



**NOAA
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CONSERVATION
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Research Center

Updating bycatch genetics workflow

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Who I am

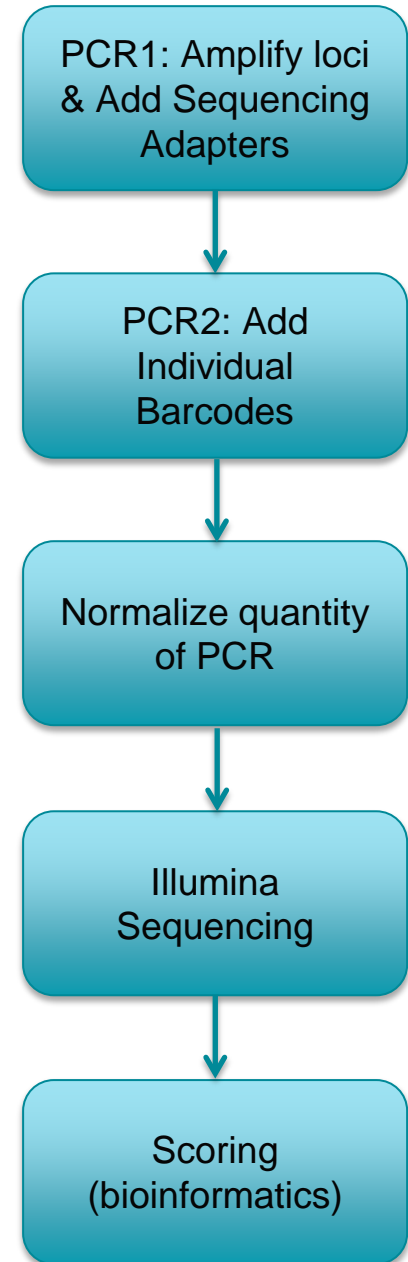
- UAF CFOS
 - PhD. work with Tony Gharrett and Megan McPhee.
 - Population genetics of sockeye salmon in SE Alaska.

- Skillset:
 - Population genetics, quantitative genetics, eDNA, R coding, molecular biology



New Genotyping Chemistry

- Genotyping in the thousands by sequencing (GTseq)
- Amplify hundreds of loci for thousands of individuals in a single run.
- Concordance (TaqMan):
 - Chum – 99.88%



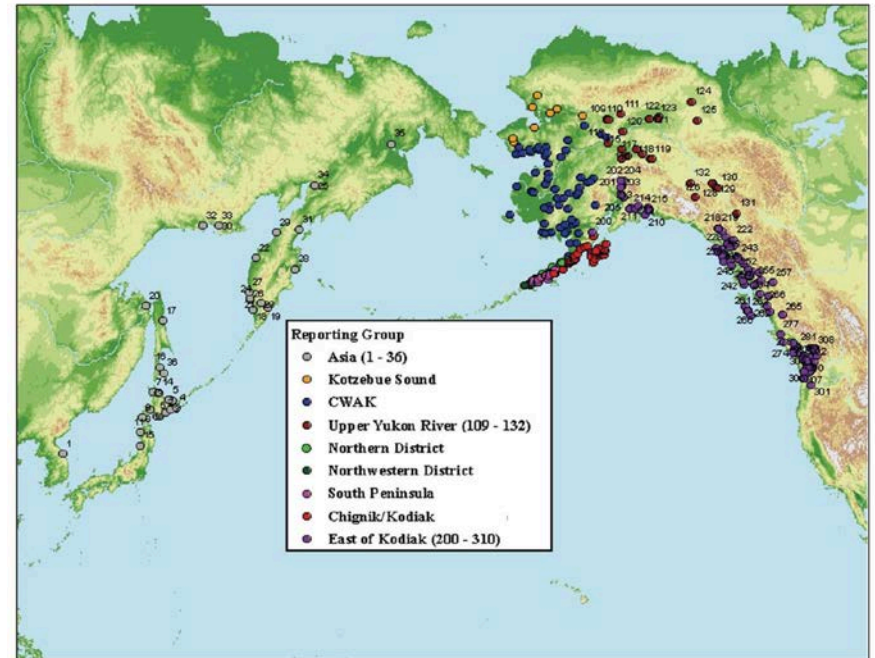
New Chum Baseline

Old (11 microsatellites)

- 381 populations
 - 77 pops Yukon, Western, & Coastal AK

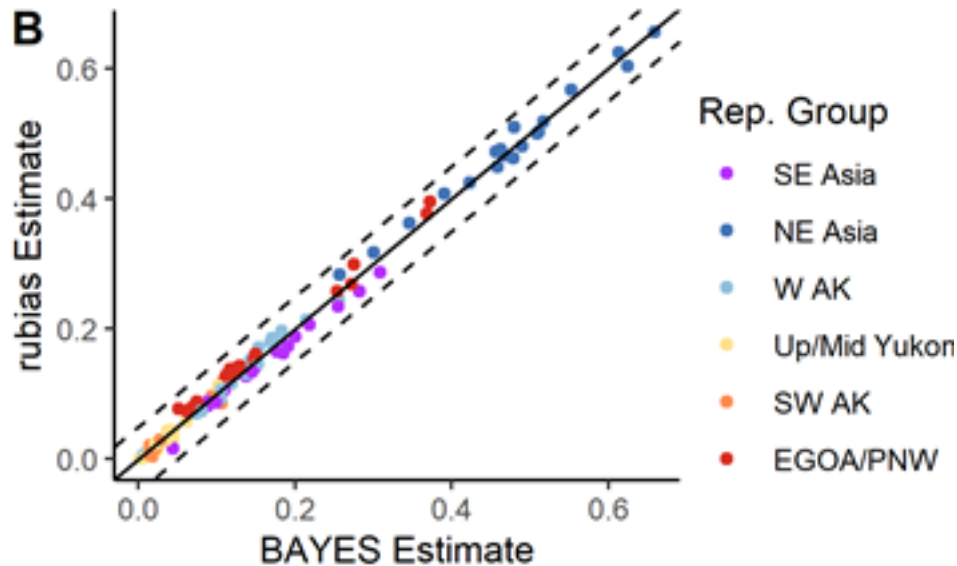
New (91 SNP loci)

- 310 populations
 - 163 pops Yukon, Western, & Coastal AK

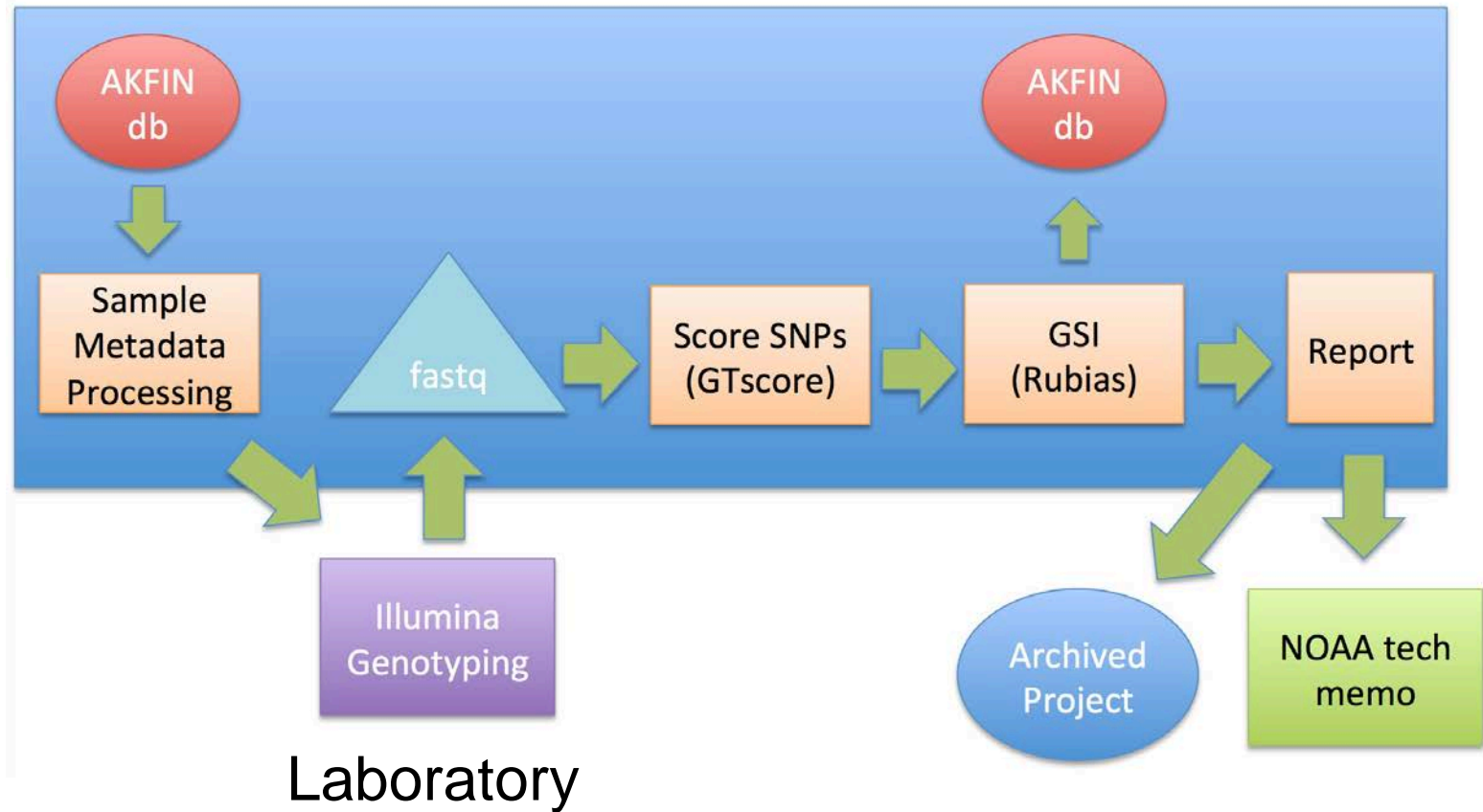


Changing Analysis Methodology

- Bayes (Pella & Masuda 2001)
 - Windows gui
- *rubias* (Moran and Anderson 2019)
 - R library
 - Integrated into data analysis pipeline
 - 2018 Analysis:
 - 0.94% (0.71%SD)



Data Analysis Pipeline



AKFIN database

Alaska Fisheries Information Network
Established under direction of Pacific
States Marine Fisheries Commission (PSMFC)

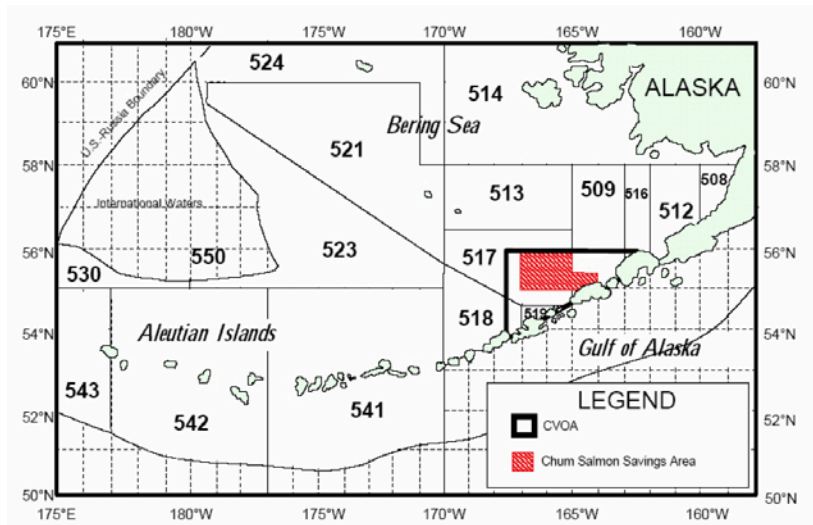


Goal:

- Link observer records to genetic and age information (confidentially)
- Facilitate data exploration and spatio-temporal modeling (PCCRC funded project).

AKFIN database: Trivial example

- Do static closures preserve the same stocks of fish from year to year?



www.npfmc.org

year	MixSize
2011	1784
2012	129
2013	1849
2014	1037
2015	1143
2016	2853
2017	3333
2018	2111
2019	1242

- Pull genetic records
- Format mixture
- *MSA rubias*

Spatio-temporal dynamics of chum salmon

PSC

- Quantify the inter- and intra-annual patterns of genetic stock composition across space, time, fishing sector, and fish age
- Evaluate how age- and stock-specific distributions of chum salmon vary with biotic and abiotic factors in the Bering Sea.
- End goal: Move to predictive framework for bycatch avoidance

Data visualization: R shiny (*interactive web*) application

- pdbarry.shinyapps.io/gsi_salmon_comparisons/



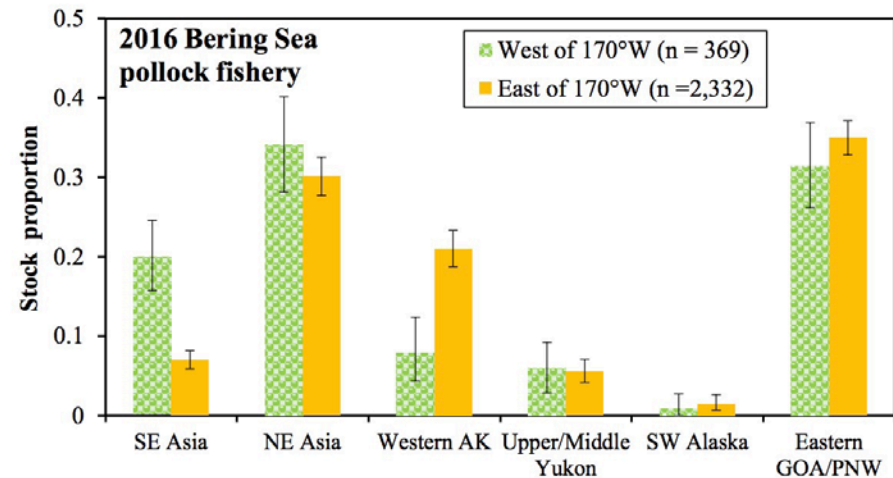
NOAA Technical Memorandum NMFS-AFSC-366
doi:10.7289/57M-AFSC-366

Genetic Stock Composition Analysis of Chum Salmon from the Prohibited Species Catch of the 2016 Bering Sea Walleye Pollock Trawl Fishery and Gulf of Alaska Groundfish Fisheries

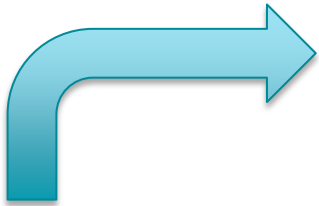
J. A. Whittle, C. M. Kondzela, H. T. Nguyen, K. Hauch, D. Cuadra, and J. R. Guyon

U.S. DEPARTMENT OF COMMERCE
National Oceanic and Atmospheric Administration
National Marine Fisheries Service
Alaska Fisheries Science Center

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Data visualization



Select:

Region

- Bering Sea / GOA

Spatial strata

- NMFS area
- East/West 170

Temporal strata

- Early/Middle/Late
- A/B season

Year

Genetic Stock Composition of salmon bycatch

1) Region
 Bering Sea

2) Group barplot (by color):
 Spatial Strata

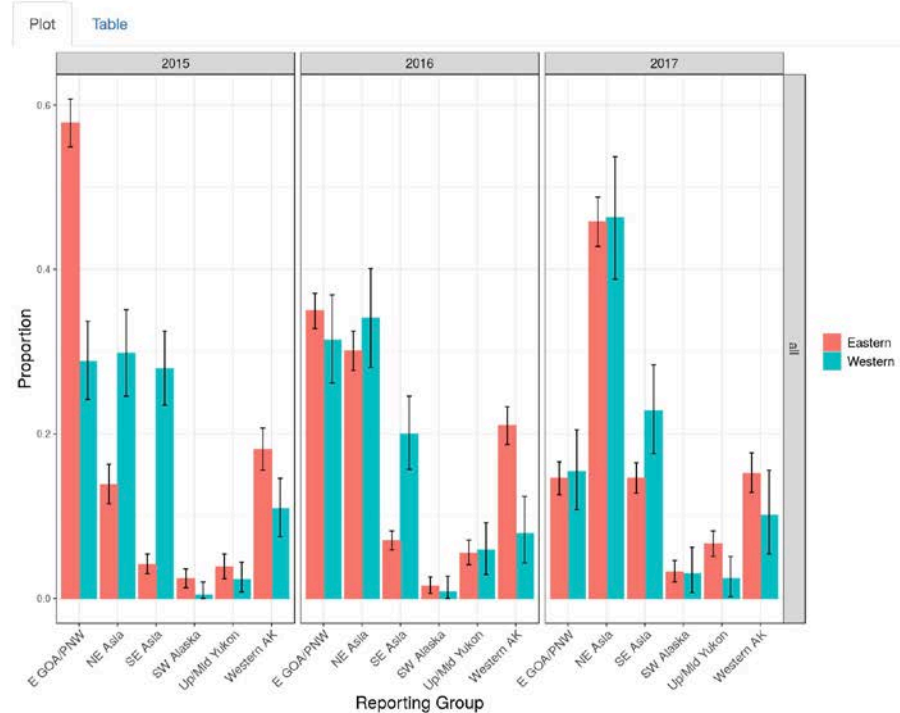
Include:
 Eastern Western

3) Separate graphs horizontally by:
 Year

Include:
 2015 2016 2017

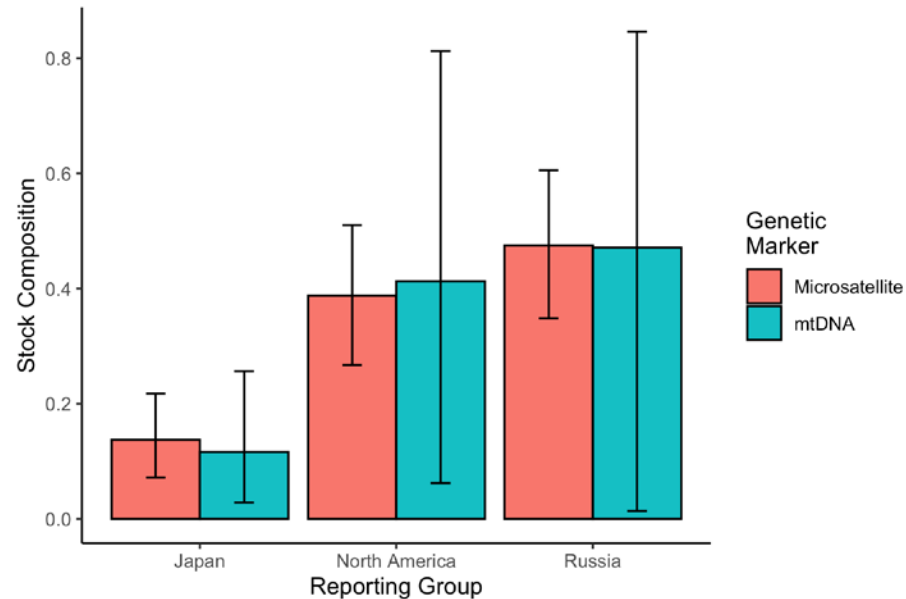
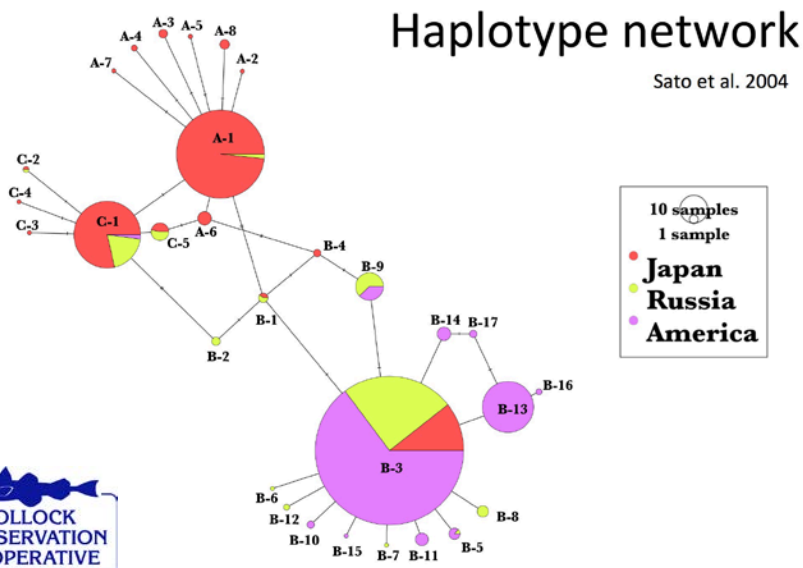
4) Separate graphs vertically by:
 Temporal Strata

Include:
 temporalstrat



Shipside stock identification of chum salmon bycatch with nanopore sequencing

- Can we estimate Asia vs. North America contributions to mixtures?



Acknowledgements

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