

Malheur Bull Trout Workshop

Topic #4: Monitoring and Evaluation

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Malheur Bull Trout Workshop

Topic #4: Monitoring and Evaluation

- How do we define and measure success in the Malheur associated with future chemical treatment actions? What about partial eradication, loss of life history variation, etc.?
- How do we measure population response by bull trout and other native species? I.e., metrics and methods.
- What monitoring methods should occur to maintain confidence brook trout remain absent from treated reaches?
- What course of action will be taken if brook trout are found in the treated reaches at any point in time.

Response of bull trout and other native species to treatment: metrics

Abundance

of spawners

Genetic diversity

Survival

Emigration

Recruitment

Population viability

Pop. growth rate

Effective pop. size

Life-history variation

Occupancy

Response of bull trout and other native species to treatment: metrics and methods

Abundance

Capture-Recapture

Prob. sampling

eDNA surveys

of spawners

Genetic diversity

Design based

Survival

Emigration

Recruitment

Snorkeling

Genetic assessment

Population viability

Pop. growth rate

Effective pop. size

Electrofishing

Model based

Redd surveys

Life-history variation

Occupancy

Occupancy model

Telemetry

Malheur Bull Trout Workshop

Topic #4: Monitoring and Evaluation

Traditional and new technologies for monitoring
bull trout and other fishes

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Topic #4: Monitoring and Evaluation

Traditional and new technologies for monitoring
bull trout and other fishes

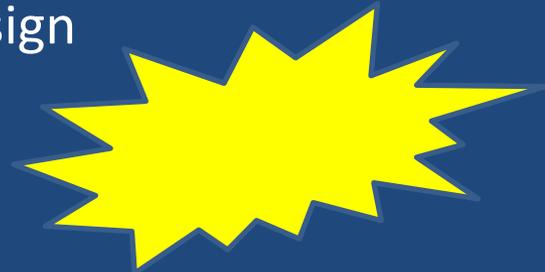
- Traditional (commonly performed) abundance estimate
- Occupancy modeling
- eDNA
- Genetic assessment and monitoring
- Capture-recapture models

Traditional (commonly performed) abundance estimate

- Visit sample sites based on some type of probability sampling design
 - Random, stratified random, cluster, GRTS., etc.
- Sample fish using some appropriate method
 - Electrofishing, snorkeling
- Estimate abundance at the site-level using some appropriate method
 - Mark-recapture (Chapman 1951), depletion (Zippin 1958)
- Extrapolate abundance based on the sampling design

Traditional (commonly performed) abundance estimate

- Visit sample sites based on some type of probability sampling design
 - Random, stratified random, cluster, GRTS., etc.
- Sample fish using some appropriate method
 - Electrofishing, snorkeling
- Estimate abundance at the site-level using some appropriate method
 - Mark-recapture (Chapman 1951), depletion (Zippin 1958)
- Extrapolate abundance based on the sampling design
- Gold-like standard
- Time consuming to measure precisely
 - Possibly problematic for rare or patchily distributed species



Occupancy modeling

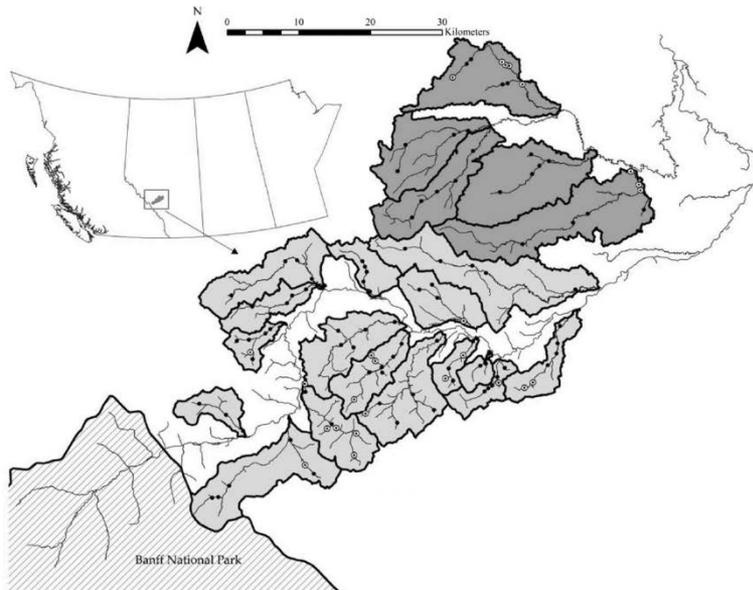
- Visit sample sites based on some type of probability sampling design or not
 - Amenable to design-based or model-based framework
 - Extrapolation based on statistical design or statistical model
- Sample fish using some appropriate method
 - Electrofishing, snorkeling, eDNA*
- Estimate capture probability and occupancy probability
 - Requires spatial or temporal revisits
- Estimate occupancy at various scales
 - Possibility for nested designs, etc.
- Gaining popularity
- Can be implemented relatively quickly (relative to abundance est.)
- May be well suited for rare species with patchy distributions

Occupancy modeling

Rodtka et al.

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Fig. 1. Location of the 21 patches and 92 sample sites (solid circles) and 25 nonresponse sites (open circles with center dot) in the Clearwater River study area in west-central Alberta, Canada. Patches in the Prairie Creek drainage are shaded darker.



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ARTICLE

Estimating occupancy and detection probability of juvenile bull trout using backpack electrofishing gear in a west-central Alberta watershed

Mike C. Rodtka, Chad S. Judd, Peter K.M. Aku, and Kevin M. Fitzsimmons

Abstract: Occupancy modeling is well suited to quantitative assessment of bull trout (*Salvelinus confluentus*) distribution at multiple scales. We used models to estimate occupancy of juvenile bull trout (5150 mm fork length) in a west-central Alberta watershed. Based on a backpack electrofishing survey of 92 sites, we assessed the relative importance of stream habitat characteristics on detection probability (\hat{p}) and potential for false absences to bias occupancy estimates. Median distance to first bull trout detection was 16 m (range 0–289 m). Models including ambient water conductivity as a covariate of detection probability were most supported with an $85 \mu\text{S}\cdot\text{cm}^{-1}$ increase resulting in over a tenfold increase in detection. Conditional detection probability using backpack electrofishing gear approached 95% in the first 200 m of effort in streams with a conductivity around $200 \mu\text{S}\cdot\text{cm}^{-1}$. The potential for false absences in our study area was relatively low. Modeled site ($\hat{\theta} = 0.53$; SE = 0.13) and patch-scale ($\hat{\Psi} = 0.47$; SE = 0.12) occupancy closely corresponded to naïve (i.e., assuming $p = 1$) estimates (0.47 and 0.43, respectively). Our results highlight the potential efficiencies of an occupancy modeling approach when assessing fish distribution, but careful consideration of model assumptions is necessary.

Résumé : La modélisation de l'occupation se prête bien à l'évaluation quantitative de la répartition des ombles à tête plate (*Salvelinus confluentus*) à différentes échelles. Nous avons utilisé des modèles pour estimer l'occupation des ombles à tête plate juvéniles (longueur à la fourche ≤ 150 mm) dans un bassin versant du centre-ouest de l'Alberta. À la lumière de levés par pêche électrique à l'aide d'engins dorsaux dans 92 sites, nous avons évalué l'importance relative des caractéristiques d'habitats lotiques en ce qui concerne la probabilité de détection (\hat{p}) et la possibilité que de fausses absences biaisent les estimations d'occupation. La distance médiane avant la première détection d'un omble à tête plate était de 16 m (fourchette de 0 m à 289 m). Les modèles intégrant la conductivité ambiante de l'eau comme covariable de la probabilité de détection performaient le mieux, une augmentation de $85 \mu\text{S}\cdot\text{cm}^{-1}$ se traduisant par plus de dix de la détection. La probabilité de détection conditionnelle à l'aide de l'engin de pêche électrique dorsal approchait les 95 % dans les premiers 200 m d'effort dans les cours d'eau présentant une conductivité de l'ordre de $200 \mu\text{S}\cdot\text{cm}^{-1}$. Le potentiel de fausses absences dans la région à l'étude était relativement faible. L'occupation modélisée à l'échelle du site ($\hat{\theta} = 0.53$; SE = 0.13) et de la parcelle ($\hat{\Psi} = 0.47$; SE = 0.12) correspondait étroitement aux estimations naïves (0.47 et 0.43, respectivement, en présument que $p = 1$). Nos résultats soulignent les gains d'efficacité possibles découlant d'une approche de modélisation de l'occupation pour l'évaluation de la répartition de poissons, un examen soigné des hypothèses qui sous-tendent de tels modèles étant toutefois nécessaire. [Traduit par la Rédaction]

Introduction

Assessed as Threatened in the coterminous United States (USFWS 2008) and Alberta (Saskatchewan–Nelson rivers populations; COSEWIC 2012), bull trout (*Salvelinus confluentus*) are considered particularly sensitive to habitat change and are thought to reflect general ecosystem health (COSEWIC 2012), and their widespread decline is cause for concern. However, assessment of bull trout status has been hampered by a lack of standardized protocols for quantifying species distribution and abundance at a watershed scale (USFWS 2008; COSEWIC 2012). Current assessment protocols often focus on estimating fish abundance either directly (e.g., electrofishing, snorkel surveys) or indirectly (e.g., visual counts of redds) (USFWS 2008; COSEWIC 2012), but the patchy distribution of bull trout, variable habitat use, and demographic stochasticity make timely detection of meaningful trends in abundance difficult (Ham and Pearsons 2000; Al-Chokhachy et al. 2009). Estimates of abundance or its underlying processes (survival and

reproduction) are also expensive to acquire, require extensive field surveys, and often involve the capture and marking of individuals (Al-Chokhachy et al. 2009; Noon et al. 2012). The various sampling methods used to capture and enumerate bull trout are also subject to a variety of biases, further complicating the issue (COSEWIC 2012).

The presence-absence or area occupied approach (Marsh and Trenham 2008) is an increasingly popular alternative to estimating abundance when monitoring wildlife populations. This approach involves estimation of the proportion of an area (or habitats within an area) that is occupied by a target species (MacKenzie et al. 2006). Given the difficulty of monitoring bull trout abundance, occupancy estimation appears to provide an attractive alternative for assessment of the species at the watershed scale. Indeed, assessment of the geographic distribution of bull trout is included in both the USFWS and COSEWIC status assessments (USFWS 2008; COSEWIC 2012). The detection–nondetection data

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eDNA

- Environmental DNA (eDNA)
 - DNA that originates from feces, saliva, urine and skin cells of animals
 - Can be extracted from an environmental sample such as soil, sediment, water, or snow
- GREAT deal of interest in this technology/methodology
 - Including bull trout range-wide eDNA surveys
 - Some kinks to work out
 - Degradation, detection probabilities, etc.
- Likely valuable for detection of rare or patchily distributed species
- Likely valuable for detecting small numbers of brook trout
- Low-cost
 - Limited personnel requirements

eDNA

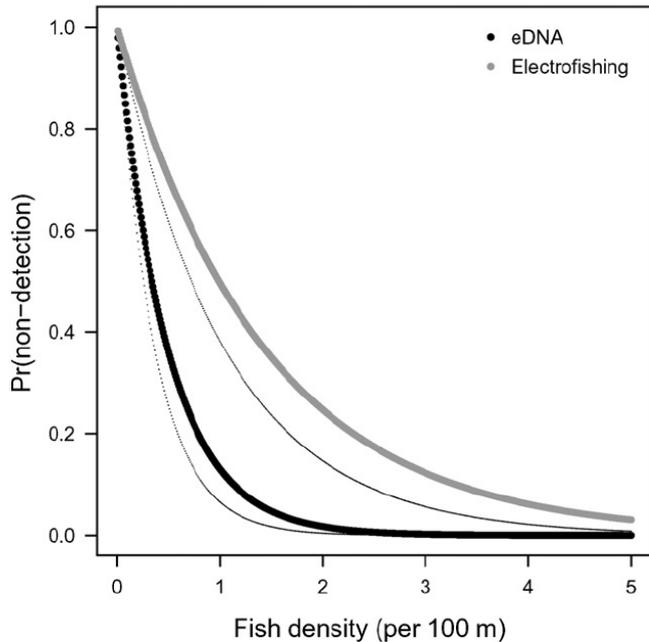


Fig 5. Predicted non-detection rates for electrofishing (gray) and eDNA (black) for randomly-distributed 0.01–5 fish per 100 m reach using protocols described in this study. Thick black points show calculations using eDNA production and downstream persistence ($1 - k$ per 100 m) mean estimates from the observational study. Thin black points show calculations using the lower and upper bounds of the 95% CI around these estimates. These results are consistent with stochastic simulations (Appendix C) and suggest lower costs for eDNA relative to electrofishing when animals are rare (Appendix D).



Understanding environmental DNA detection probabilities: A case study using a stream-dwelling char *Salvelinus fontinalis*



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ABSTRACT

Environmental DNA sampling (eDNA) has emerged as a powerful tool for detecting aquatic animals. Previous research suggests that eDNA methods are substantially more sensitive than traditional sampling. However, the factors influencing eDNA detection and the resulting sampling costs are still not well understood. Here we use multiple experiments to derive independent estimates of eDNA production rates and downstream persistence from brook trout (*Salvelinus fontinalis*) in streams. We use these estimates to parameterize models comparing the false negative detection rates of eDNA sampling and traditional backpack electrofishing. We find that using the protocols in this study eDNA had reasonable detection probabilities at extremely low animal densities (e.g., probability of detection 0.18 at densities of one fish per stream kilometer) and very high detection probabilities at population-level densities (e.g., probability of detection >0.99 at densities of ≥ 3 fish per 100 m). This is substantially more sensitive than traditional electrofishing for determining the presence of brook trout and may translate into important cost savings when animals are rare. Our findings are consistent with a growing body of literature showing that eDNA sampling is a powerful tool for the detection of aquatic species, particularly those that are rare and difficult to sample using traditional methods.

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1. Introduction

Environmental DNA (eDNA) sampling has recently emerged as a powerful tool for detecting aquatic animals. These methods detect genetic material in environmental samples (e.g., stream water) to indirectly infer the presence of a species (Jerde et al., 2011). This approach is especially useful for detecting species that are difficult to sample using traditional methods (Taberlet et al., 2012), for non-invasively sampling critically endangered species (Sigsgaard et al., 2015), and for distinguishing cryptic species (Fukumoto et al., 2015). Since it was first used to detect aquatic animals (Ficetola et al., 2008) there has been an explosion of research on eDNA methods, particularly with respect to rare invasive species (e.g., Dejean et al., 2012; Goldberg et al.,

2013; Moyer et al., 2014) and threatened native species (Spear et al., 2015; Thomsen et al., 2012).

Previous research suggests that eDNA methods may be substantially more sensitive and cost-effective than traditional sampling for species detection (Biggs et al., 2015; Jerde et al., 2011; Sigsgaard et al., 2015). However, there has been large variation in reported sensitivities, and eDNA production rates are still unknown for most species. Several studies have related eDNA concentration to animal abundance or biomass (Klymus et al., 2015; Pilliod et al., 2013; Takahara et al., 2012), but variation in eDNA production rates among individuals is also very high (Klymus et al., 2015; Pilliod et al., 2014; Strickler et al., 2015).

The eDNA produced by aquatic organisms is distributed in the environment and lost as a function of degradation, dilution, deposition, and re-suspension (Strickler et al., 2015; Turner et al., 2015). Several studies have assessed rates of eDNA degradation, which usually occurs over hours to days (Barnes et al., 2014; Pilliod et al., 2014; Strickler et al., 2015), but the other processes affecting eDNA concentrations in aquatic systems are less understood. For example, the downstream transport of eDNA in lotic systems implies that animals can be detected some distance from their location (e.g., <50 m to up to 12 km; Deiner and Altermatt, 2014; Jane et al., 2015; Pilliod et al., 2014), but because little

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Genetic assessment and monitoring

- Influence of sample design and intensity on estimates of effective number of breeders (N_b)
 - Index of abundance
- Optimum sampling design was sampling 75 individuals from 3 sample sites

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RESEARCH ARTICLE

Sampling strategies for estimating brook trout effective population size

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Mark Hudy · Zachary Robinson · Keith H. Nislow ·
Benjamin H. Letcher

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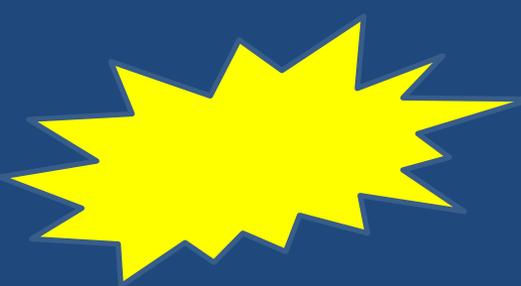
Abstract The influence of sampling strategy on estimates of effective population size (N_e) from single-sample genetic methods has not been rigorously examined, though these methods are increasingly used. For headwater salmonids, spatially close kin association among age-0 individuals suggests that sampling strategy (number of individuals and location from which they are collected) will influence estimates of N_e through family representation effects. We collected age-0 brook trout by completely sampling three headwater habitat patches, and used microsatellite data and empirically parameterized simulations to test the effects of different combinations of sample size ($S = 25, 50, 75, 100, 150, \text{ or } 200$) and number of equally-spaced sample starting locations ($SL = 1, 2, 3, 4,$

or random) on estimates of mean family size and effective number of breeders (N_b). Both S and SL had a strong influence on estimates of mean family size and \hat{N}_b , however the strength of the effects varied among habitat patches that varied in family spatial distributions. The sampling strategy that resulted in an optimal balance between precise estimates of N_b and sampling effort regardless of family structure occurred with $S = 75$ and $SL = 3$. This strategy limited bias by ensuring samples contained individuals from a high proportion of available families while providing a large enough sample size for precise estimates. Because this sampling effort performed well for populations that vary in family structure, it should provide a generally applicable approach for genetic monitoring of iteroparous headwater stream fishes that have overlapping generations.

Electronic supplementary material The online version of this article (doi:10.1007/s10592-011-0313-y) contains supplementary material, which is available to authorized users.

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Keywords Genetic monitoring · Effective population size · Effective number of breeders · Brook trout · Headwater streams · Linkage disequilibrium · LDNe



Genetic assessment and monitoring

- Effective number of breeders (N_b) may be used to approximate population size (N)

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Spatiotemporal relationship between adult census size and genetic population size across a wide population size gradient

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Abstract

Adult census population size (N) and effective number of breeders (N_b) are highly relevant for designing effective conservation strategies. Both parameters are often challenging to quantify, however, making it of interest to determine whether one parameter can be generalized from the other. Yet, the spatiotemporal relationship between N and N_b has not been well characterized empirically in many taxa. We analysed this relationship for 5–7 consecutive years in twelve brook trout populations varying greatly in N (49–10032) and N_b (3–567) and identified major environmental variables affecting the two parameters. N or habitat size alone explained 47–57% of the variance in N_b , and N_b was strongly correlated with effective population size. The ratio N_b/N ranged from 0.01 to 0.45 and increased at small N or following an annual decrease in N , suggesting density-dependent constraints on N_b . We found no evidence for a consistent, directional difference between variability in N_b and/or N_b/N among small and large populations; however, small populations had more varying temporal variability in N_b/N ratios than large populations. Finally, N_b and N_b/N were 2.5- and 2.3-fold more variable among populations than temporally within populations. Our results demonstrate a clear linkage between demographic and evolutionary parameters, suggesting that N_b could be used to approximate N (or vice versa) in natural populations. Nevertheless, using one variable to infer the other to monitor trends within populations is less recommended, perhaps even less so in small populations given their less predictable N_b vs. N dynamics.

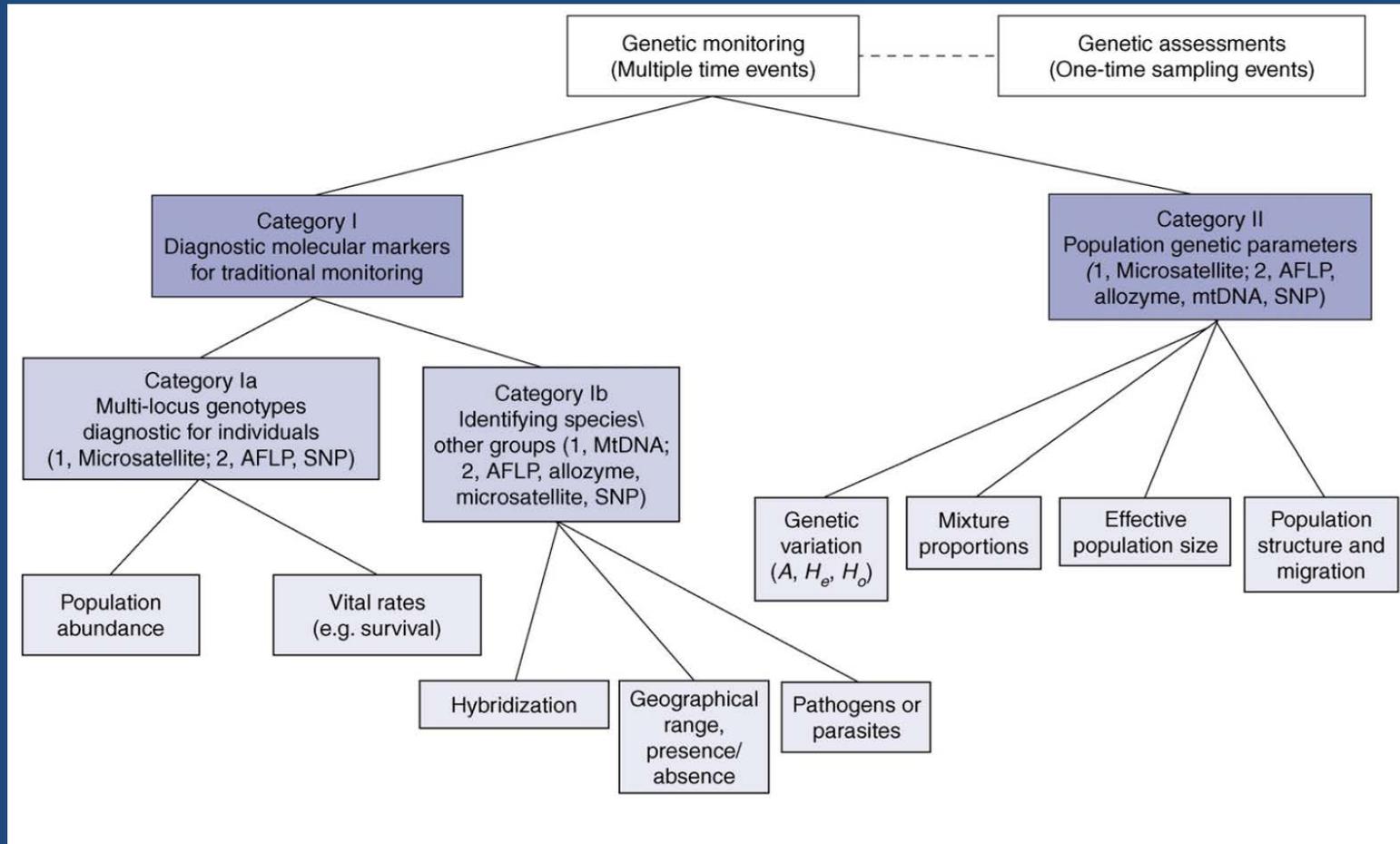
Keywords: census population size, effective number of breeders, effective population size, genetic monitoring, mark–recapture, stream fish

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Genetic assessment and monitoring

- Can you obtain other relevant population genetic information while estimating N_b ?

Genetic assessment and monitoring



Schwartz, M.K., G. Luikart, and R.S. Waples. 2007. Genetic monitoring as a promising tool for conservation and management. *Trends in Ecology & Evolution* 22:25-33.

Genetic assessment

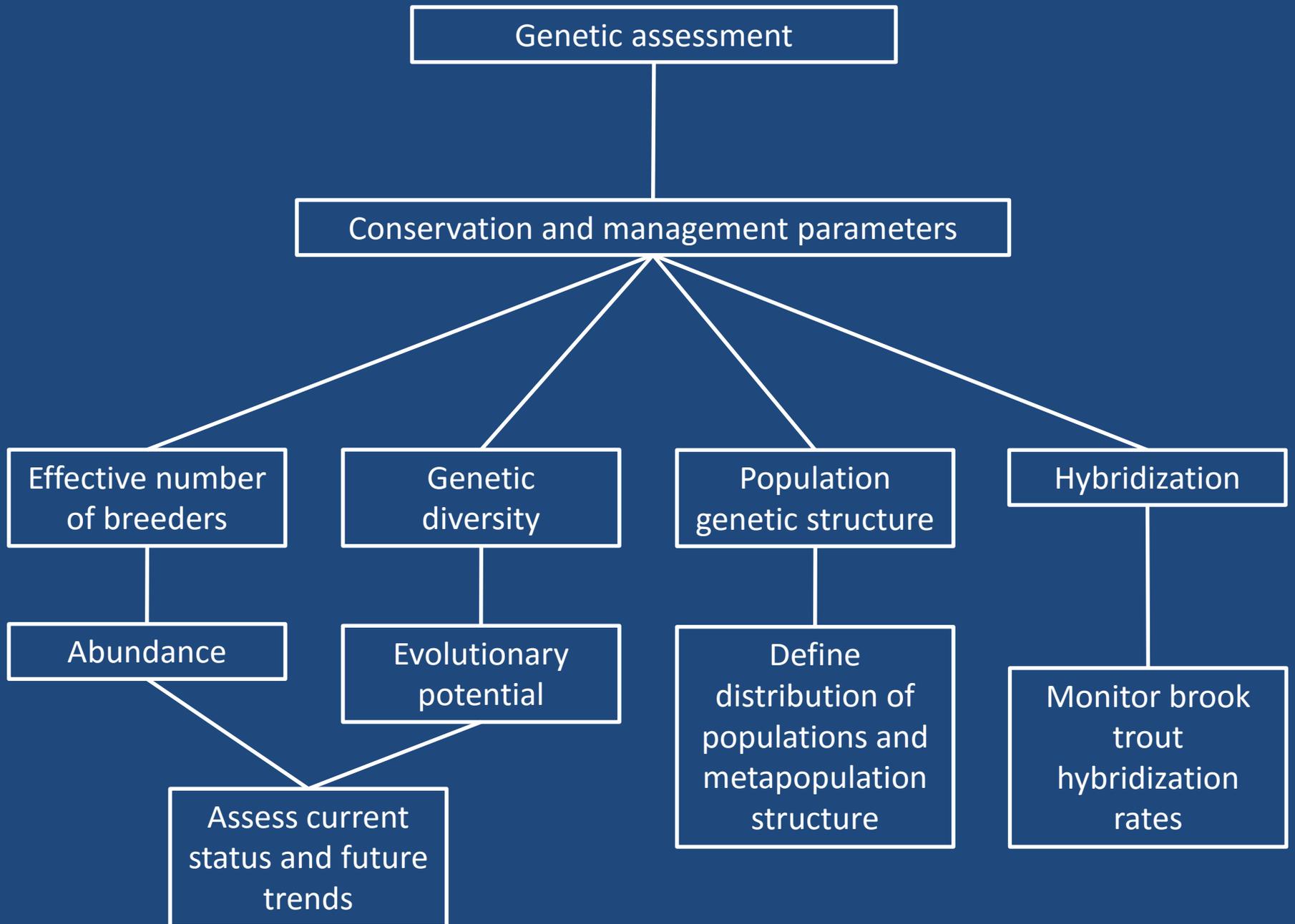
Population genetic parameters

Effective number
of breeders

Genetic
diversity

Population
genetic structure

Hybridization



Genetic assessment and monitoring

- Previous published studies have shown promise, **BUT**
 - N_b may not be a great tool for tracking trend
 - N_b may not be a great tool for estimating population of 'large' populations
- ODFW efforts in Jack Creek and Long Creek have shown promise

Genetic assessment and monitoring

- Previous published studies have shown promise, **BUT**
 - N_b may not be a great tool for tracking trend
 - N_b may not be a great tool for estimating population of 'large' populations
- ODFW efforts in Jack Creek and Long Creek have shown promise
- Efforts in Malheur Basin and John Day Basin have identified limitations
 - Sample size requirements

Capture-recapture models

- Model-based method
 - Extrapolation of estimator based on statistical model
- Closed or open population models

Capture-recapture models

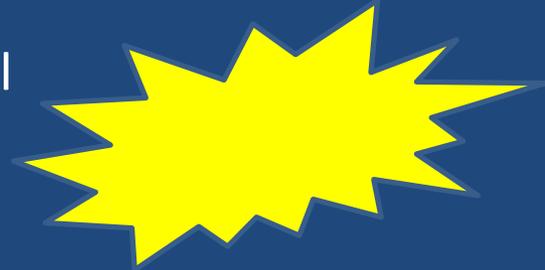
- Model-based method
 - Extrapolation of estimator based on statistical model
- Closed or open population models
- Closed population models
 - Examples: Lincoln-Petersen, Schnabel, Huggins, etc.
 - Estimate: capture probability and abundance

Capture-recapture models

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 - Extrapolation of estimator based on statistical model
- Closed or open population models
- Closed population models
 - Examples: Lincoln-Petersen, Schnabel, Huggins, etc.
 - Estimate: capture probability and abundance
- Open population models
 - Examples: Recovery models, Cormack-Jolly-Seber models, multi-state models, reverse-time models, Link-Barker models, etc.
 - Estimate: capture probability, survival, recruitment, exploitation, movement

Capture-recapture models

- Model-based method
 - Extrapolation of estimator based on statistical model
- Closed or open population models
- Closed population models
 - Examples: Lincoln-Petersen, Schnabel, Huggins, etc.
 - Estimate: capture probability and abundance
- Open population models
 - Examples: Recovery models, Cormack-Jolly-Seber models, multi-state models, reverse-time models, Link-Barker models, etc.
 - Estimate: capture probability, survival, recruitment, exploitation, movement
- Robust design: hybrid open/closed population model
 - Abundance



Other considerations

- Measure covariates
 - Will likely help you with your estimates
- Monitor temperature
 - Consider developing your own basin-specific temperature model

Relative cost guestimates

	Low	Medium	High
Traditional abundance estimate		X	X
Occupancy	X	X	
eDNA	X		
Genetic assessment		X	
Capture-recapture	X	X	X