-derived resources into lowland streams and rivers, thereby contributing to freshwater food webs (Engman et al. 2021). Stewart et al. (2022) further demonstrated with δ13C and δ15N that amphidromous fish prey serve as an important trophic subsidy for the threatened New Zealand endemic longfin eel (*Anguilla dieffenbachii*), emphasising the need for conservation efforts to extend beyond upstream riverine habitats to include coastal barrier beach lagoons, key 'food-producing habitats' (Table 2). Even within foodscapes, prey movements can serve as an important determinant of trophic connectivity and the ultimate source of energy supporting fisheries production. For example, along the US Atlantic coast, the consumption of mysids (small shrimp-like crustaceans that undergo diel vertical migrations) by epibenthic fishes resulted in bottom-associated fishes having tissue δ13C stable isotope values comparable to small pelagic forage fishes in the same region (Woodland and Secor 2013). In this region, the movement of mysids serves as a biological vector transporting fresh pelagic production to benthic pathways, contributing an estimated 32%–55% to the growth of certain epibenthic fishes based on two-end member stable isotope modelling (Woodland and Secor 2013). In the Baltic Sea, Kiljunen et al. (2020) used stable isotopes to identify a similar, albeit inverse, trophic interaction between mysids and Atlantic herring (*Clupea harengus*) in which mysids served as a vector of benthic production to the pelagic zone. In both instances, prey movements provided a mechanism for the transport of biomass and energy between habitats, enhancing trophic connectivity within the foodscape and yielding an important trophic subsidy to consumers.

SIA is not without limitations as interpretation can be confounded by preservation techniques, overlapping isotope values among habitats or prey resources, temporal variability in baseline values and uncertainty in trophic discrimination factors, all of which may reduce ecological inferences (Kelly et al. 2006; Bond and Diamond 2011; Shipley and Matich 2020). Further, while stable isotopes have been used to describe spatial patterns of movement at various scales as noted in the examples listed above, studies are most typically conducted at larger spatial scales (e.g., continental; Durbec et al. 2010) with relatively few studies conducting finer spatial scale analysis (e.g., within a few kilometres, though see Haas et al. 2009; Cunjak et al. 2005; Harrod et al. 2005). A promising development in SIA for understanding fish connectivity is Compound-Specific Isotope Analysis (CSIA), using individual amino acids or fatty acids rather than bulk tissue. While the cost of CSIA can be prohibitive, it allows clearer separation of baseline and trophic processes, reducing uncertainty in trophic enrichment estimates (McMahon and McCarthy 2016).

3.3.2 | Otoliths

Otoliths are calcified structures located within the inner ear of teleost fishes that accrete layers over time, incorporating trace elements and isotopes from the surrounding environment (Thorrold et al. 2001). The shape, chemical signatures (stable isotopes) and/or trace elements (most frequently Strontium [Sr], Barium [Ba], Manganese [Mn] and Magnesium [Mg]) found in otoliths can be used to reconstruct environment or habitat use histories and infer associated movement patterns and natal origin, providing a useful tool to assess functional and demographic connectivity (reviewed in Secor 1999 and S. E. Campana 2005; Elsdon et al. 2008). In freshwater, estuarine and marine systems, otoliths and/or other calcified structures (e.g., statoliths of cephalopods, vertebrae of elasmobranchs, fin rays and fin spines in bony fishes) have been widely used to investigate connectivity of organisms (Gillanders 2002; Reis-Santos et al. 2015; Zampatti et al. 2021; Figure 3C). Otoliths have the advantage in that all fish are inherently 'marked' from an early age (i.e., relative to other manual methods such as biotelemetry), whereby information in the form of isotopes and trace elements is usually permanently stored in the otolith and is related to the age of the fish (Elsdon et al. 2008). The simplest approach focuses on examining otolith shape (Ferguson et al. 2011) or whole otolith elemental and SIA to assess population associations (Campana 1999). The premise is that differences in otolith shape and/or chemistry among populations or communities suggest a lack of ecological connectivity, although similar otoliths do not necessarily imply connectivity (Campana et al. 2000).

Increasingly, lifetime movements and life-history patterns are extracted based on different 'signatures' being incorporated as fish move throughout environments. For example, Sr and Ba tend to be positively and negatively related to salinity, respectively; if a fish moved from freshwater to marine waters it would likely have lower Sr:Ca and higher Ba:Ca associated with freshwater compared to when it was in marine waters (Sr and Ba are usually ratioed to Ca). Chronological information in relation to age and growth can then be extracted and used to better understand aspects of landscape and ecological connectivity. For example, Brophy et al. (2020) used δ13C and δ18O values derived from Atlantic bluefin tuna otoliths to infer natal origins and assess the timing and degree of mixing between individuals from geographically separated spawning stocks (i.e., functional and demographic connectivity). In another example, Tulp et al. (2013) evaluated otolith strontium (^{88}Sr) patterns of European smelt (*Osmerus eperlanus*) collected from the Wadden Sea (marine) and landlocked lakes IJsselmeer and Markermeer (freshwater) in the Netherlands, regions fragmented by a large dam (Table 2). They found

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significantly higher ^{88}Sr concentrations in marine fish, with no indication of mixing between the marine and landlocked populations. Given declines in the landlocked stocks and their important ecological role as key prey for piscivorous birds, this study shows how otolith chemistry confirmed that an artificial barrier is disrupting ecological and trophic linkages and reducing demographic connectivity.

Several methods exist for determining fish movement and migration using otoliths, varying based on the number of fish groups studied, the use of chemical profiles across otoliths, and whether natural environmental signatures or applied chemical tags are evaluated (Elsdon et al. 2008; Walther and Limburg 2012; Thomas and Swearer 2019). Much of the work has focused on natural tags (information naturally acquired in otoliths) but several studies also demonstrate ecological connectivity among groups using applied tags such as tetracycline (Jones et al. 1999) or an unnatural isotopic ratio of a common element (Almany et al. 2007). For example, Jones et al. (1999) marked embryos in the field with tetracycline, subsequently collected larvae settling onto a reef, and examined their otoliths to determine if they were marked. Using this approach, researchers were able to examine functional and demographic connectivity by demonstrating return to natal reefs and self-recruitment of 15%–60%. Almany et al. (2007) used a different marking approach whereby they marked mothers with enriched ^{137}Ba isotopes that were transmitted to offspring before hatching. Two months after marking, recently settled fish were collected and researchers examined daily growth increments in otoliths to confirm they were born after mothers were marked and then examined the core of the otolith to determine if the fish were tagged. Using this approach, they demonstrated return of larval fish to natal reefs with 17%–60% returning depending on the species. Other approaches trace juvenile or adult fish back to their larval (in the case of juveniles) or juvenile (in the case of adults) habitats (Gillanders and Kingsford 1996; McMahon et al. 2012) based on naturally occurring elements or isotopes in otoliths. For example, Gillanders and Kingsford (1996) demonstrated functional connectivity between estuarine nursery habitats and adult rocky reef habitats by analysing trace elements in otoliths of juvenile fish from estuarine seagrass and rocky reef habitats.

Similarly, naturally occurring elements or isotopes can be analysed in profiles across otoliths with variation used to identify functional connectivity among different water bodies. For example, Elsdon and Gillanders (2005) assessed whether freshwater occupancy of black bream (*Acanthopagrus butcheri*) could be inferred from otolith Ba:Ca ratios whereby otolith Ba:Ca of fish was correlated with ambient Ba:Ca. They discovered a strong correlation, with fish caught in freshwater showing roughly double the Ba:Ca of fish captured in saltwater. These ratios successfully identified fish residency patterns and revealed multiple migratory behaviours of fish within the same estuary. This approach has also been used to determine partial migration in fish whereby some individuals in a population moved and others remained resident (Gillanders et al. 2015). Interestingly, a study by Pan et al. (2024) used otolith biochemistry to assess effects of a climate event—El Niño—on population connectivity of Spanish mackerel (*Scomberomorus niphonius*) along China's coast during the 2015–2016 event (Figure 2C). They analysed elemental ratios (Ba:Ca, Mg:Ca) in otoliths from age-1 individuals across three consecutive years (2016–2018), observing significant increases in these ratios during the El Niño year. Their results indicated that during the El Niño year, there was large-scale movement of mackerel between the East China Sea and the Yellow Sea, but in the following years, local spawning groups appeared to be more self-sustaining, suggesting that extreme climate events like El Niño can profoundly affect the functional connectivity of migratory fish populations. Collectively, these studies demonstrate the importance of otolith chemistry for spatially reconciling population structures, life histories and movement patterns of fishes. However, researchers have cautioned that otolith chemistry can come with limitations like overlapping chemical signatures in similar habitats and that data interpretation requires assumptions about water chemistry stability that may not capture movements if environmental gradients are ephemeral or weak (Elsdon et al. 2008; Sturrock et al. 2012).

3.4 | Genetics

Genetic connectivity among populations is imperative for the maintenance of genetic diversity and adaptive potential in wild populations of fish (Rubidge et al. 2012; Klingler et al. 2021; Figure 3D). Habitat fragmentation erodes structural connectivity and can ultimately affect functional and genetic connectivity, resulting in isolation and acceleration of the loss of genetic variation through demographic and genetic stochasticity within populations (Pflüger et al. 2019; Klingler et al. 2023). Genetic data collection, beginning with protein electrophoresis and continuing into the present genomic sequencing era, has allowed biologists to genotype individuals at specific loci within populations and characterise the gene pool. Statistical comparison of alleles and allele frequency across multiple loci within and among populations provides an estimate of gene flow (Hamilton 2021). Subsequent breeding among immigrant and resident individuals acts to increase genetic connectivity and similarity among populations and provide novel genotype combinations that may increase fitness. By comparing genetic similarity and structure, researchers can determine whether fish from different locations are mixing, isolated, or have restricted movements, offering insights into genetic connectivity among wild and/or farmed populations (e.g., Spies et al. 2018; Fazzi-Gomes et al. 2021; O'Dwyer et al. 2021). Allozymes, mitochondrial DNA, and nuclear microsatellites were the genetic marker systems that dominated the conservation and population genetic field for the past 20–30 years (Grover and Sharma 2016); today, whole genome sequencing, RADseq approaches and the development of GTseq panels have increased our ability to characterise all or significant portions of the genome of individuals, whole populations, watersheds, regions and entire management units (Saglam et al. 2017; Supple and Shapiro 2018; Amish et al. 2019; Bohling et al. 2021; Chang et al. 2021). With the advent of genomic sequencing methodology, we can now characterise large portions of the entire genome at both neutral genetic and adaptive trait loci to more accurately quantify gene flow and connectedness and estimate genetic diversity and adaptive potential.

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Patterns of genetic variation provide statistical power to understand the effects of anthropogenic changes that may be impeding the ability of fishes to move among habitats and fulfil their life history. This is a comparatively powerful framework, as tracking physically tagged individuals in real time can be logistically challenging and provides no information on subsequent breeding or historical patterns of movement. In addition to Wright's F statistics (Weir and Hill 2002), which measure the extent of genetic differentiation through allele frequency differences and the presence of unique variants, Bayesian genotype clustering analysis (Pritchard et al. 2000; Gompert et al. 2014) uses the probability of specific genotypes based upon allele frequencies and assumptions of Hardy–Weinberg equilibrium to identify groups (clusters) of interbreeding individuals. Bayesian analysis assigns individuals to a genotype cluster (population) of origin. Genetically identified populations overlaid onto landscapes can identify real boundaries and reveal generational movement (Brown et al. 2016; Neville et al. 2016; Peacock et al. 2016). In cases of individuals with mixed ancestry (i.e., proportional membership in multiple genotype clusters), the parents reflect different genotype clusters and therefore interbreeding and admixture.

Landscape genetics/genomics combines population genetics and landscape ecology to help elucidate genetic connectivity, as well as effects of habitat fragmentation and other human disturbances on functional connectivity. The literature is replete with studies using genetic data to characterise movement patterns of fish species and the landscape correlates of these patterns. For example, Whiteley et al. (2010) used spatial patterns of allelic variation to show that coastal cutthroat trout (*Oncorhynchus clarkii clarkii*) above natural waterfall barriers in western North America were highly differentiated from populations below the barriers, therefore demonstrating natural inhibition of functional and genetic connectivity (Figure 2D). Geological evidence suggests that above-barrier populations have been isolated from downstream populations for 8000–12,500 years and that gene flow was also unidirectional from upstream to downstream with the isolated upstream populations having lower levels of genetic variation. In another example, Neville et al. (2006) used genetic data to characterise the functional connectivity of the endangered Lahontan cutthroat trout (*O. c. henshawi*) in one of the last large, interconnected stream systems it inhabits (Table 2). They identified both resident and migratory life histories, with spatial genetic structure in tributaries indicating isolation by barriers or distance. Evidence of extirpation and recolonisation supported a metapopulation dynamic, dependent on the connectivity and habitat diversity of large watersheds. Migratory individuals play a key role in recolonising extirpated tributary populations, while tributaries act as refugia during droughts. Similar genetic patterns supporting the historical importance of large, connected watersheds have been documented in other inland cutthroat trout subspecies (e.g., *O. c. lewisi*, *O. c. utah*, *O. c. bouvieri*; Eaton et al. 2018; Budy et al. 2017, 2020; Kaeding 2023).

Environmental DNA (eDNA) is an additional genetic method that can be used to monitor fish connectivity by detecting species' genetic material in water, indicating where fish are present and how/if they move across geographic regions or barriers. This noninvasive method has improved our ability to detect fish species while reducing sampling bias, removing the need to handle animals and has proven useful for assessing functional connectivity across both marine and freshwater ecosystems (see Yamanaka and Minamoto 2016). In freshwater ecosystems, eDNA has been used to track recolonisation after dam removal, such as in the Elwha River (Washington, USA) where anadromous fishes were newly detected upstream post-barrier removal (Duda et al. 2021). In marine environments, eDNA has been used to compare fish community structures (also see Section 3.5: Community Structure Analysis) across different coastal habitat types to evaluate functional connectedness, indicating key differences in species present at embayment habitats versus open coastal regions (Waters et al. 2023). In a different marine study, Wu et al. (2025) used eDNA to sample fish communities from three habitat types near Hainan Island (China): a natural Sargassum seaweed field, an adjacent natural *Enhalus acoroides* seagrass bed, and a cultivated *Eucheuma gelatinae* seaweed zone (Table 2). They detected 156 fishes, but only 7% were detected across all habitat types; the fish assemblages in the natural seaweed and seagrass habitats were analogous, indicating demographic connectivity; however, the cultivated bed was significantly different and had the lowest number of species present. This work underscores how habitat type and management (i.e., natural versus cultivated) can influence fish community composition and connectedness. Although eDNA provides a number of benefits, including its ability to detect cryptic species, capture a greater number of species compared to conventional methods, and sample at a greater spatial and temporal scale due to ease of use, it currently has known limitations such as false positives and its ability to only apply basic species data (i.e., cannot offer size frequency, sex ratio or absolute abundance data; discussed in Waters et al. 2023). Regardless, the above examples provide valuable insights into local biodiversity and how fish populations are functionally linked across seascapes and riverscapes.

Levels of genetic variation, measures of effective population size and extent of genetic differentiation can be used to develop recovery strategies and for effective monitoring of species at risk. Although researchers have cautioned the use of genetics to evaluate fish connectivity given potential lag times in detecting connectivity changes and/or capturing short-term changes in connectedness (e.g., it may take up to 200 generations for microsatellite markers to reach equilibrium after isolation begins; Cossu et al. 2022), advances in next-generation genomic approaches, such as single nucleotide polymorphism (SNP) analyses, can detect divergences more rapidly. For example, SNP data have been used to detect the effects of fragmentation due to dams, and subsequent post-dam removal, on timescales far less than 200 generations; Fraik et al. (2021) detected significant shifts in the genetic structure of steelhead (*Oncorhynchus mykiss*) populations on the Elwha River within two generations (< 5 years) following dam removal. Regardless, if researchers require the actual or fine-scale use of specific habitats, genetic methods may need to be combined with complementary tagging or behavioural studies (Cooke et al. 2008; Washburn et al. 2020).

3.5 | Community Structure Analysis

Unlike the previously listed methods that directly quantified fish connectivity, community structure analysis instead offers

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indirect inference based on spatial and/or temporal patterns in species assemblages to examine demographic connectivity (Figure 3E). Examples of tools to assess fish community structure include traditional fisheries approaches (e.g., passive and active nets), backpack and/or boat electrofishing, eDNA, and telemetry. These techniques allow researchers to detect species presence, relative abundance, community composition or individual movements across geographic regions and seasons (Evans et al. 2017; Radinger et al. 2019). Though community composition metrics, like alpha diversity (a community's species richness) and beta-diversity (difference in species composition between two or more sites/habitats) (Whittaker 1972), do not themselves quantify connectivity, spatial patterns such as a high composition overlap would suggest landscape and demographic connectivity among habitats/sites/regions. These inferences can become more powerful when combined with species traits like dispersal capacity or life history, abiotic environmental or habitat data, and hydrological models of movement pathways or corridors. For example, Felin et al. (2025) investigated the role of local and whole-basin functional and structural connectivity in fish species distribution, designing connectivity indices based on river network characteristics and each species' mobility characteristics, and including them in a species distribution model to consider habitat suitability and quantify their role in fish distribution patterns. They found that connectivity indices that took the local context of the area into account performed consistently better than others, noting that fragmentation caused lower likelihood of presence for many non-diadromous river fish species.

Moreover, integrating community structure with complementary tools can connect compositional patterns with a mechanistic understanding of movements. For example, fish community sampling was conducted in the Lower Boardman (Ottaway) River (Michigan, USA) to provide a baseline assessment and migratory patterns of fishes that may encounter a fish passage structure being constructed by the Great Lakes Fishery Commission in North America called “FishPass” (www.glfc.org/fishpass.php; Figure 2E). The FishPass project aims to reconnect the Boardman River with Lake Michigan by replacing a deteriorating dam with a complete barrier (to all fish) and an adaptable fishway designed to support automated or semi-automated selective, bidirectional fish passage. This system would enable native species to pass while blocking harmful invaders like sea lamprey. Swanson et al. (2023) evaluated fish community assemblage and associated fish movement patterns using a suite of methods (e.g., boat and backpack electrofishing, PIT and radio telemetry) to determine which species would encounter FishPass and if seasonal patterns of occurrences existed. Their study demonstrated phenological variation in movement patterns across their study species coinciding with seasonal shifts in the relative abundance of species observed within the fish community sampling (i.e., demographic connectivity). A large proportion of radio telemetered (73%) sea lamprey encountered the dam, with observations suggesting they challenged the barrier multiple times. Native species had variable tendencies to encounter the dam, and their tendency to encounter decreased after subsequent entry events into the river. This study is an on-the-ground example of a community structure analysis that identified species that managers should consider in a management intervention and functional aspects of such movements, offering the evidence necessary for effective management of a fish passage solution. By leveraging innovative approaches (i.e., this could also be considered an emerging technology, see section below), FishPass aims to address one of the greatest challenges in fisheries management: ensuring the passage of desirable fish at a barrier while preventing the spread of invasive fishes (i.e., ‘selective fragmentation’, Rahel and McLaughlin 2018; Zielinski et al. 2020), with the long-term goal of fully automated selective passage.

Community structure analyses that integrate species traits can reveal how habitat fragmentation and flow alteration affect fish connectivity in regionally specific contexts. Perkin et al. (2015) investigated fish communities in Great Plains streams (USA), where intermittent flows and extensive agricultural water use have altered hydrologic regimes (Table 2). They documented declines in headwater specialists, such as the plains minnow (*Hybognathus placitus*) and western silvery minnow (*H. argyritis*), species particularly sensitive to fragmentation and dewatering. By combining beta-diversity metrics with trait data, the researchers showed that fragmentation and flow reductions disproportionately affected small-bodied, dispersal-limited fishes, resulting in an altered community structure downstream of water withdrawals and anthropogenic barriers. Research like this emphasises the critical role of maintaining hydrological connectivity to support vulnerable species and informs water management policies that balance human use with ecological integrity. Linking shifts in community structure to species' functional traits and environmental stressors offers a nuanced approach for conservation prioritisation in fragmented river systems that experience dewatering, providing insights beyond those obtained through direct movement tracking alone.

Although community structure analysis provides valuable information about fish connectivity, this method, too, has limitations. The approach relies heavily on detecting changes in species presence or relative abundance, which may be affected by numerous confounding factors beyond connectivity itself, including seasonal variability, sampling biases or habitat heterogeneity (Gotelli and Colwell 2001; Legendre and Legendre 2012). Moreover, compositional overlaps do not always differentiate between transient movements and actual demographic exchange, potentially overestimating true demographic connectivity (Lowe and Allendorf 2010). As such, community structure analysis may be most powerful when integrated with other methods such as movement data, genetic analyses or hydrological modelling to provide a comprehensive and mechanistic understanding of connectivity. Careful study design and multimethod approaches appear essential to overcome these limitations and effectively estimate demographic connectivity to inform conservation and management decisions.

3.6 | Emerging Tools and Technologies

Recent advances in data analyses and technology have revolutionised the way we can monitor fish connectivity, enhancing our understanding of fish passage and movements, water flow and overall ecosystem health. These technologies span remote sensing, biological monitoring, and data integration and analytics. In some cases, emerging technologies may be a standalone

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technique to evaluate connectivity, whereas in other examples they have been blended with the above-mentioned methods to achieve more comprehensive results.

Remote sensing can be used to evaluate structural connectivity of the land- and water-scape. High-resolution satellite imagery, freely accessible through services like Google Earth and Sentinel-2 via the Copernicus browser (https://browser.dataspace.copernicus.eu/), has been used to identify seasonal hydrologic or geomorphological patterns related to fish movements that may affect connectivity in freshwater environments (Galia et al. 2023). For example, high-resolution (10 m horizontal RGB) Sentinel-2 images were used to determine ice-on and ice-off periods and combined with acoustic telemetry data to investigate potential seasonal barriers (i.e., ice) to fish movement, providing key information to managers related to both structural and functional connectivity, as well as overwintering habitats (Bergman et al. 2023, 2025—Figure 2F). Similarly, light detection and ranging (lidar) data can be used to create digital elevation maps (DEMs) or digital terrain models (DTMs) to study water flow (i.e., reconstruct stream networks) at basin-wide scales to provide broad scale information on water-scape features that may hinder structural connectivity (e.g., water falls, velocity barriers) (Hedger et al. 2020; Andualem et al. 2024; Figure 3F). Together, these remote sensing tools can help map and evaluate the impact of potential natural and artificial disruptions to structural connectivity at broad scales more efficiently than on-the-ground surveys (Parks et al. 2024—Table 2).

Underwater imagery using ultrasonic sensors (e.g., ARIS, DIDSON, recreational side-scan, forward-facing sonar, live-view sonar) or visual spectrum photography are also useful for monitoring fish passage and community assemblages (i.e., functional and demographic connectivity, respectively; Schramm et al. 2020; Haas et al. 2024—Table 2). Baited Remote Underwater Video Systems ('BRUVs') offer a noninvasive, fishery-independent method that can be used to assess demographic connectivity via fish assemblages and provide valuable insights into species presence and diversity, relative abundance and spatial distribution. When BRUVs are deployed strategically across habitats or management zones (e.g., protected areas, spatial closures), they can offer information on functional connectivity by capturing patterns of habitat use and occurrences over time (Santana-Garcon et al. 2014; Hall et al. 2021). While underwater cameras provide high-resolution images of fish in controlled settings (i.e., a fish counter within a fishway) or automated remote settings, they can be hindered by high turbidity or low light levels. Sonar techniques such as hydroacoustics are not impacted by water clarity or light levels, but object identification can be more difficult (Le Quinio et al. 2023). For example, Piczak et al. (2025) used down-looking hydroacoustic surveys and trawls (bottom and mid-water) to evaluate fish community composition inside versus outside harmful algal bloom areas, revealing no significant differences between areas, and suggest that bloom zones in their study were not a total barrier or 'dead zone' to fishes. Advances in machine learning and image detection or recognition software that reduce the need for significant investment in data storage and analyses have made these technologies more widespread in their deployment (Barbedo 2022) and can also be integrated into selective fish passage solutions (Grasty et al. 2021). Passive acoustic monitoring ('ecoacoustics') is another emerging technology that has been used more extensively in marine habitats to record animal sounds or track movement of vocal animals (Miller 2012), offering insights beyond communication, but also community composition and functioning of the ecosystem, and is not limited by turbidity like BRUVs (Stowell and Sueur 2020). In addition, artificial intelligence and machine learning approaches have benefited from the analyses of large datasets to identify patterns in structural connectivity and predict disruptions (Buchanan et al. 2022). Machine learning techniques have been applied to the analysis of telemetry data to (1) improve the accuracy of resource selection functions, which are used to determine and predict relative habitat selection by animals (Griffin et al. 2021—Table 2), (2) infer differential movement and space use patterns by fish in areas where receiver coverage is poor (Williamson et al. 2021) and (3) integrate with environmental data to identify potential spawning aggregation sites (Brownscombe et al. 2020).

Thanks to the prevalence of smartphones with GPS capabilities, high-resolution cameras and continuous internet connections, crowdsourcing biological data collection has become a more common approach to collecting near real-time data on fish distributions (Radinger et al. 2019). An innovative application of crowdsourcing to inform functional connectivity of freshwater fishes is the 'fish doorbell', where people from around the world are able to monitor a live feed of an underwater camera for fish and report (i.e., ring the doorbell) fish presence to fisheries scientists in Utrecht, NL to operate a gate, allowing fish to pass (https://visdeurbel.nl/en/). Apps can also provide information to managers and scientists on distributions of fishes, like 'AquaInvaders' (http://naturelocator.org/aquainvaders.html), which focuses on nonnative aquatic species.

4 | Knowledge Gaps

While current and emerging technologies have provided opportunities to gain a better understanding of landscape and ecological connectivity to effectively manage fish populations, several knowledge gaps remain. There is often a taxonomic bias with respect to conservation-related studies with certain species or groups of species receiving more funding and prioritisation over others (Donaldson et al. 2016). Whether charismatic megafauna (e.g., sharks; Mazzoldi et al. 2019), flagship, or umbrella species (Kalinkat et al. 2017), or a focus on recreationally or commercially important or invasive species (Landsman et al. 2011; Rypel et al. 2021; Brown et al. 2025), a lack of understanding of fish connectivity on all trophic levels undermines comprehensive management strategies. Management paradigms are changing where ecological knowledge of species across trophic levels and recreational importance are valued to understand ecosystem functioning.

Similar to taxonomic biases, it is important to be aware of geographic biases that exist in the literature due to remoteness of access and/or limited accessibility of funds/resources/technologies to researchers in different parts of the world (Kot

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et al. 2023). These biases present opportunities for capacity and relationship building and can be mitigated by coordinated programs such as large tracking networks that could leverage infrastructure across regions (e.g., OTN, ETN; Matley et al. 2022). Despite diverse methodologies for studying connectivity, access to understanding deep-water movements in marine and freshwater environments is limited by logistics and abilities to sample these areas given the technologies available to date. Even in more accessible urban areas, knowledge gaps remain; LaPoint et al. (2015) reviewed ecological connectivity research conducted in urban areas and discovered strong taxonomic and geographic biases, with most studies focusing on large mammals and birds in North America and Europe (only 2 of 148 articles evaluated fish). The authors emphasise that these biases are concerning given urban stressors like fragmentation and pollution already limit functional connectivity of many species and that climate change will likely exacerbate negative effects by increasing species' need to shift ranges or access new habitats.

Advances in current and emerging technologies for studying connectivity represent a significant promise for addressing many of the gaps outlined above. The miniaturisation of biotelemetry tags allows for the tagging of younger and smaller fishes, helping to fill life history, taxonomic and trophic gaps, while also enabling the tracking of individuals over longer time periods (Cooke et al. 2022; Lennox, Mastrodimitropoulos, et al. 2025). The call for a global library of underwater biological sounds (Parsons et al. 2022) will enhance the utility of the emerging technology ecoacoustics by practitioners because they will no longer need to start from the ground up. In addition to the ability of machine learning to recognise fish images (Barbedo 2022), it can also be used to detect and classify fish sounds (Barroso et al. 2023). Calls for archiving data from peer-reviewed literature would benefit knowledge exchange in future studies (Kot et al. 2023), ultimately benefiting fisheries management and conservation.

Many opportunities remain to further our understanding of fish connectivity by working together. An area that is receiving more attention for filling in gaps for connectivity studies is the use of participatory science using visual surveys. For example, engaging volunteers in documenting the migration phenology of various fish species is not only responsible for increased data collection, but it mobilises a new set of advocates for habitat connectivity for all fish species (e.g., sucker migration phenology, Murchie et al. 2024; Run Herring Run, Metcalfe et al. 2022). Similarly, groups such as Redmap (https://www.redmap.org.au/about/how-you-can-help-redmap/) rely on volunteers to share observations of marine species to document range extensions, with data typically shared to researchers via cell phone apps (Happel et al. 2020). The opportunity to collaborate with others that have expertise across different technologies, geographies, and taxa (including terrestrial) for studying animal connectivity will further enhance our current understanding of fishes. This includes the Two-Eyed Seeing Approach (Reid et al. 2021) where Indigenous Knowledge can be paired with Western science in a complementary and co-existing manner for future studies.

Although the focus of this article was to review methods used to assess fish connectivity, we acknowledge that there are a number of fundamental questions that persist. Understanding the degree of connectivity needed to maintain or restore fish populations in different contexts (e.g., when installing a fish passage device) is difficult to assess, but wholly vital to ensure wild populations persist. Moreover, there are fascinating and fundamental questions about the interplay between structural and functional connectivity that enable fish to occupy the same site, yet there are also questions about the extent to which individuals or subpopulations that come from different areas exchange genetic material. Integrating methods and disciplines has the potential to reveal novel ecological processes while informing management. As such, continued efforts to address knowledge gaps that span disciplines, organisations and ways of knowing for researchers to collaboratively work together will provide critical insight in fish connectivity.

5 | Conclusion

Connectivity is a fundamental concept in aquatic ecosystems with particular salience to fishes. For decades, researchers have attempted to understand and document the extent and consequences of connectivity—or its corollary, fragmentation. Many of the fundamental studies about why and how fish move have come from applied research focused on addressing issues with physical barriers (e.g., dams) or to define fisheries management units (e.g., stocks). Today, connectivity is routinely considered within an applied context by fisheries managers in decisions related to stocking, fisheries regulations and planning, invasive species management and habitat management including restoration and protection (Cooke et al. 2016; Hays et al. 2019). This article emerged from a conference symposium on marine and freshwater fish connectivity where the diverse ways in which different methods were being applied were remarkable and spanned species, ecosystems, methods and objectives. Here, we synthesise the diverse toolbox available to assess fish connectivity which has expanded since previous reviews (e.g., Lucas and Baras 2000). Despite impressive technological developments that have revolutionised our understanding of fish connectivity, many questions remain. To that end, we anticipate and welcome future efforts to develop novel methods and approaches for combining tools to further refine our understanding of fish connectivity. Connectivity is of fundamental importance to ecology and fisheries management; we are convinced that efforts will continue to unravel the mysteries of how fish interact with each other, their environment and humans for many decades to come.

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Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

The authors have nothing to report.

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