

Single parent and grandparent genetic assignments: What is possible and what is not?

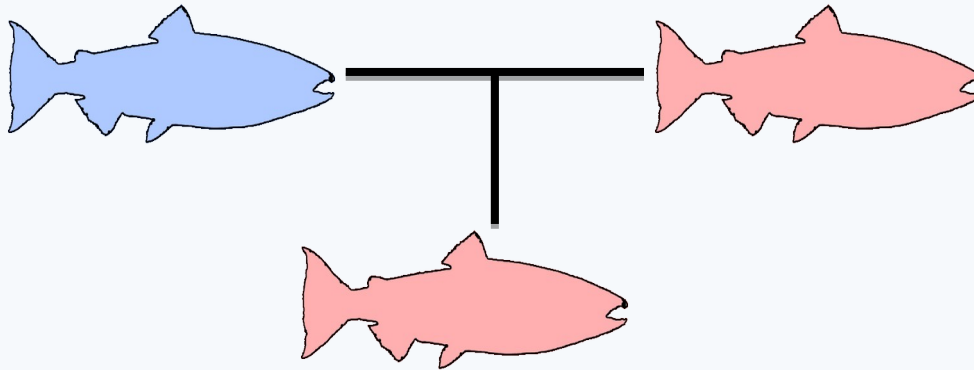
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Parentage-based tagging (PBT)

- Genetic sampling of all Snake basin hatchery broodstock began in 2008
- Allows identification of hatchery origin fish
 - Compare genotypes and determine whether a sample is an offspring of the broodstock

Dual-parent assignment

- Identification of hatchery origin fish by matching them to both parents:



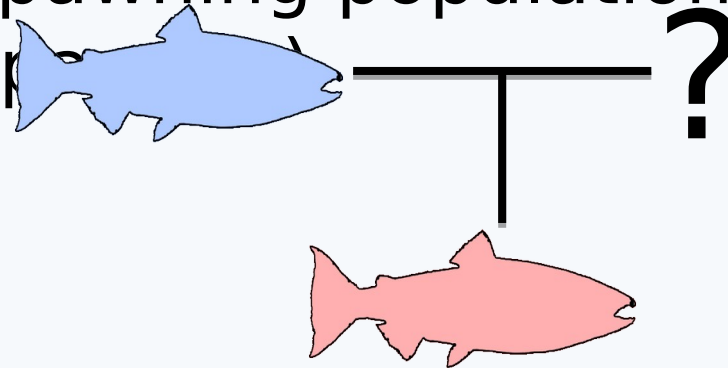
- Must have genotypes of both parents to identify offspring

Can you identify other relationships?

- There are many projects that dual-parent assignments do not inform
 - Single parent assignment
 - Grandparent assignment
- This talk will focus on the current state and near-future of steelhead panels we use in the Snake basin
 - Almost anything is possible with the right set of markers

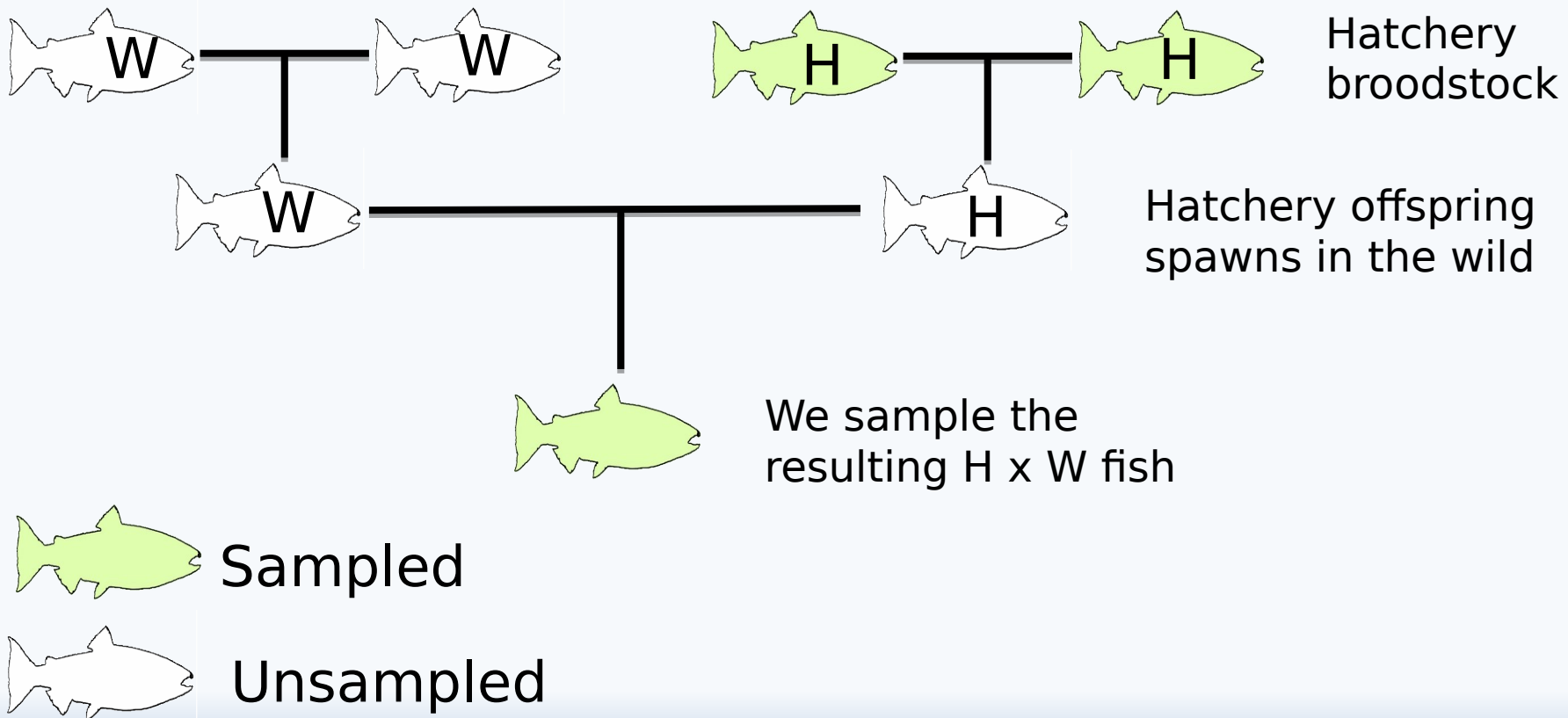
Single parent assignment

- Allows identification of offspring even when one parent is not genotyped
 - Low quality DNA collected from potential parents
 - Naturally spawning populations (hard to sample all parents)



Grandparent assignment

- Some relevant situations have no parents sampled



Grandparent assignment

- Assigning a single grandparent to a single grandchild is **not** possible with current and near-future panels we use
 - Maybe one day
- But consider assigning trios
 - 2 grandparents, 1 grandchild

Can you infer these relationships?

- To decide if single-parent or grandparent assignments are possible, calculate the expected error rates
 - Genetic panel and population specific
- Choose assignment criteria to balance false-positive and false-negative errors
 - Typically minimize false-positive

False negative errors

- What is the probability a true parent-offspring relationship is not assigned?
- “Per-comparison” error rates
 - 1000 offspring, 4000 potential parents
 - 500 true parent-offspring pairs
- A false negative rate of 0.10 is expected to yield 50 false negatives

False positive errors

- What is the probability two unrelated fish are assigned as parent-offspring?
- “Per-comparison” error rates
 - 1000 offspring, 4000 potential parents
 - $1000 * 4000 = 4,000,000$ single parent comparisons
 - 500 true parent-offspring pairs
- A false positive rate of 10^{-6} is expected to yield 3.9995 false positives

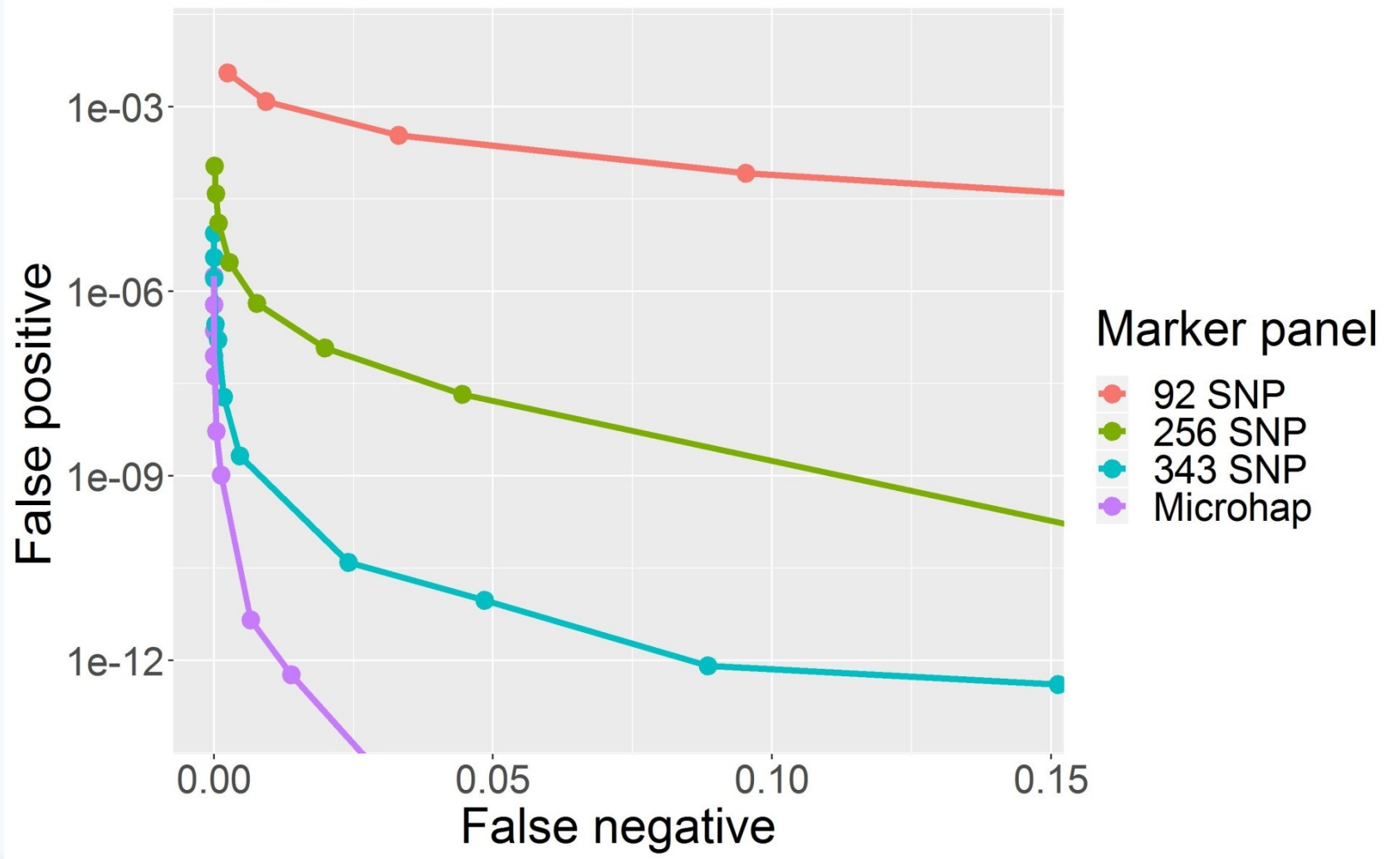
Error rates

- Larger analyses require smaller false-positive rates
 - More comparisons
 - Need more powerful panels
- A given panel may be fine for a small analysis, but not for a large analysis

What are your error rates?

- 92 SNPs
 - 2008 – 2015
- 2015 switched genotyping method
- 256 SNPs
 - 2016
- 343 SNPs
 - 2017 – present
- Microhap (299 SNPs and 44 microhaplotypes)
 - Retroactively 2017 – present

Single parent error rates

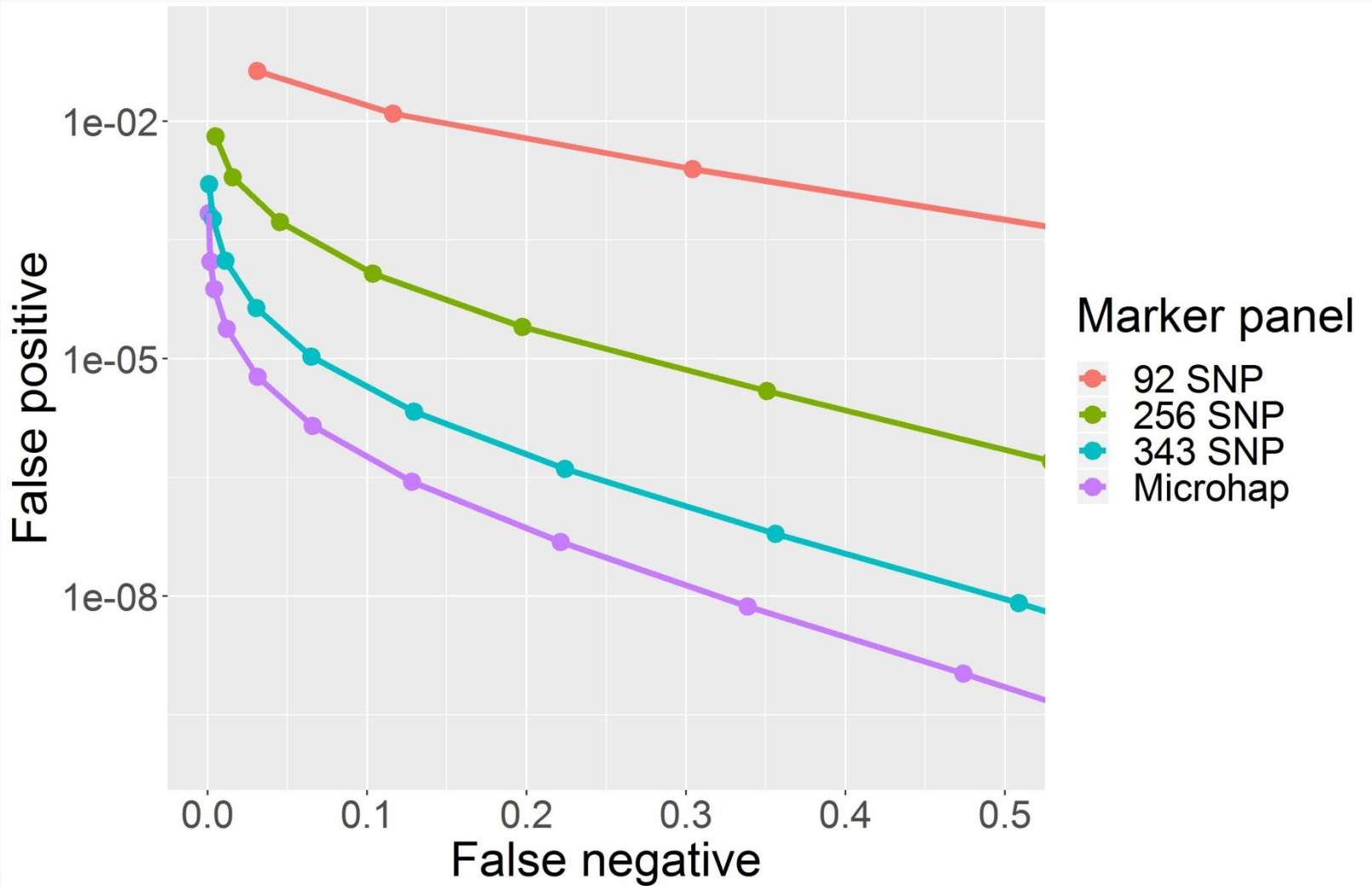


Single parent assignments

- False positive 10^{-11} , false negative .01 (microhap)
 - 1000 offspring, 4000 potential parents
 - 500 true parent-offspring pairs
- Expect:
 - 5 assignments missed (false negative)
 - 0.00004 false assignments
- Single parent assignments will soon be possible for many analyses

Spawn Year	Baseline genotypes
2021	256
2022	Microhap

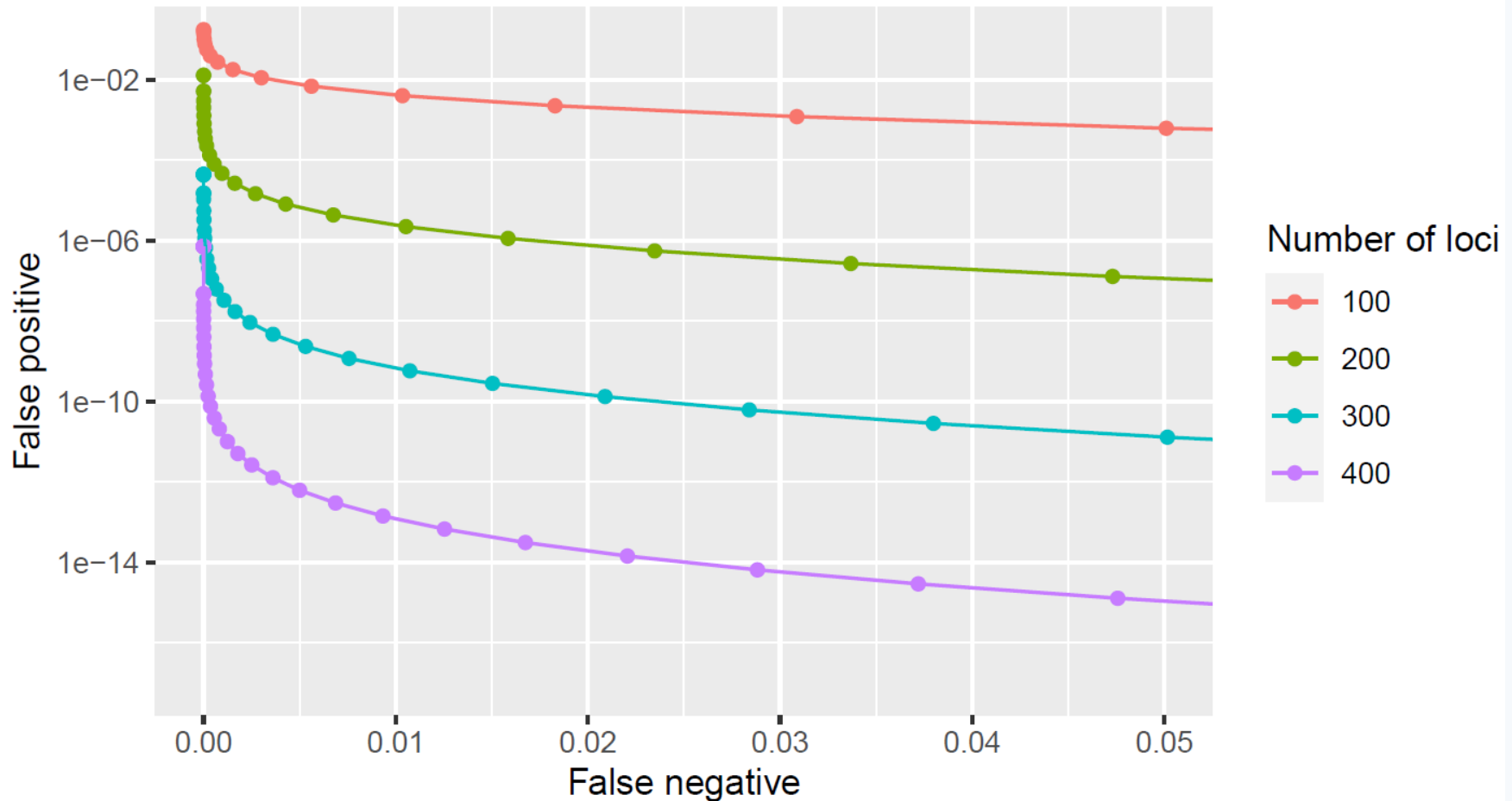
Grandparent-grandchild trio error rates



Future of marker panels?

- The number/power of markers keeps increasing
- We expect this to continue

How many microhaplotypes to identify grandparent-grandchild trios?



Grandparent-grandchild trio assignments

- Near-future panels may achieve accuracy needed in the Snake basin
- Utilize hatchery cross records to reduce the number of comparisons
 - Cross record accuracy verified by PBT
- In absence of cross records, can also use phenotypic sex, genetic sex marker, spawn date

What is possible and what is not?

- Single-parent: now for juveniles, soon for adults
 - Depending on size of analysis
- Grandparent-grandchild trio: near future
- Single-grandparent: maybe one day

Acknowledgments

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Questions