Auke Creek salmon eDNA



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But first.....the story of Nils Ryman and genetics and wildlife management.

Effective Population Size, Generation Interval, and Potential Loss of Genetic Variability in Game Species under Different Hunting Regimes

Author(s): Nils Ryman, Ramone Baccus, Christina Reuterwall and Michael H. Smith

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Rejected by *The Journal of Wildlife Management* in 1980

"genetics is not relevant to wildlife management".

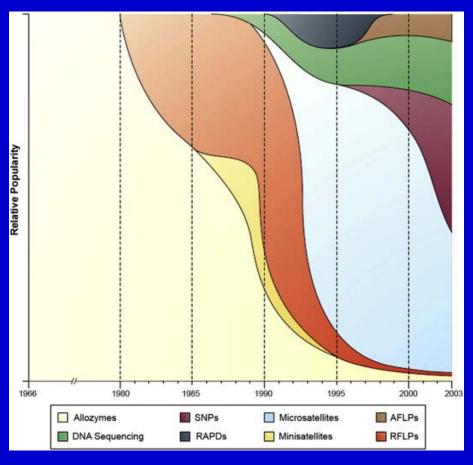
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Author(s): Nils Ryman, Ramone Baccus, Christina Reuterwall and Michael H. Smith Source: Oikos, Vol. 36, No. 3 (Mar., 1981), pp. 257-266

- published 1981 in journal Oikos, cited 137 times
- 100's of articles/year on wildlife genetics & management

Technology comes and goes.....



Schlotterer 2004

Environmental DNA for the enumeration and management of

Pacific salmon

In press. Molecular Ecology Resources

Taal Levi^{1*}, Jennifer M. Allen¹, Donovan Bell², John Joyce², Joshua R. Russell², David A. Tallmon³, Scott

C. Vulstek², Chunyan Yang⁴*, Douglas W. Yu^{4,5,6}

Thanks to Steve Heinl, ADFG.



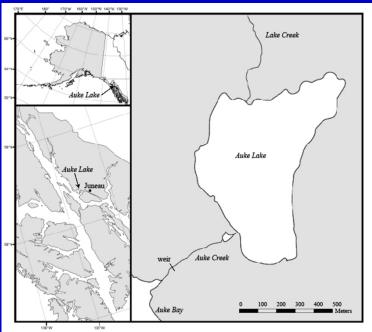
Josh Russell Donovan Bell Scott Vulstek





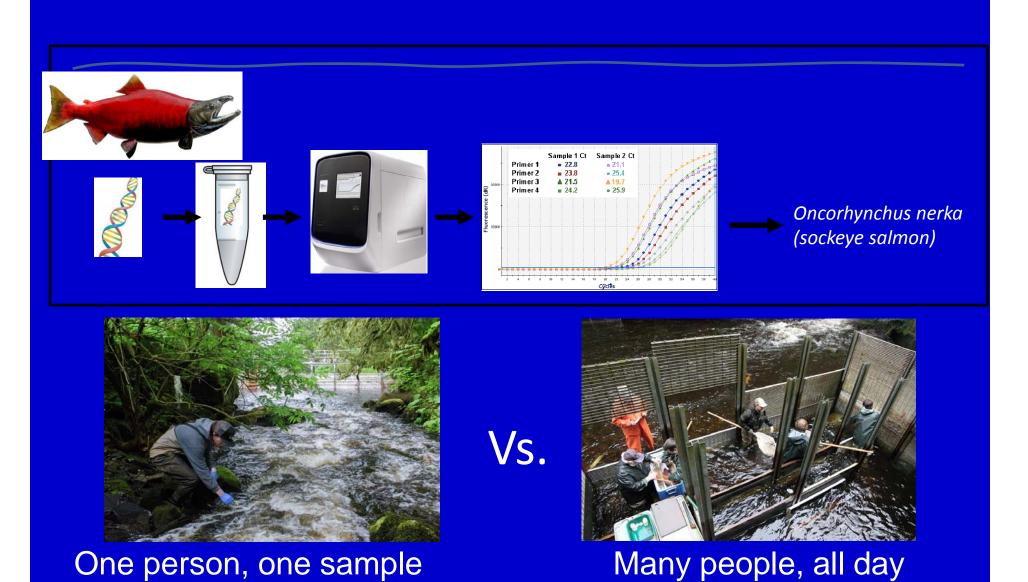
Auke Creek, Alaska

~40 year <u>census</u> of coho, sockeye, and pink salmon, Dolly Varden, & cutthroat trout



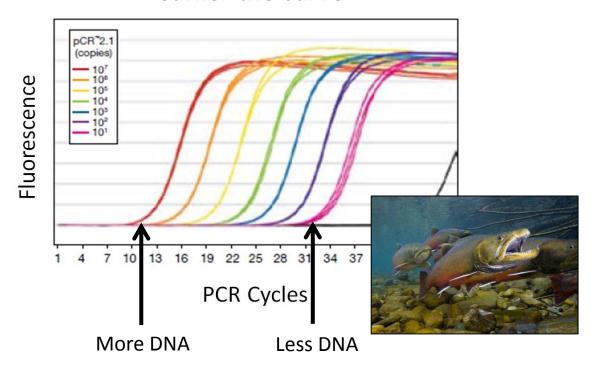


Does environmental DNA (eDNA) contain enough information to estimate salmon escapement sizes?

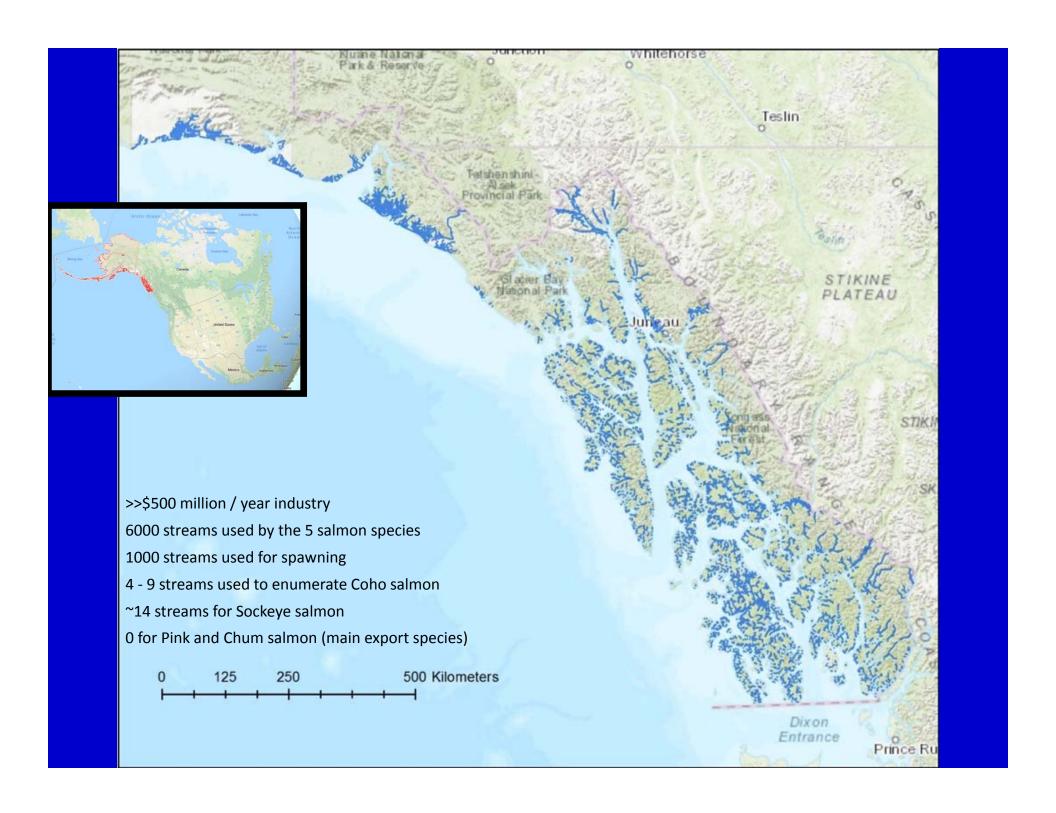


eDNA Analysis - quantitative PCR

The greater the quantity of target DNA, the earlier the curve



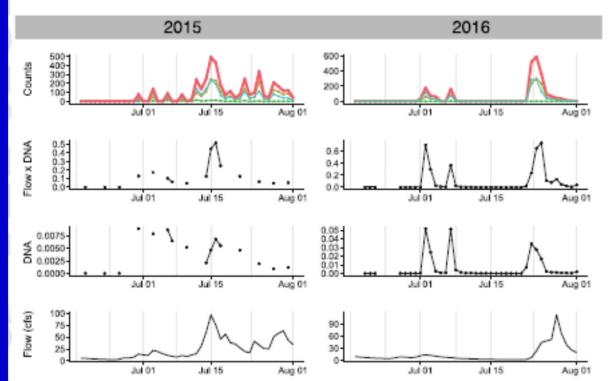




Flow x eDNA is useful.



Figure 2. Timeline from June 18 to August 1 of adult sockeye salmon counts, flow-corrected eDNA concentration (ng/µl*cfs), uncorrected eDNA concentration (ng/µl), stream flow (cfs, cubic-feet/sec), and stream temperature (°C) in 2015 and 2016. Environmental DNA results from consecutive days are connected by lines. Male and female salmon are denoted by yellow-brown and blue lines respectively, and jacks are denoted by green lines. Total adult sockeye salmon counts are denoted by thick red lines.



Sample every

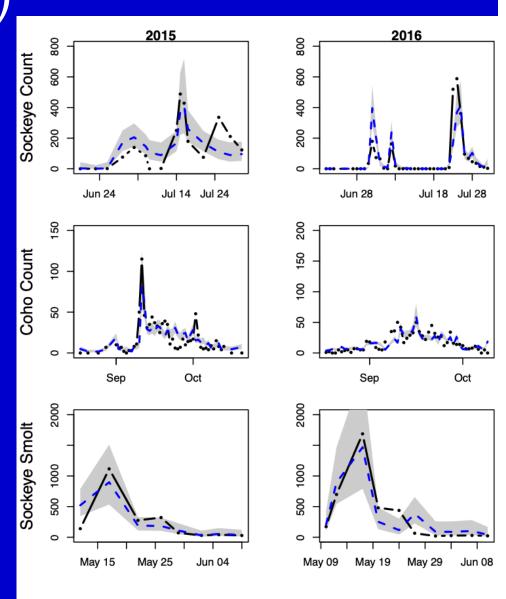
3 days

Sample daily

Fitted models (blue) vs. Fish count (black)

Consistent predictors

(eDNA count x stream flow)



Fitted models (blue) vs. Fish count (black)

Encouraging results:

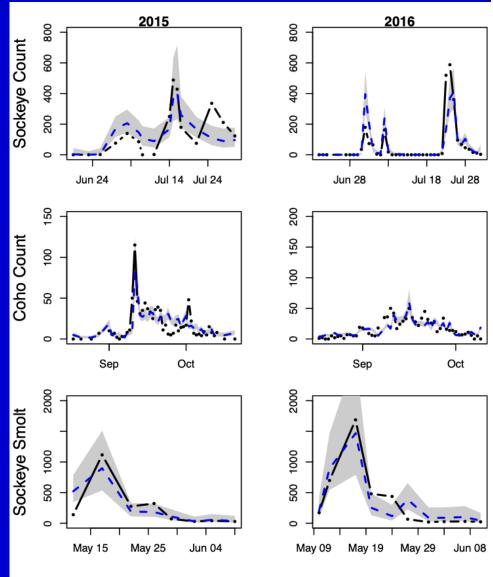
DNA predicted same-day counts

-juveniles and adults

DNA did NOT accumulate

-little 1-day & zero 2-day lag

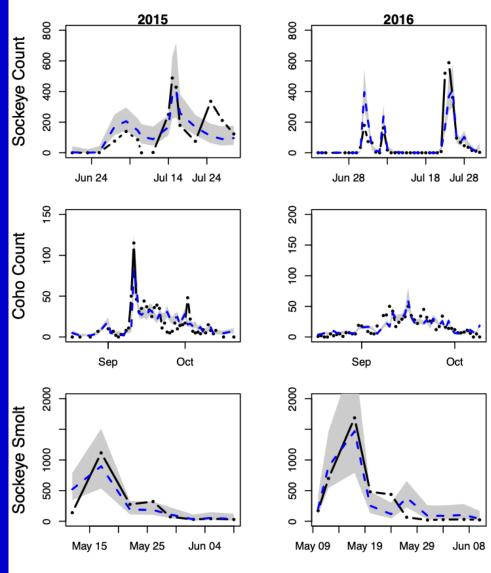
Little effect of upstream-rearing juveniles



Fitted models (blue) vs. Fish Count (black)

Considerations & Caveats

- -Need good streamflow data
- -Need daily eDNA sampling
- -eDNA varied by life stage
- -We have sample size of 1!
- -Cannot ignore molecular/lab considerations.



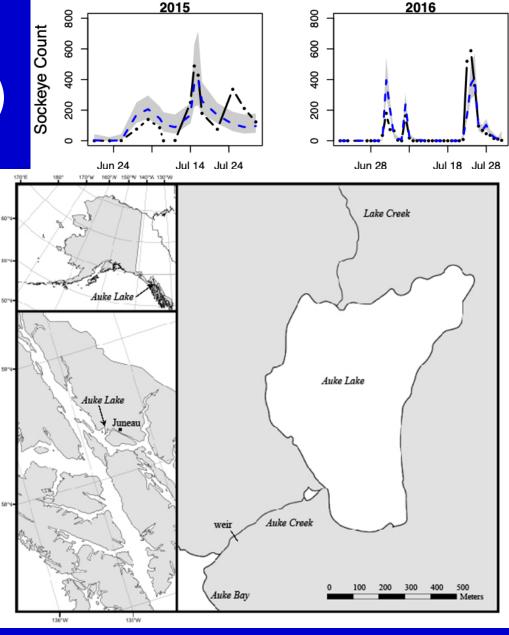
Fitted models (blue) vs.
Fish Count (black)

Considerations & Caveats

- -Need good streamflow data
- -Need daily eDNA sampling
- -eDNA varied by life stage
- -We have sample size of 1!

(lake, pH, weir location effects?)

-Cannot ignore molecular/lab considerations.



Worth future effort to explore eDNA to detect salmon run dynamics.

One technician can sample multiple streams per day

Citizen network could cover the whole landscape

Widespread eDNA sampling may be economically justified

- -if there is high variation across streams
- -if eDNA data can be used to parameterize spawner-recruit models

>>\$500 million / year industry

6000 streams used by the 5 salmon species

1000 streams used for spawning

4 - 9 streams used to enumerate Coho salmon

~14 streams for Sockeye salmon

O for Pink and Chum salmon (main export species)





eDNA Sampling Meets Information Needs at Multiple Scales

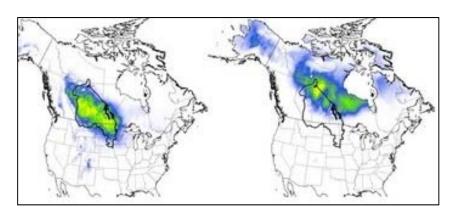
Local Scale

- Detection of Endangered Species
- Eradication of Unwanted Species



Broad Scale

- Species Distribution Model (Niche Model)
- Futuring the SDM
- Ecological Understandings





eDNA Has Become Right Tool For Detecting Rare Species

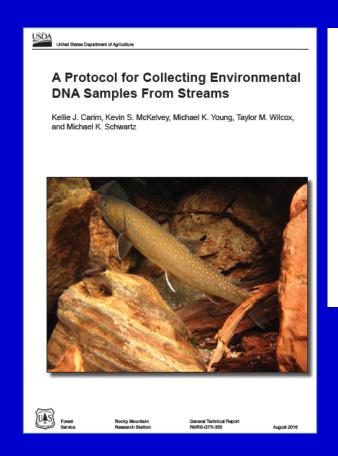


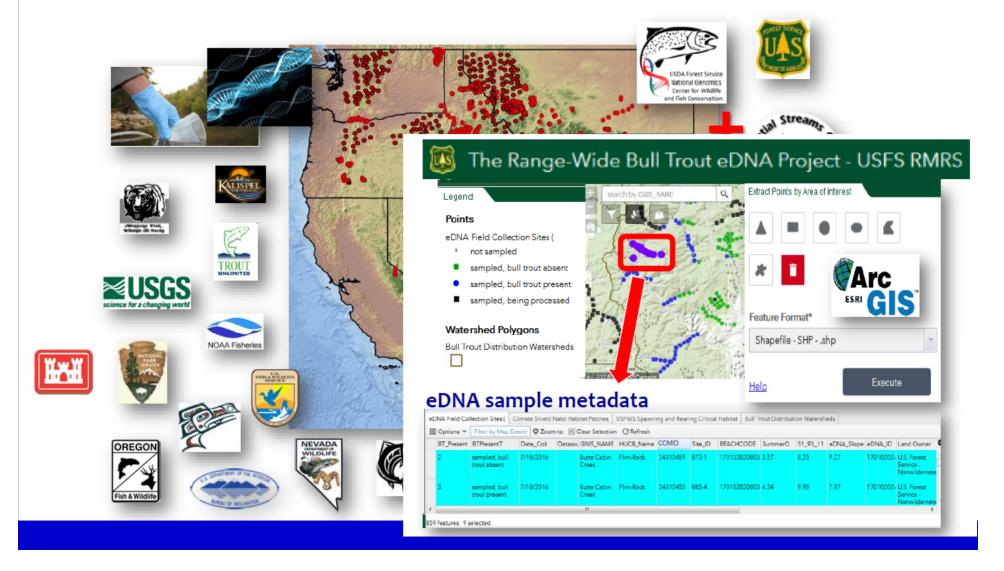


Figure 1. Complete environmental DNA kit



Take advantage of existing projects.....

Partners sampled >8,000 sites in last 4 years



Acknowledgements

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Co-authors: Taal Levi, Jen Allen, Donovan Bell, John Joyce, Josh Russell, Scott Vulstek, Chunyan Yang, Doug Yu.