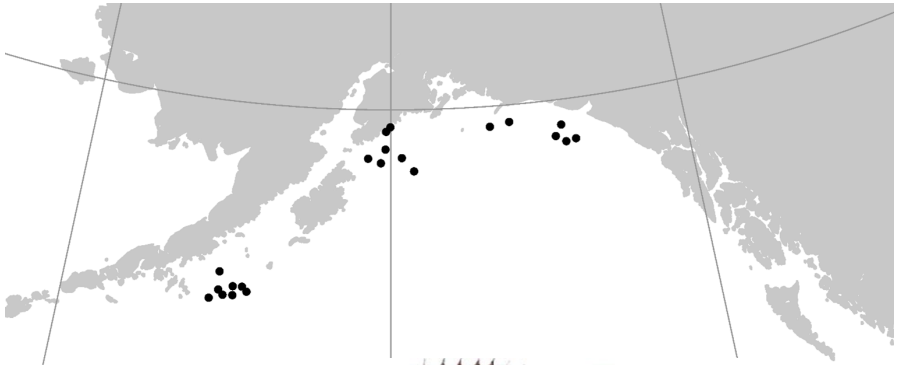
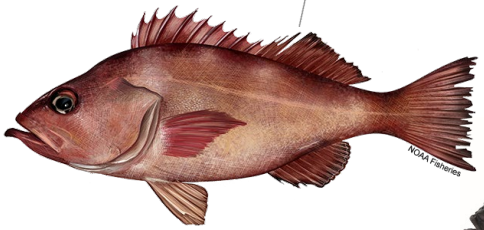
Genetic species identification of larval rockfishes from the Gulf of Alaska

Diana Baetscher, Claire Tobin, Ali Deary & Wes Larson





Western Groundfish Conference
April 27, 2023
Juneau, AK

Why use genetic identification for rockfishes?

Carr Lab photos

- juveniles & larvae
- taxonomic expertise
- cryptic species
- overlapping adult distributions
- larvae for species outside of adult distributions

Scott Groth photo

ODFW photo

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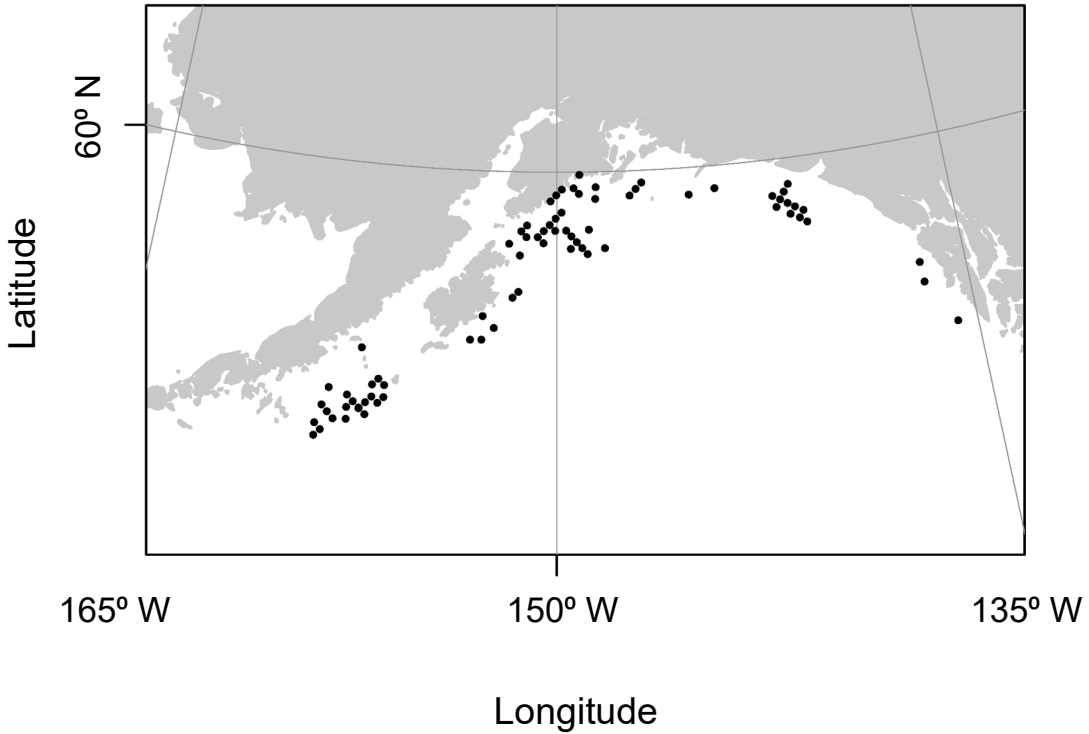
Larval rockfish collections from the Gulf of Alaska



4,660 mixed larval samples by haul/station (2011-2013, 2015)

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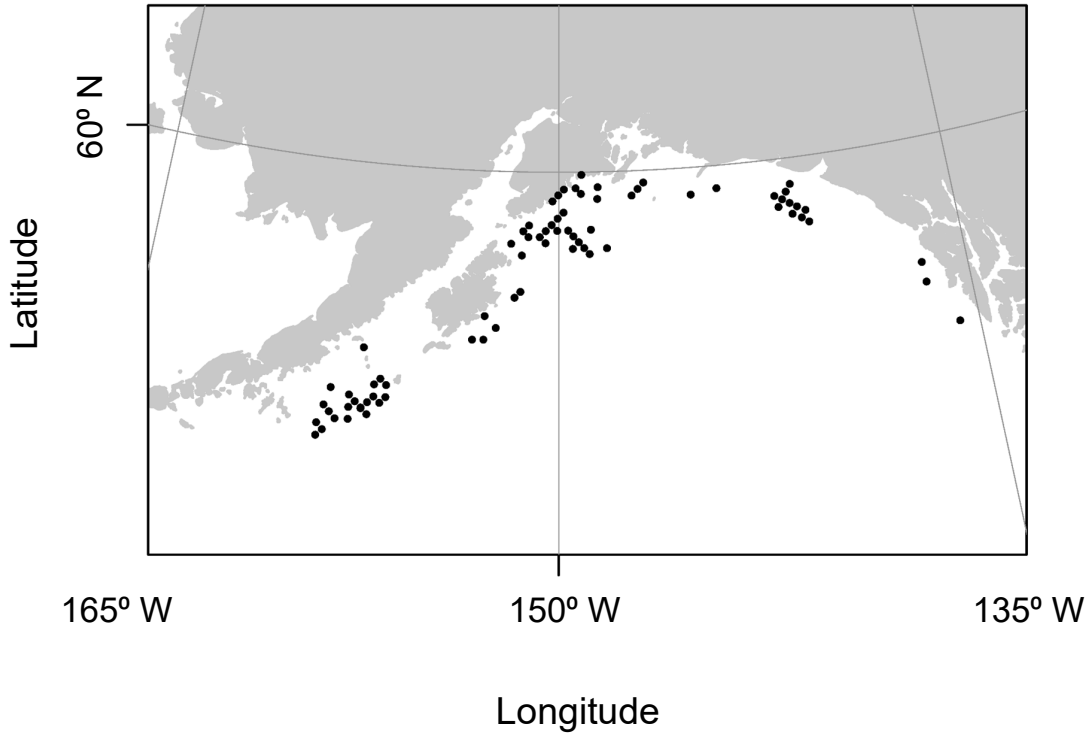
Larval rockfish collections from the Gulf of Alaska



Questions:

- species composition
- variation across space (east v. west)
- interannual conditions / oceanography

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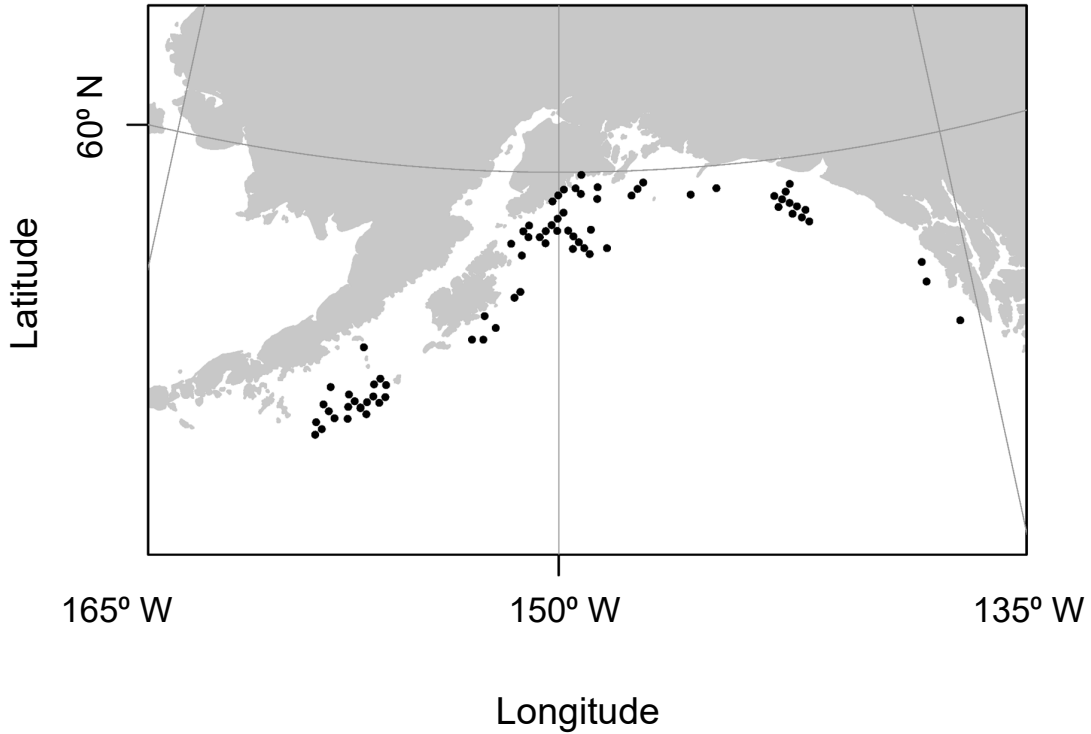
Larval rockfish collections from the Gulf of Alaska



Questions:

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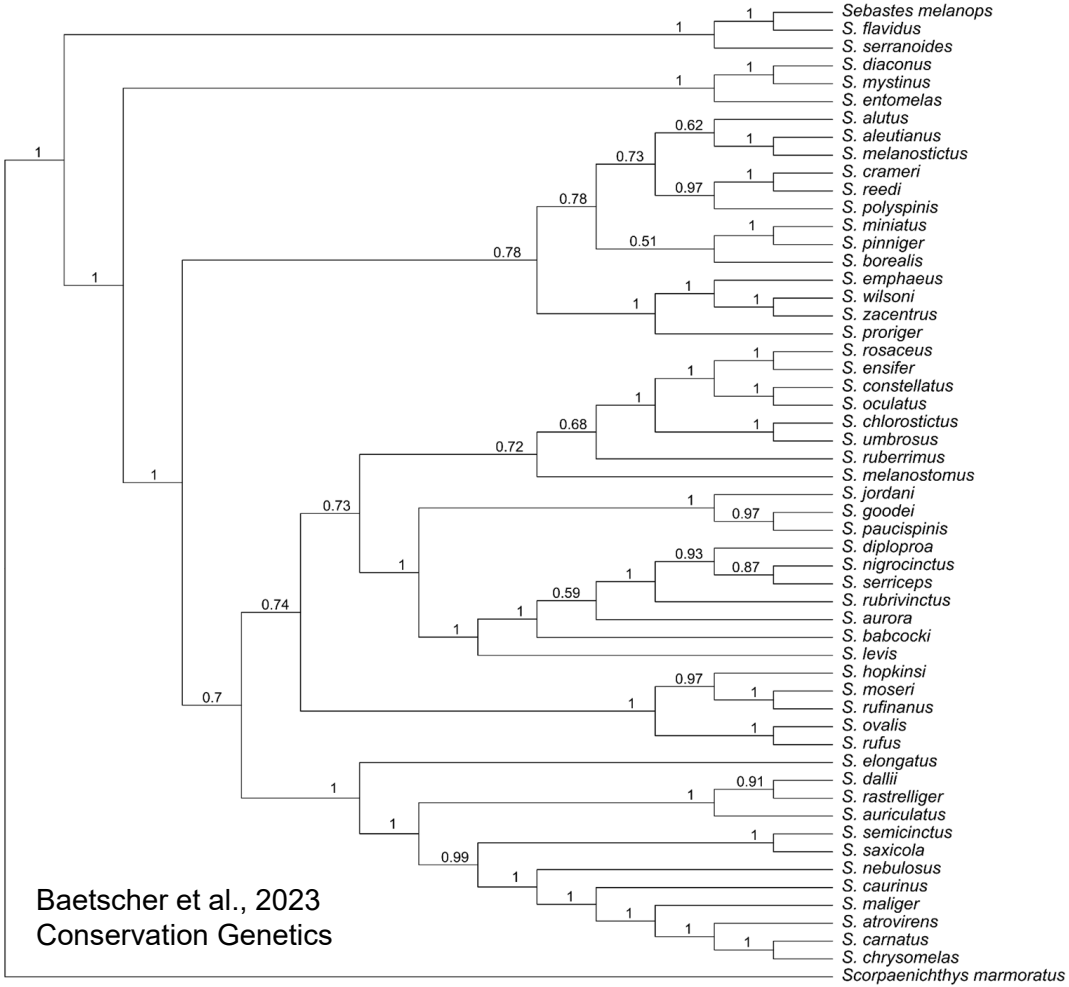
Need species ID!



Baetscher et al., 2023
Conservation Genetics

Rockfish species ID genetic markers - microhaplotypes

- 54 species, 997 samples
- NE Pacific (CA to AK)
- 90 genetic markers
- 100% accurate assignment except gopher, black-and-yellow
- flexible, extendable workflow

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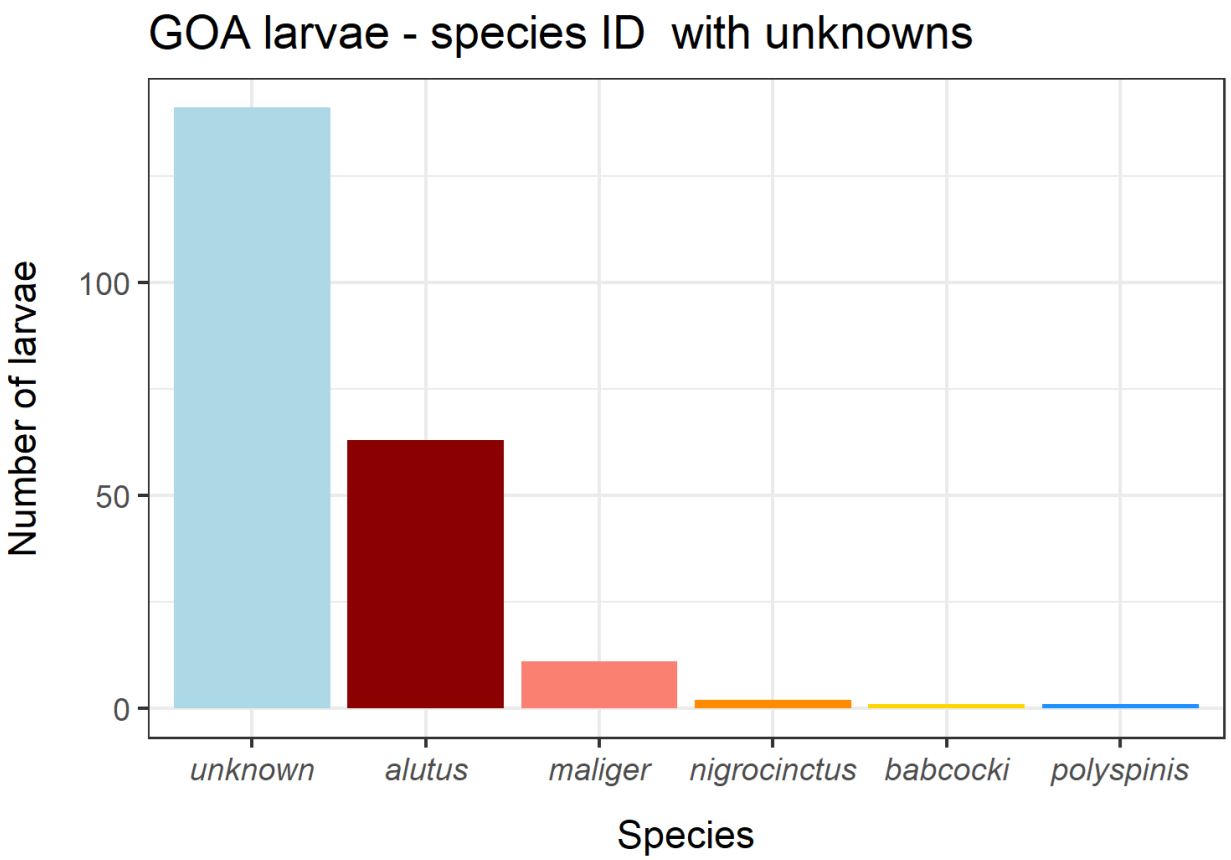

Standard species ID analysis:

Why so many unknowns?

Species not in the baseline?

Identifying species NOT in the baseline

1. Look at z-scores: The individual log-likelihood minus the expected log-likelihood and then divided by the expected standard deviation (implemented in rubias R package)

1. Test by genotyping known adult samples

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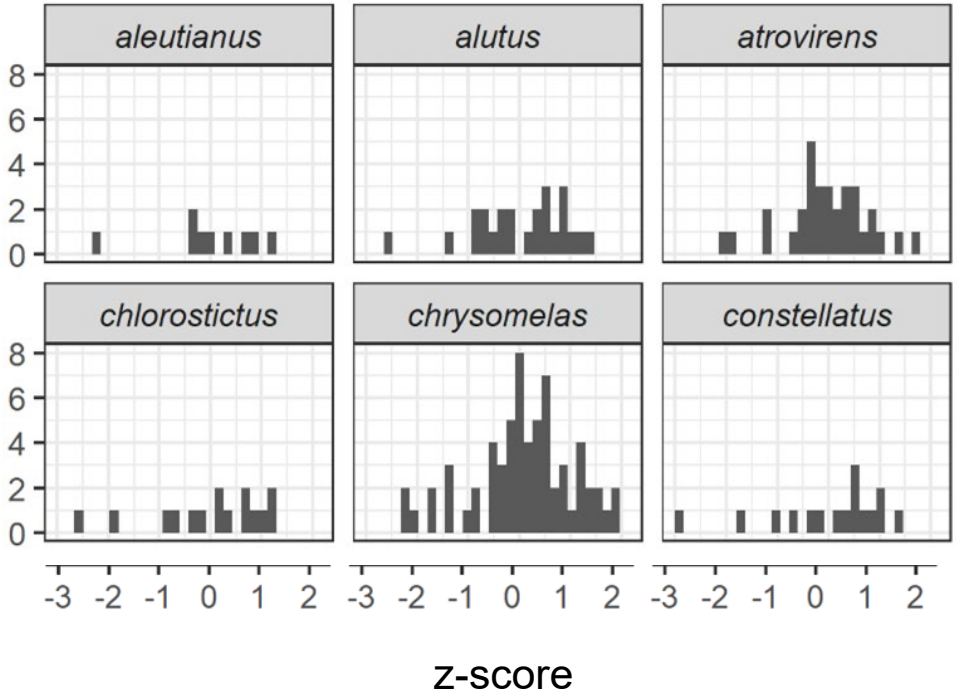

z-score distributions for baseline species

- normally distributed (between -3 and 2)
- small sample sizes - sparse patterns

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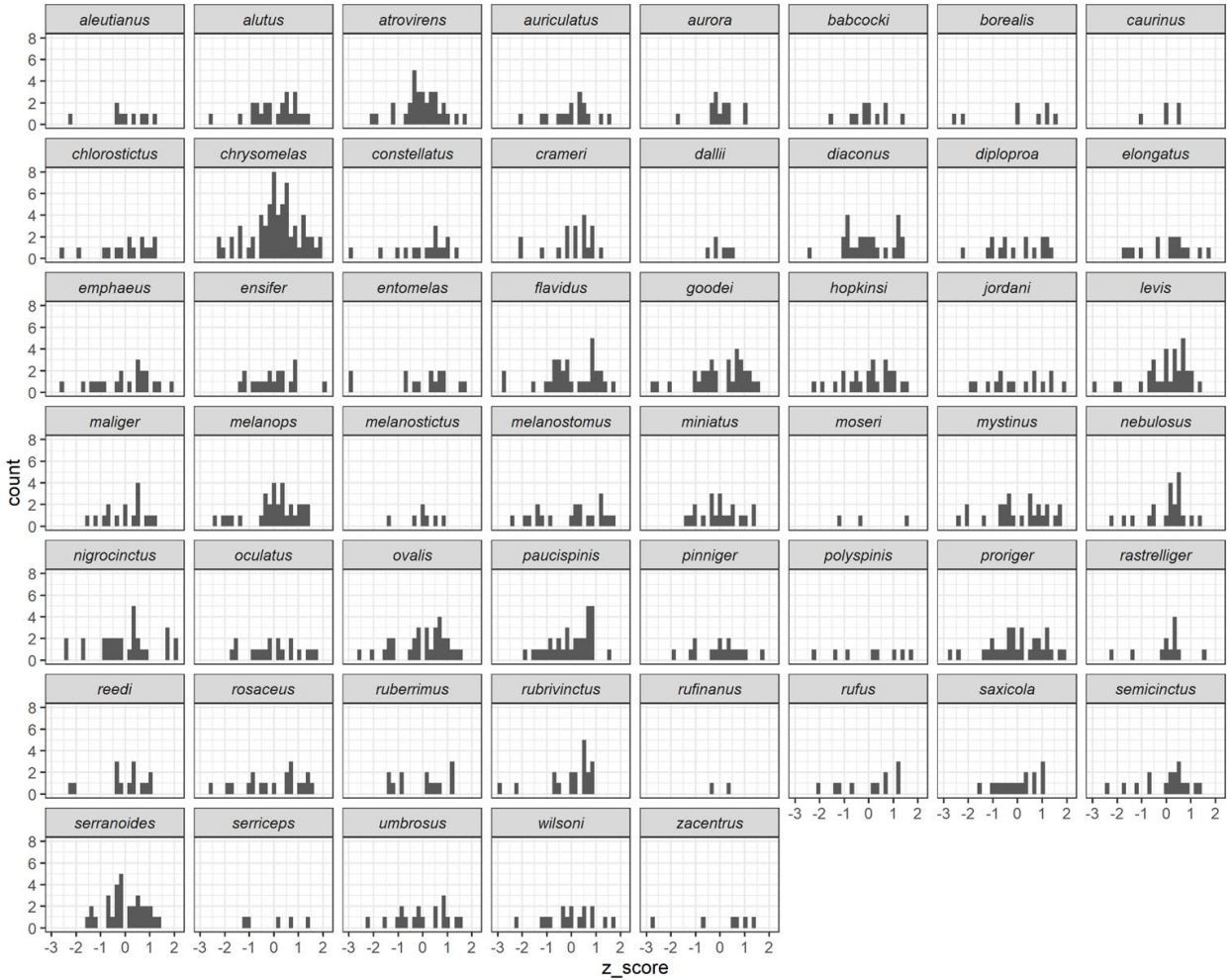

- z-score distributions for species in baseline
- normally distributed (between -3 and 2)
- small sample sizes - sparse patterns

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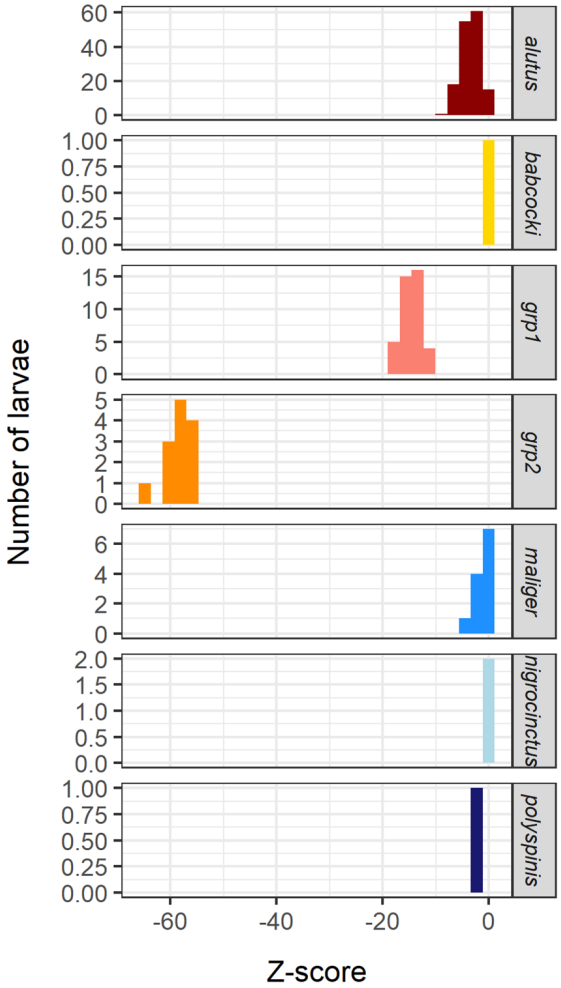

z-score distributions for larval samples and assignments

expected distributions for species included in reference

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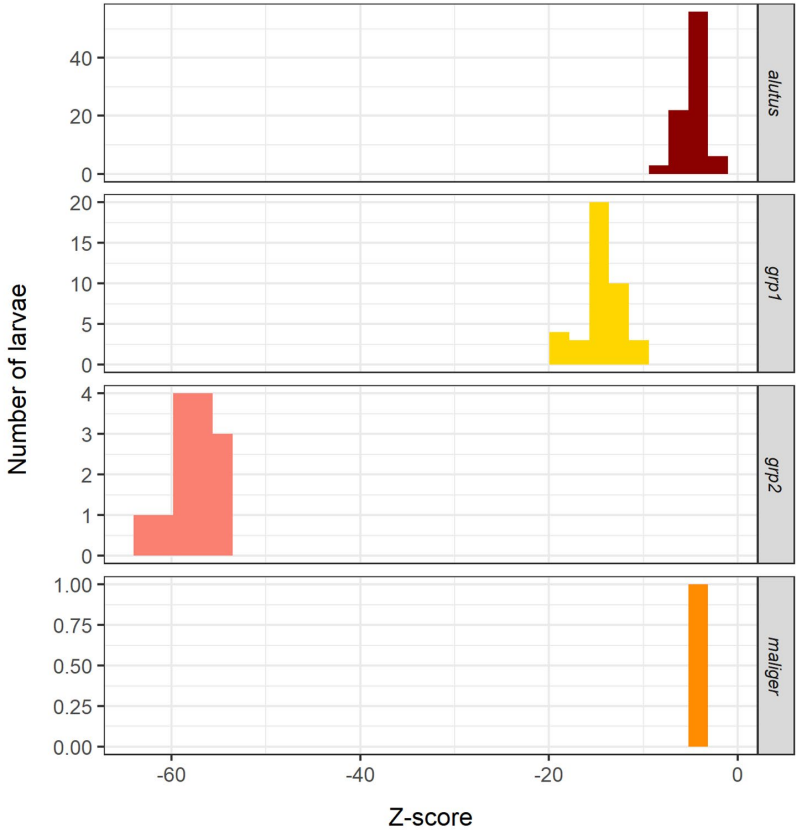
Take a look at just the unknown larvae…



→ Many assign to POP

Species not in baseline?

→ One sample outside z-score threshold

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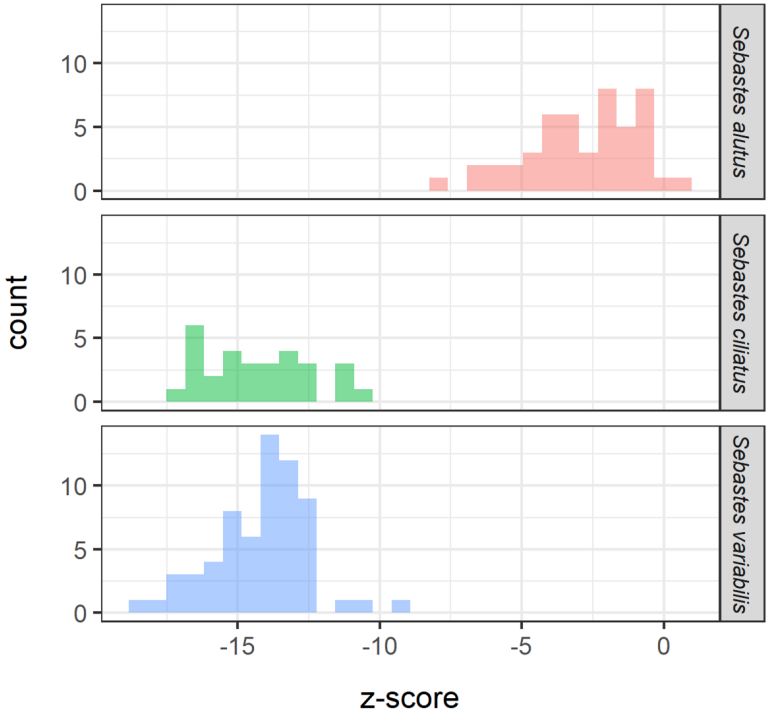
Identifying species NOT in the baseline

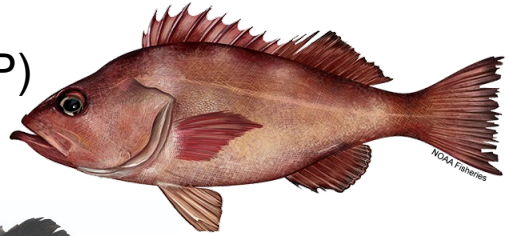
1. Look at z-scores: The fish's log-likelihood minus the expected log-likelihood and divided by the expected standard deviation (implemented in rubias R package).

1. Test by genotyping known adult samples

Known adult samples



Pacific Ocean Perch (POP)



Dark Dusky

Light Dusky

ADF&G photos

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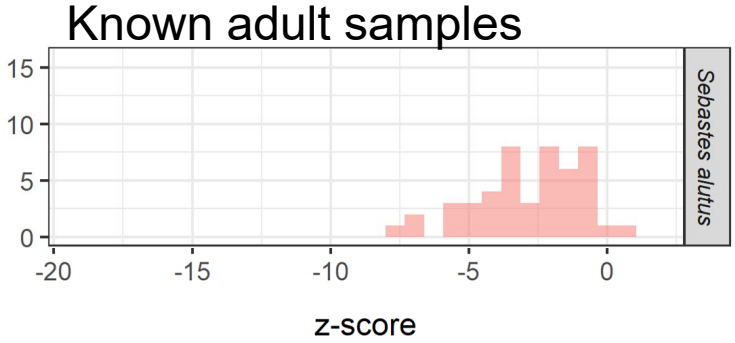

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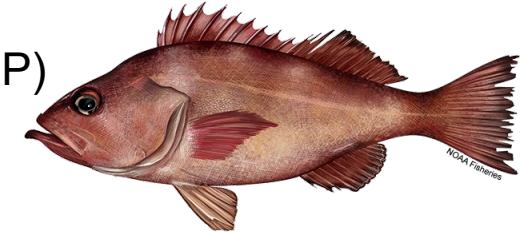

- POP has a larger spread, lower z-scores than expected for being represented in the baseline
- Multiple genetic groups (WGS data)

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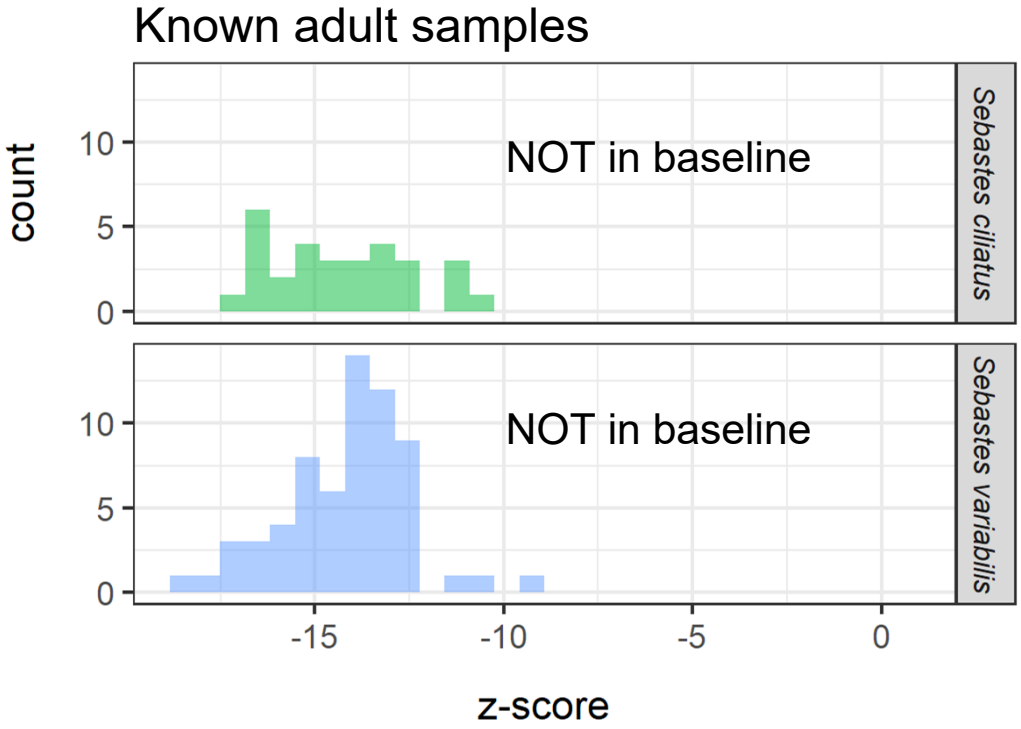

Dark Dusky

Light Dusky

ADF&G photos

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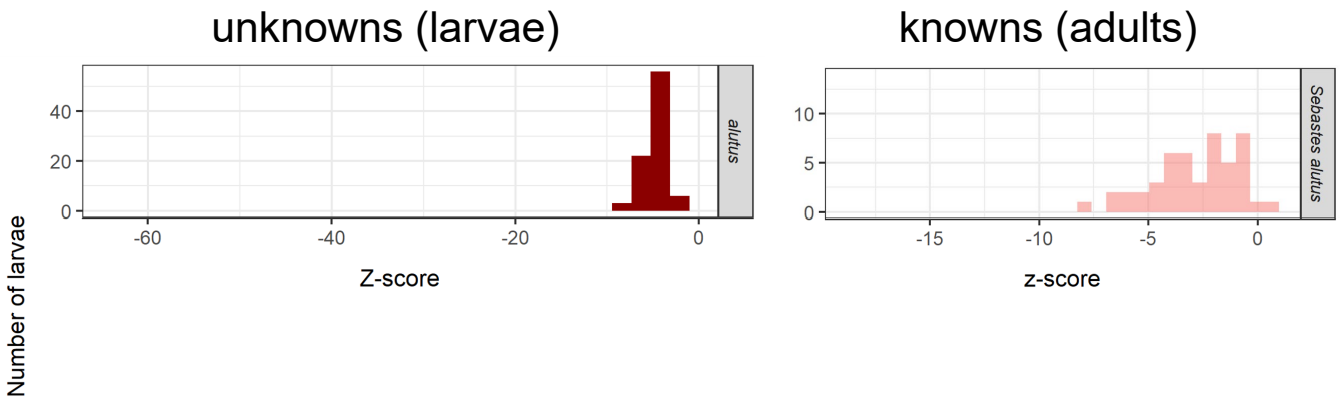
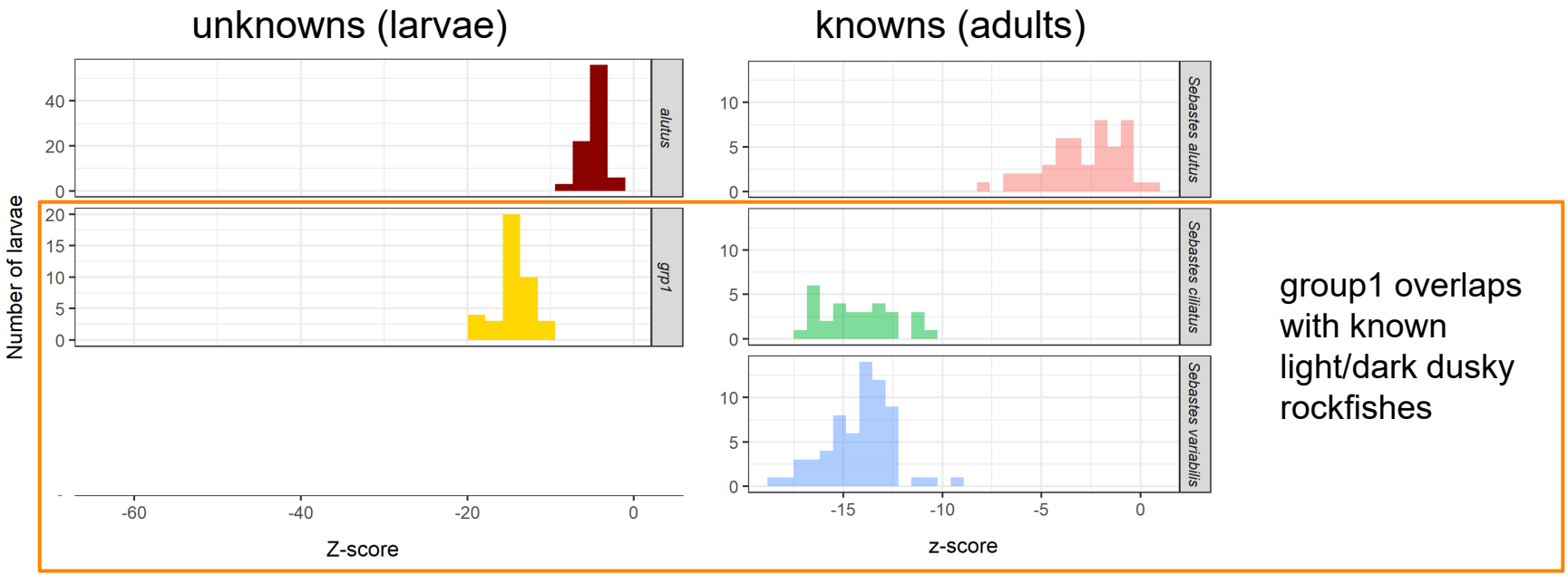
Species not in baseline: duskies, POP groups



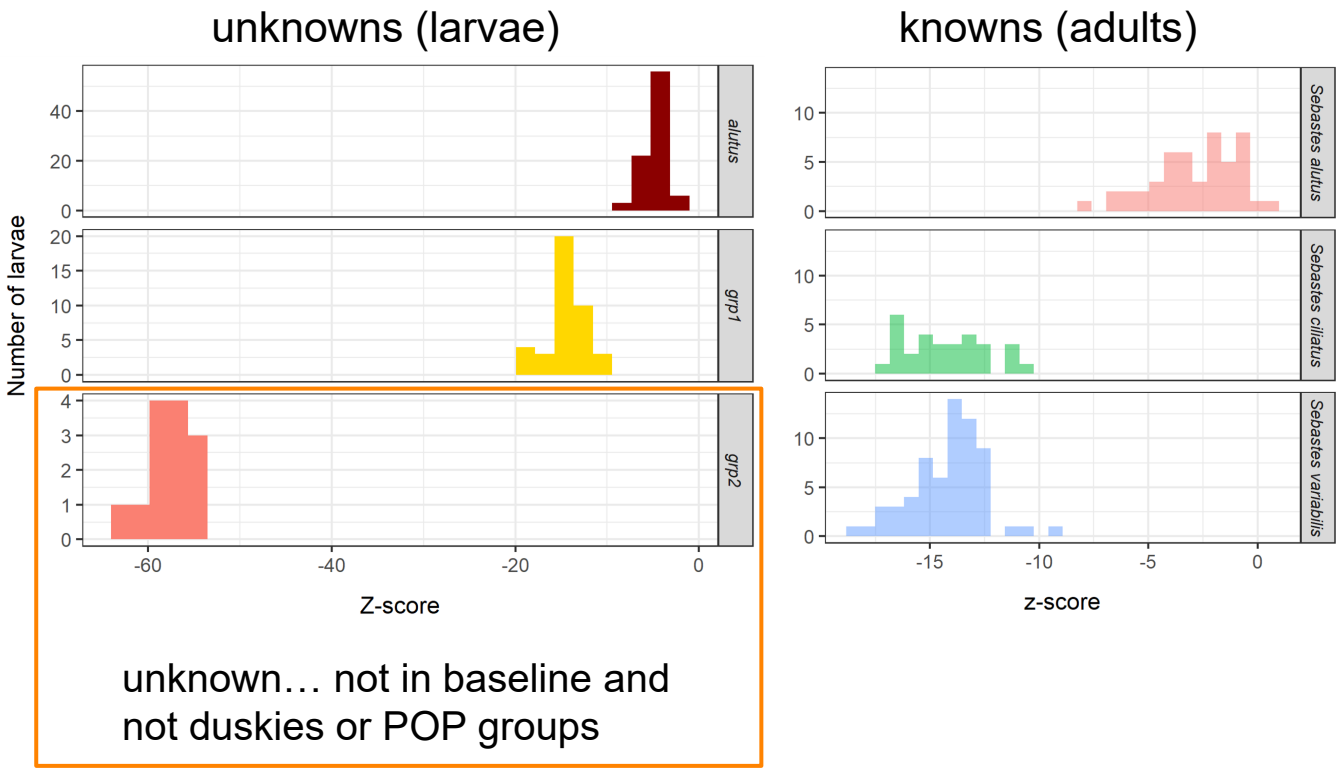
known z-score distribution of POP < -3

Species not in baseline: duskies, POP groups

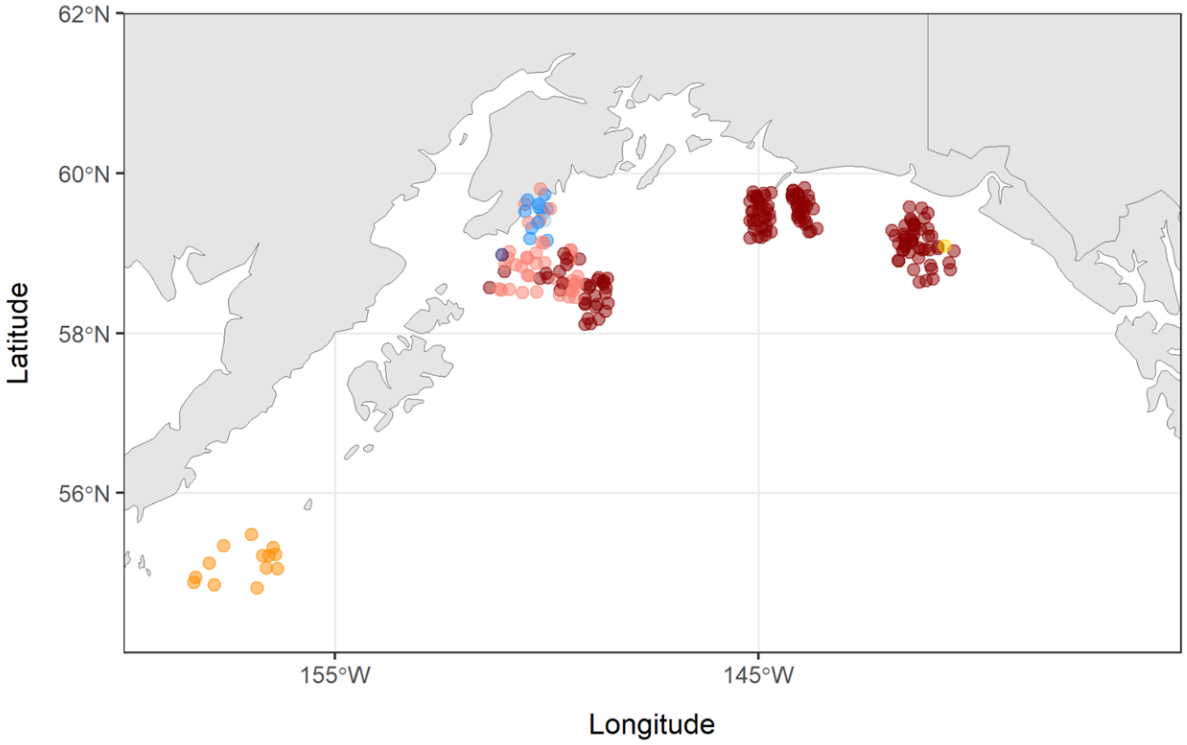


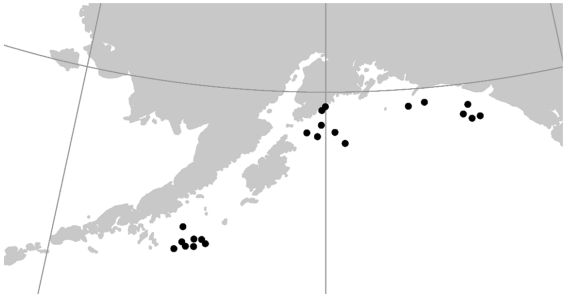
group1 overlaps with known light/dark dusky rockfishes

Species not in baseline: duskies, POP groups



Larval rockfish collections - GOA





Species	Common name
alutus	POP
babcocki	redbanded
dusky?	
grp2	
maliger	quillback
nigrocinctus	tiger
polyspinis	northern

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Acknowledgements

AFSC EcoFOCI, survey participants

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NMFS high-performance computing cluster (Sedna):
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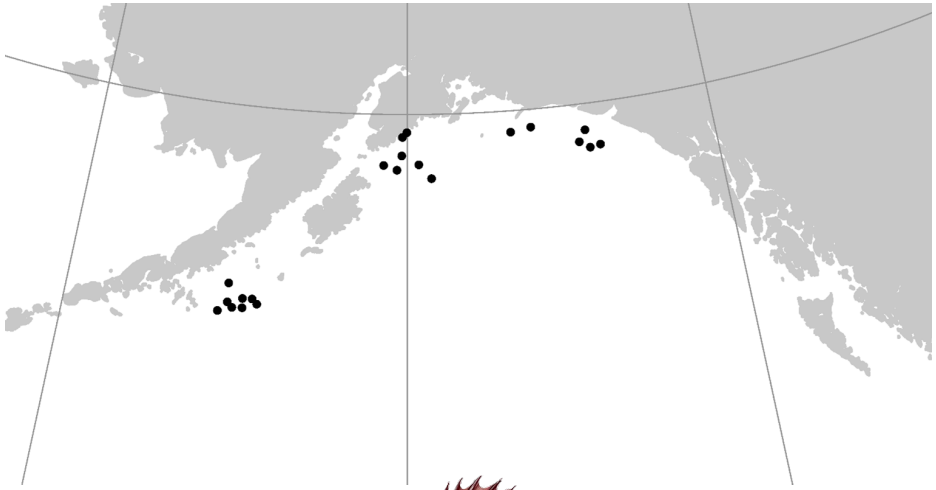

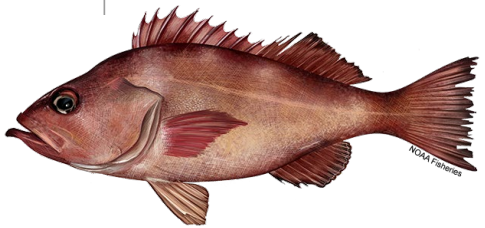

Questions?

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https://github.com/DianaBaetscher-NOAA/rockfish-species-id

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