

Overview of SALMOD for the Fall Chinook Salmon Life Cycle Production Model

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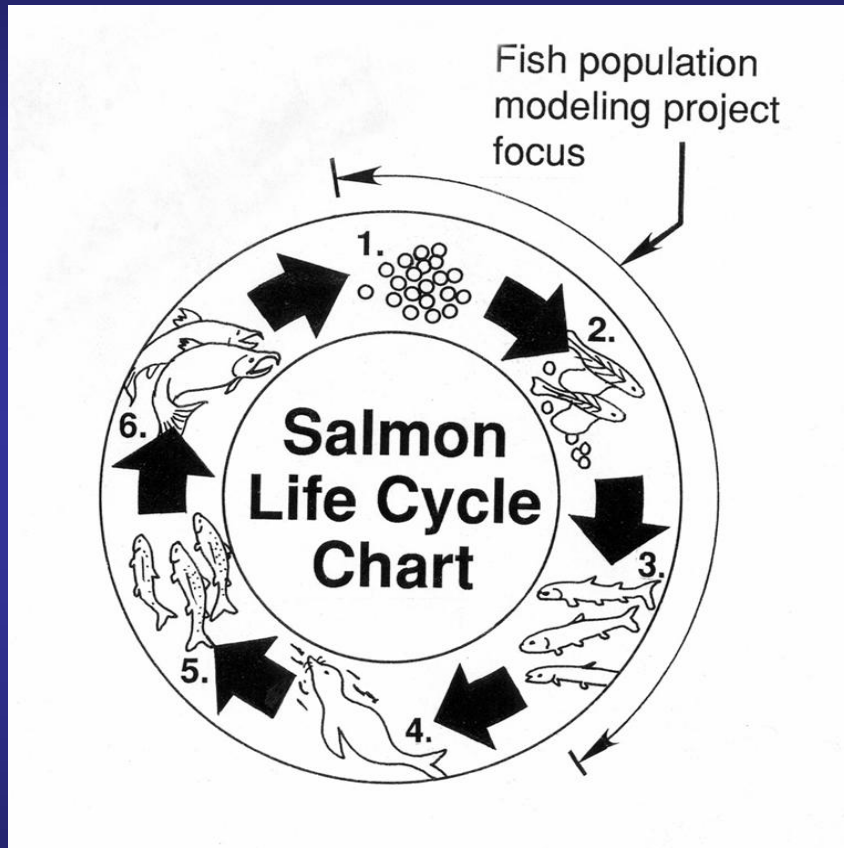
Fall Chinook Salmon Life Cycle Model
Informational Workshop

13 October 2010

Overview

- Temporal and Spatial Scale and Extent
- SALMOD's Biological Processes
- Driving Variables
- Updates to SALMOD for life cycle model
- Calibrating SALMOD

Biological Description - Lifestages



Eggs
Fry (<55 mm)
Juveniles (> 55 mm)

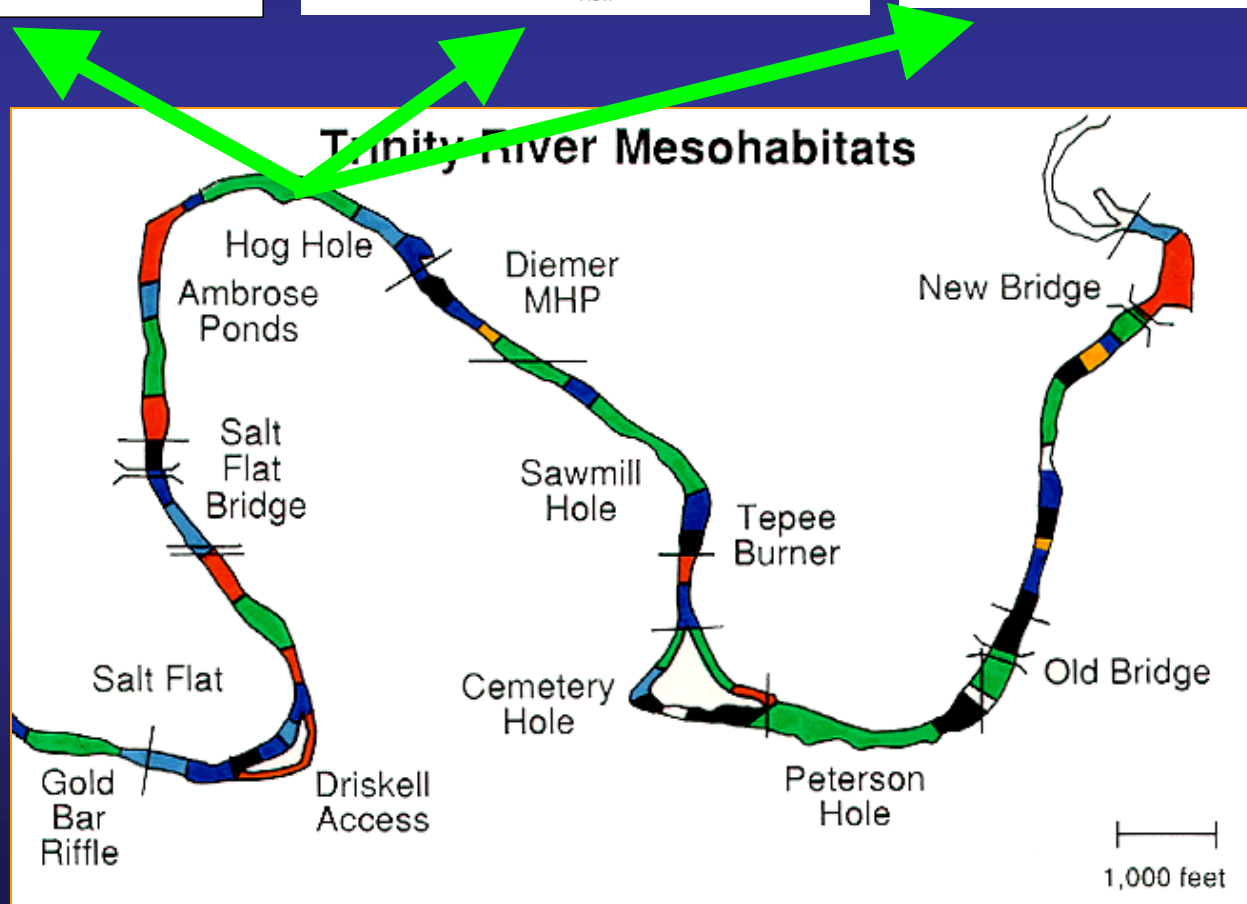
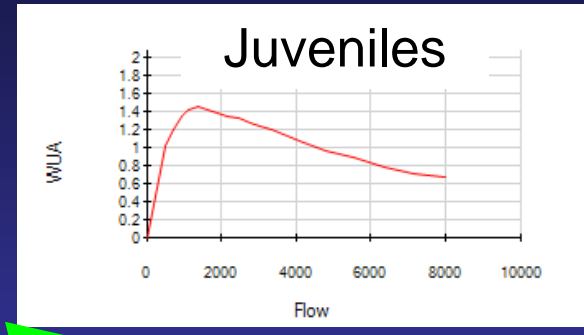
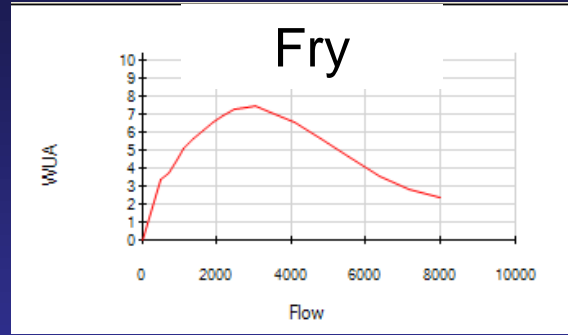
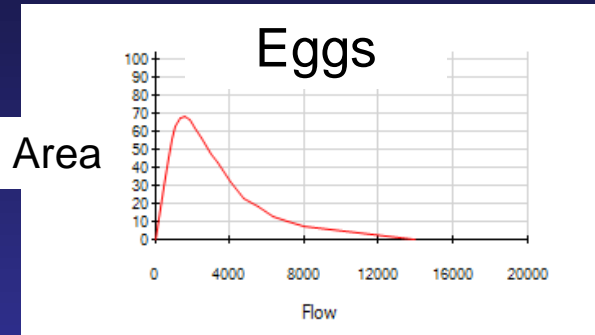
Temporal Scale and Extent: The Biological Year

- Flows and temperature
input at weekly time step
- Biological year
begins with spawning
ends with outmigration
- Biological processes
simulated through time by life stage

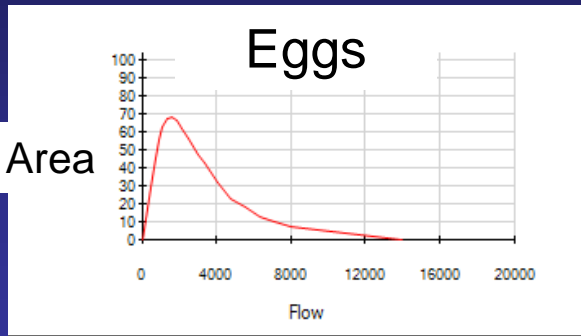
Temporal Sequence of Events



Spatial Scale: Mesohabitat Units

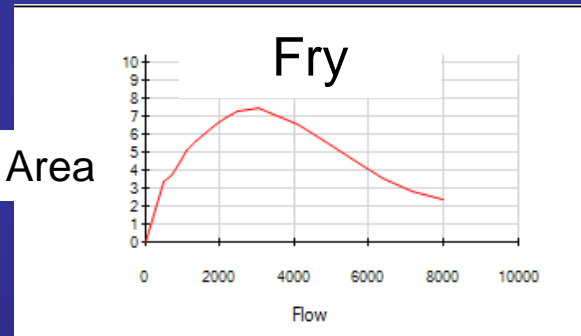


Discharge and Habitat Area Drive Dynamics by Life-stage and Habitat unit

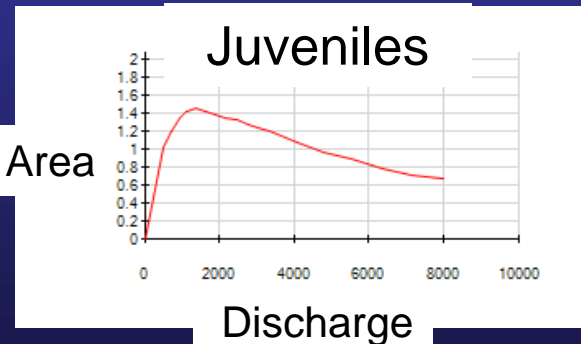


Survival

Redd Density



Density (fish/m²)
Disease (discharge)



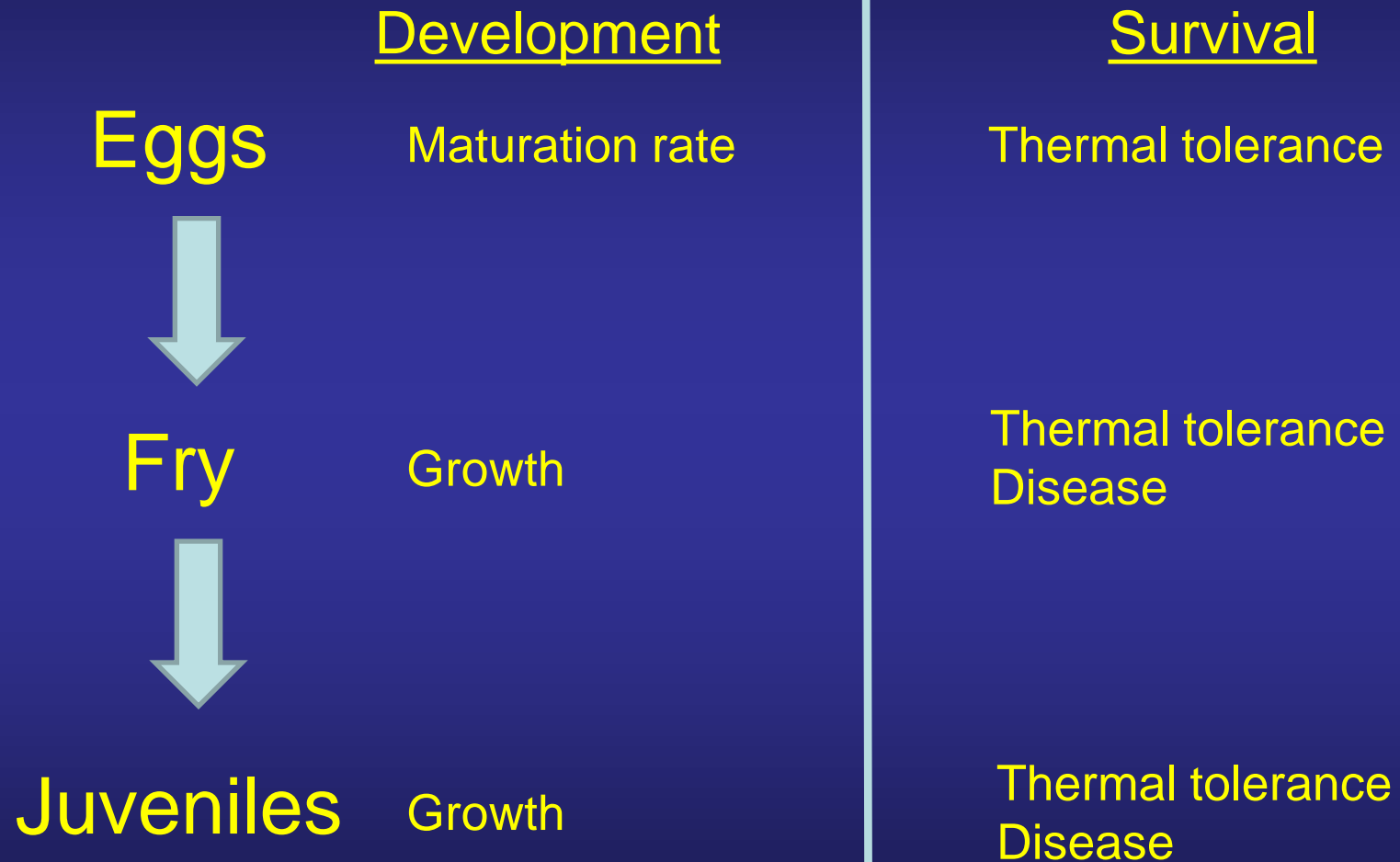
Density (fish/m²)
Disease (discharge)

Movement

Density (fish/m²)
Discharge

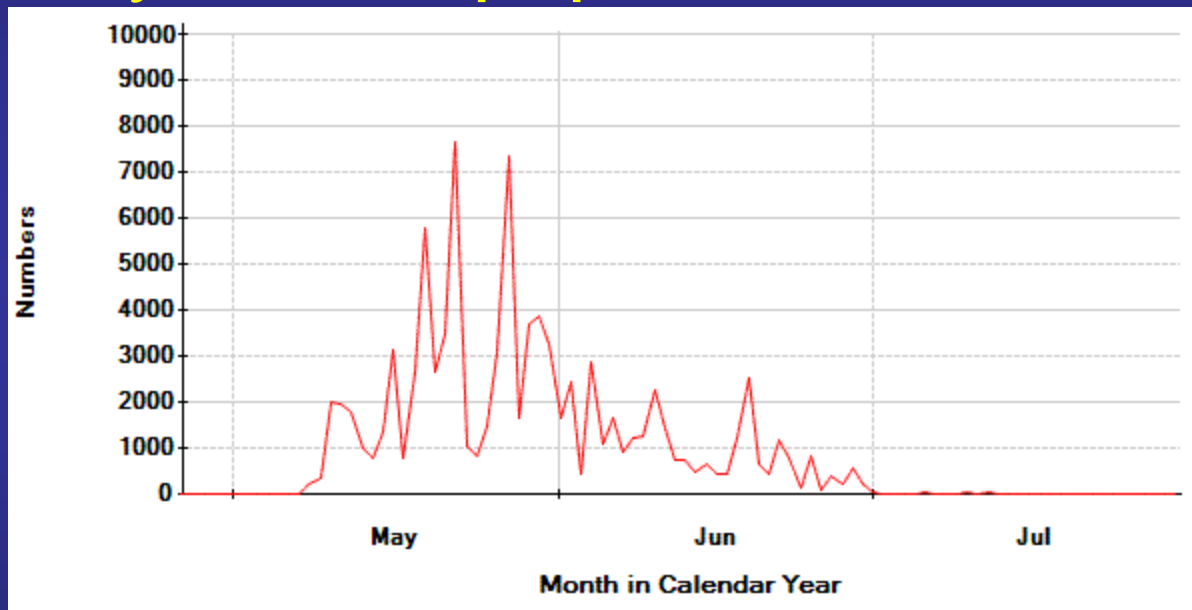
Density (fish/m²)
Discharge

Temperature Drives Dynamics by Life-stage and Habitat unit



Output for Life Cycle Model

- Abundance Time Series
 - at ocean entry
 - by source population



Ocean Life Stage

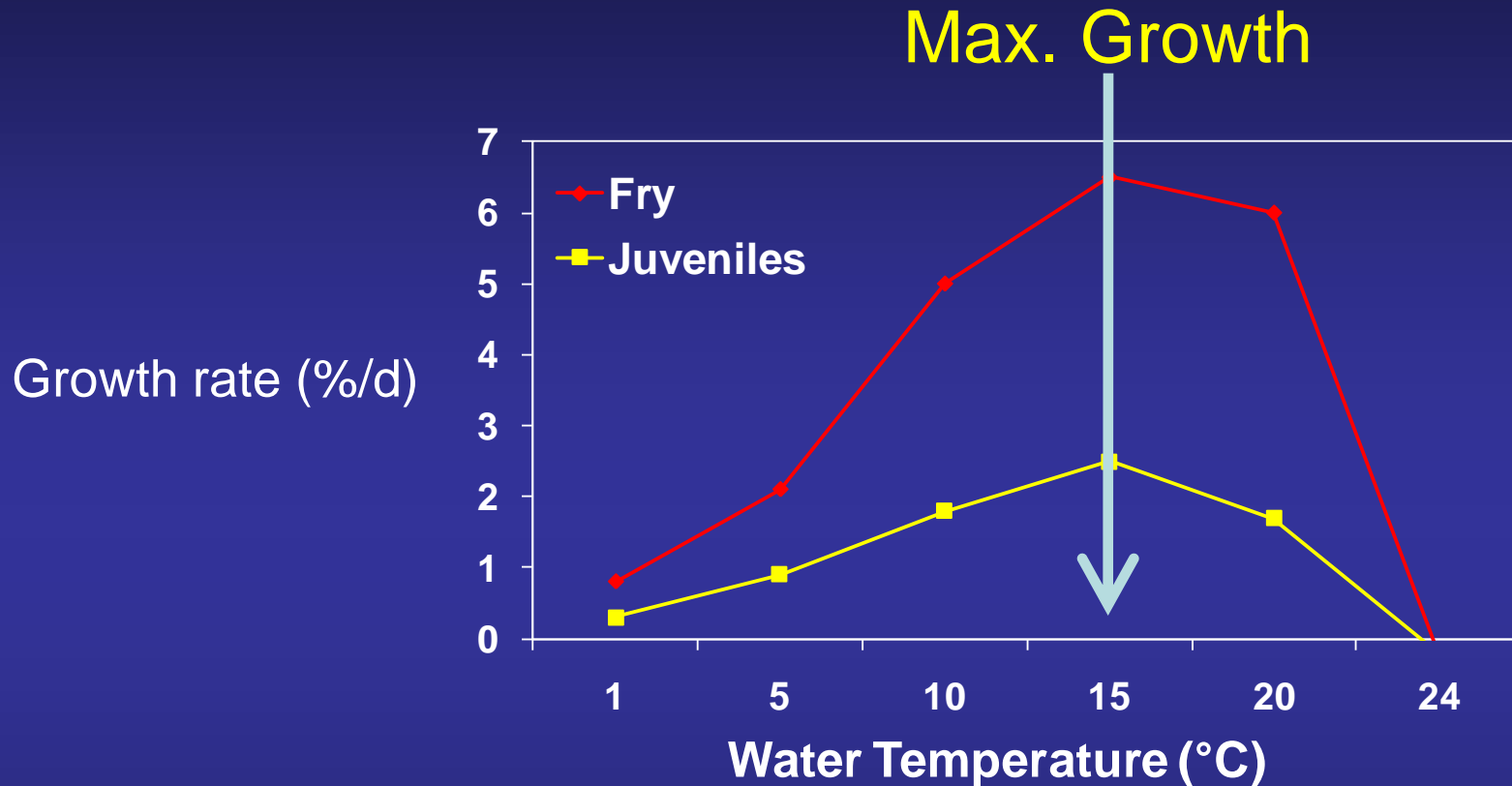
Changes to SALMOD For Life Cycle Model

- New programming platform
 - from Fortran/C++ to Visual Basic
- Tracking of source populations
- Change in Stewardship
 - from FORT to WFRC

Changes to SALMOD For Life Cycle Model

- Extended spatial domain
Keno to Ocean
- Incorporate disease model
- Update growth relationship
- Calibrate and validate against data

Update growth relationship

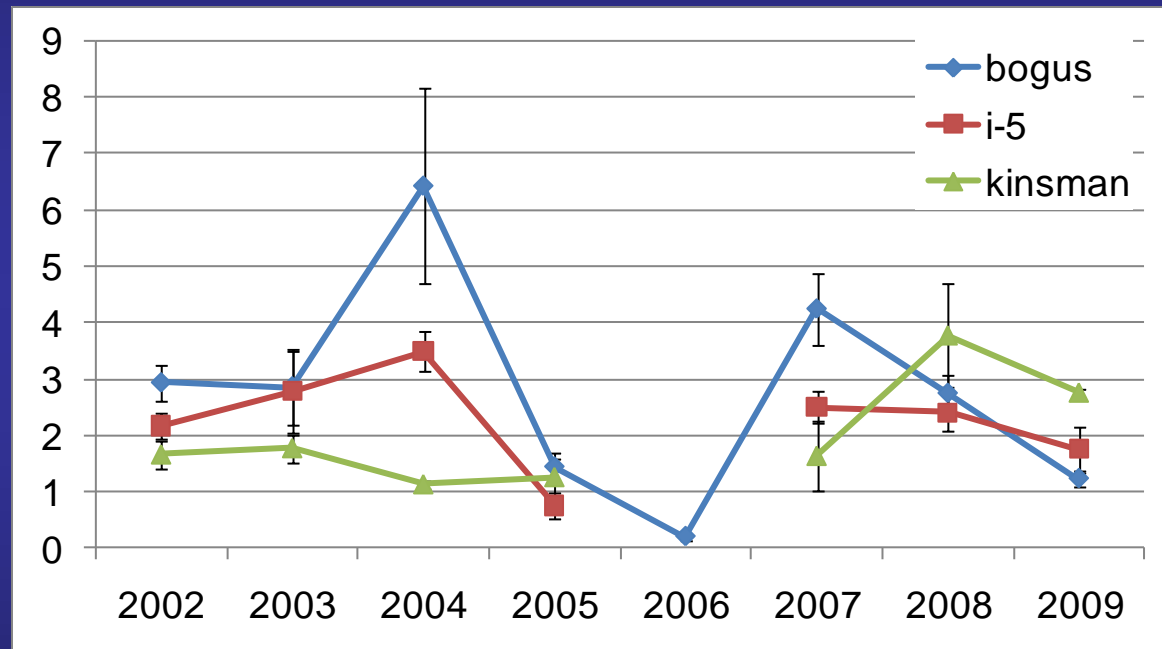


Recent data from Snake, Sac., Klamath Rivers
- Max. Growth at 19-20 °C

Calibration and Validation Data

-Trapping data on Lower Klamath
mark-recapture abundance estimates

Juvenile
abundance
(millions)



-Survival to Age 2 from cohort reconstruction

Calibration via Monte Carlo Simulation

- Draw parameter values from distribution
e.g., coefficients of logistic disease model
- Compare predicted vs. observed abundance
likelihood function, lognormal error structure
- Repeat, Repeat, Repeat
generate distribution of likelihood values
- Highest likelihood = best set of parameters
- Many plausible parameter sets
e.g., draw parameter set from best 10%

Status of SALMOD Updates

- Completed tasks
 - New platform implemented
 - Track source populations
 - Extend from Keno to Ocean

- Tasks in progress
 - Disease model
 - Growth relationship
 - Calibration

Questions?

