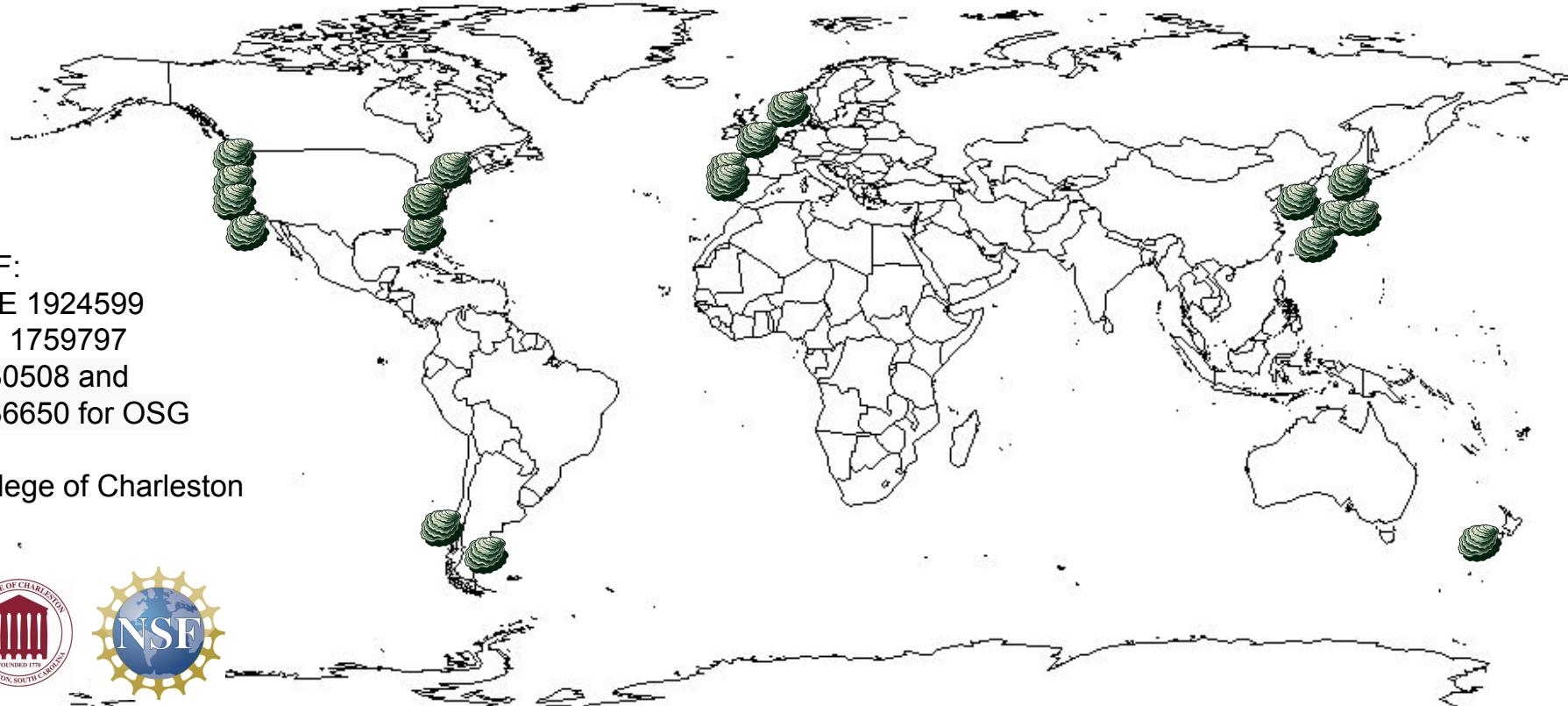


Distinguishing among alternative vectors for marine invasive species: Shipping versus Oyster transport

Allan Strand, Ryan Carnegie¹, Jim Carlton, Lucia Couceiro, Jeff Crooks, Hikaru Endo, Hilary Heyford, Masakazu Hori, Mits Kamiya, Gen Kanaya, Judith Kochmann, Kun-Seop Lee, Lauren Lees, Hannah Miller, Massa Nakaoka, Eric Pante, Jennifer Ruesink, Evangelina Schwindt, Åsa Strand, Richard Taylor, Ryuta Terada, Martin Thiel, Takefumi Yorisue, Danielle Zacherl, **Erik Sotka**



NSF:
OCE 1924599
ABI 1759797
2030508 and
1836650 for OSG

College of Charleston





“The Falls at
Tivoli”
M von Rhode,
1808

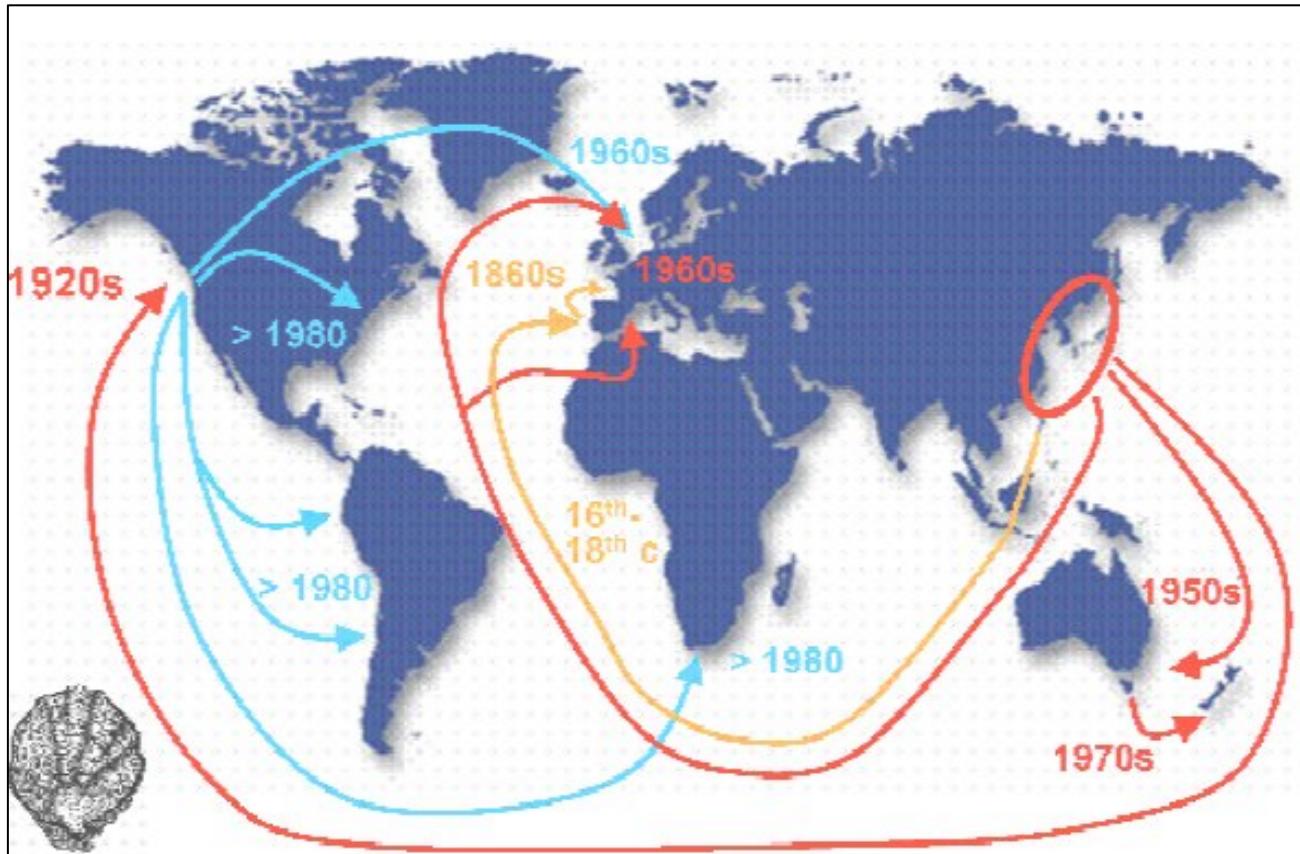


“The Falls at
Tivoli”
M von Rhode,
1808

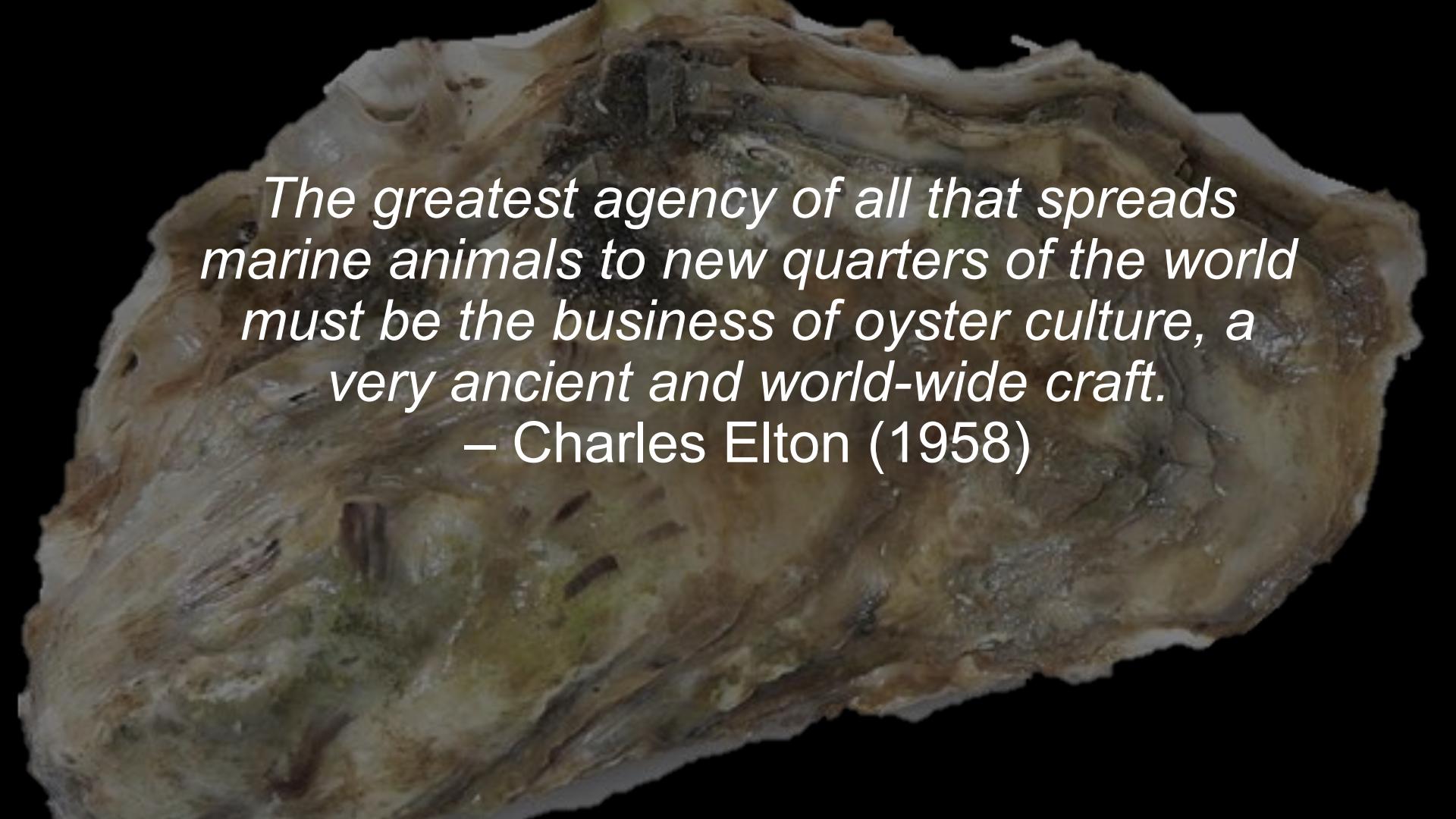
Magellana (Crassostrea) gigas occurrences (GBIF)



These global introductions were intentional



Marennes-Oléron Bay, FR

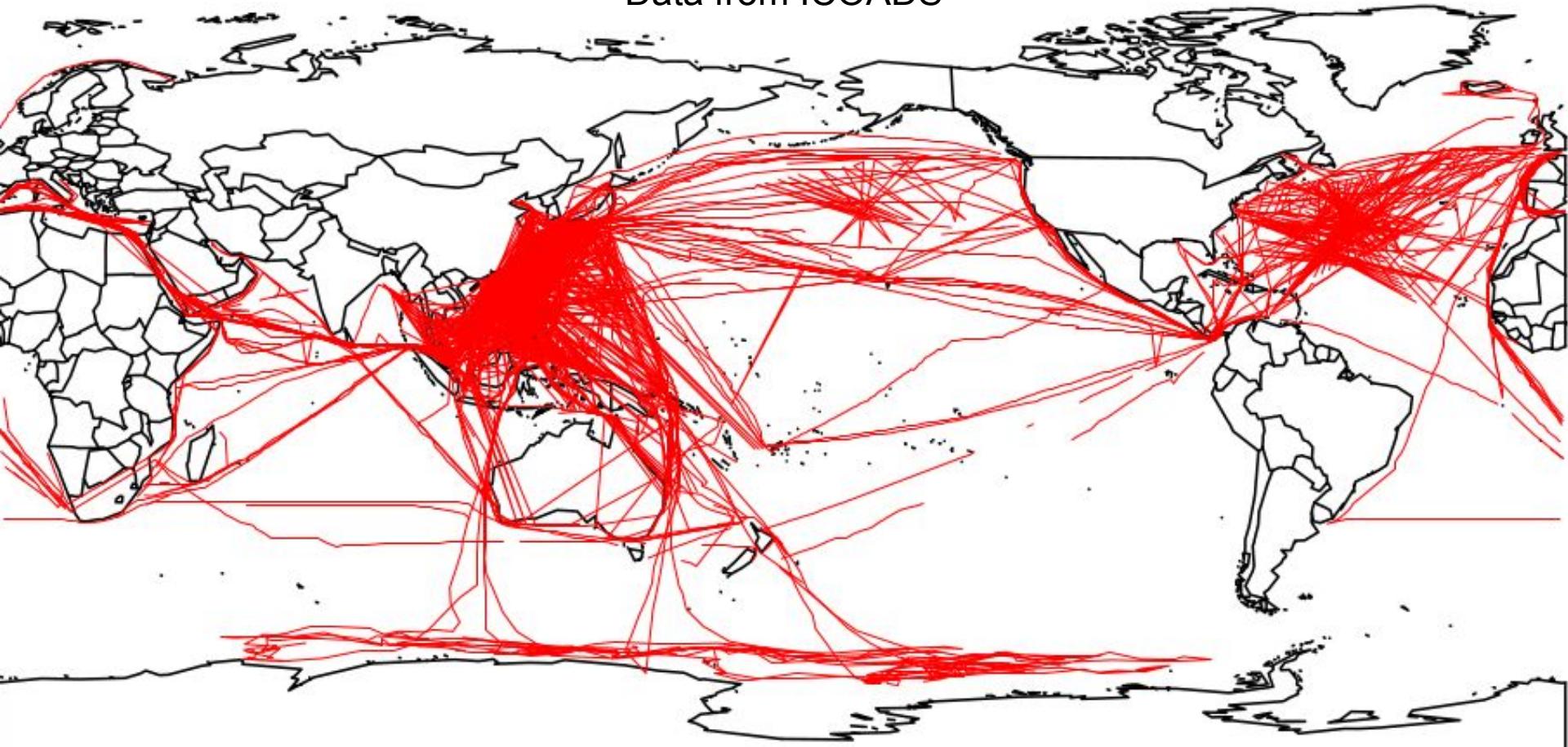
A close-up photograph of a large, open oyster shell against a solid black background. The shell is roughly triangular in shape, with a dark brown, textured interior and a lighter, yellowish-brown exterior. The lighting highlights the intricate layers and ridges of the shell's surface.

*The greatest agency of all that spreads
marine animals to new quarters of the world
must be the business of oyster culture, a
very ancient and world-wide craft.*

– Charles Elton (1958)

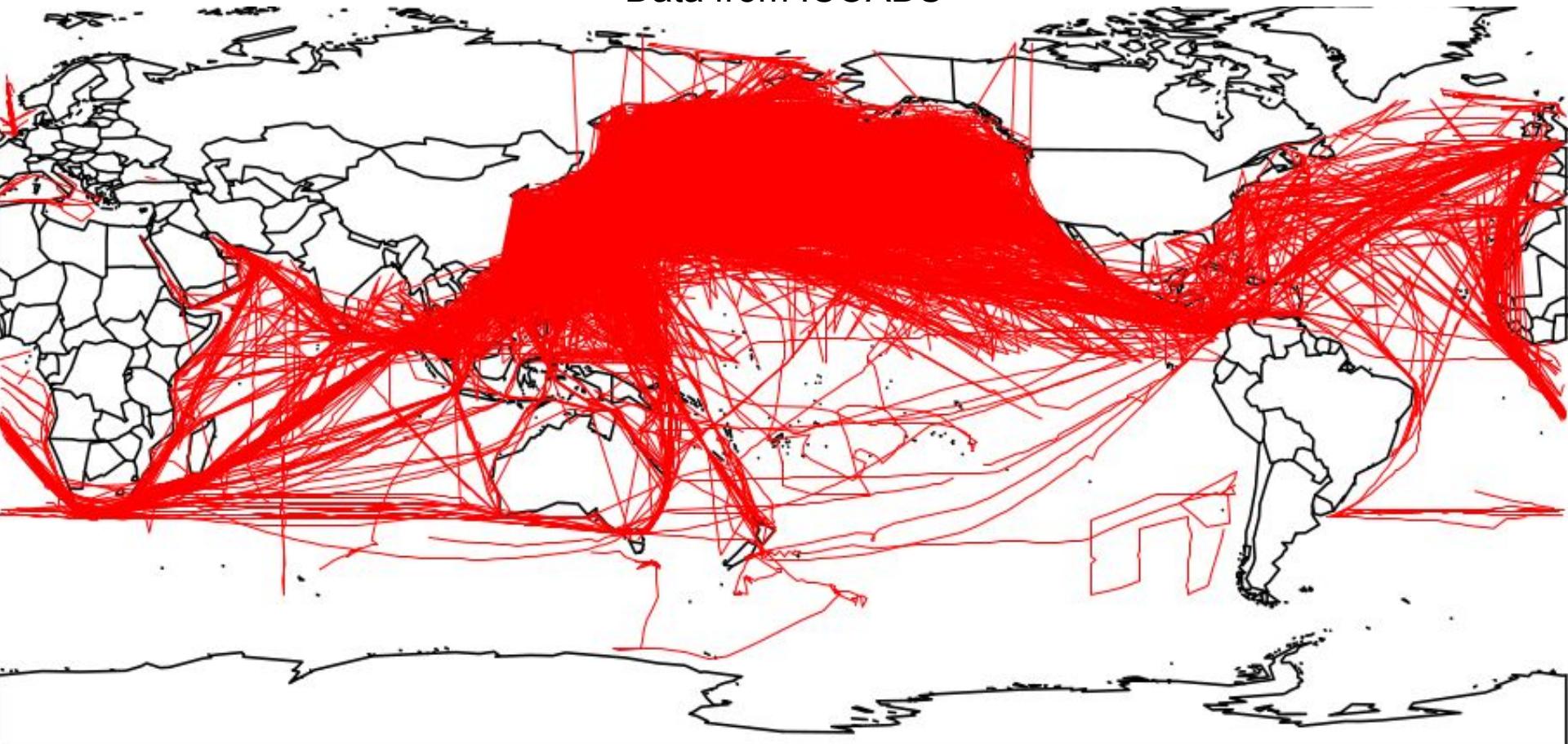
Voyages stopping or originating in Japan, 1958

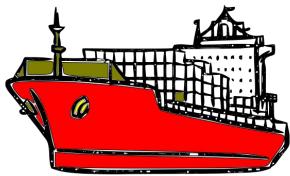
Data from ICOADS



Voyages stopping or originating in Japan, 1968

Data from ICOADS





Unified framework to differentiate among alternative introduction modes



Create contrasting introduction models.

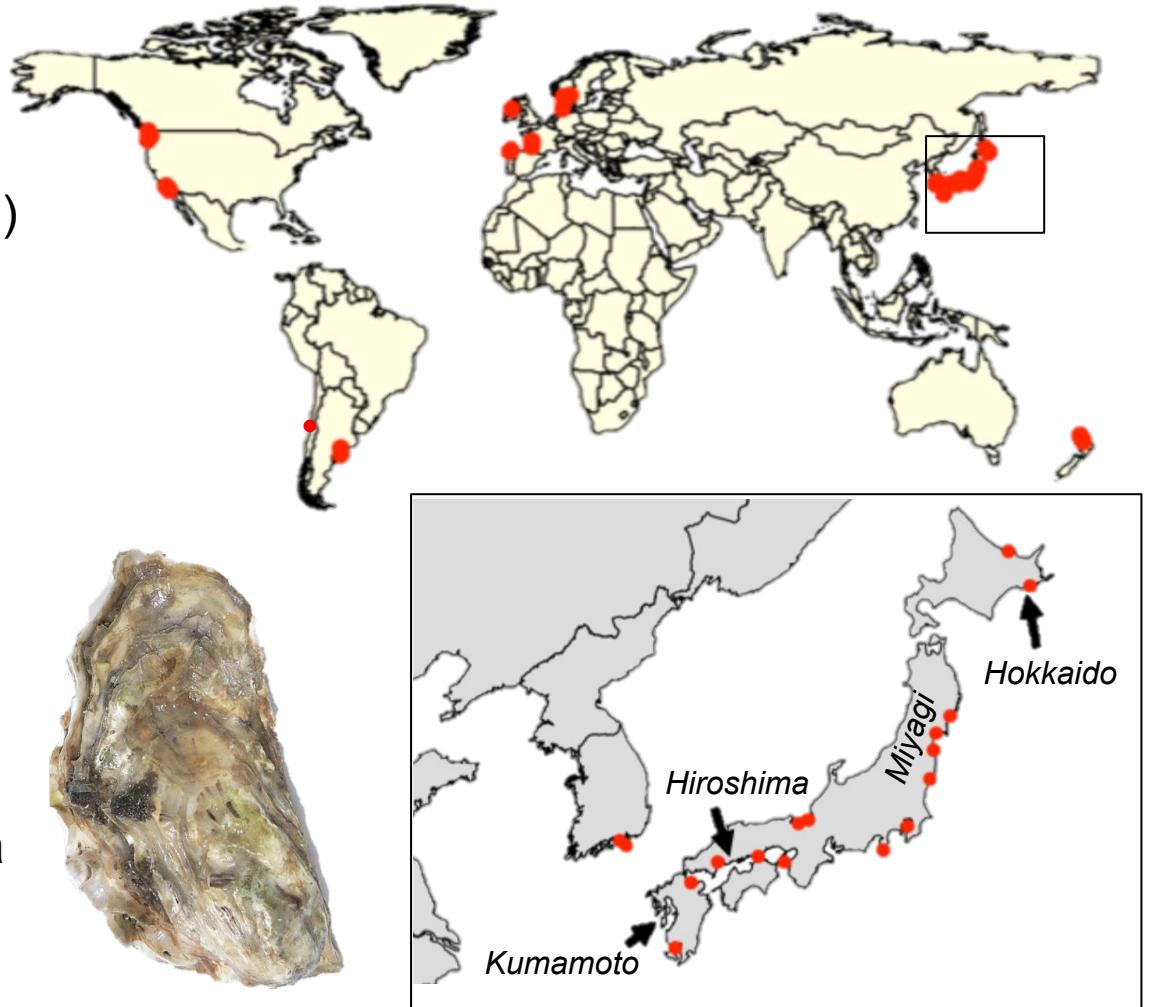
- a) Oyster mediated: population genomics
- b) Shipping mediated: Ship's log data (ICOADS)
 - i) archived by US/NOAA as part of the International Comprehensive Ocean-Atmosphere Data Set climate monitoring project

Use genetic data for introduced species to compare the models

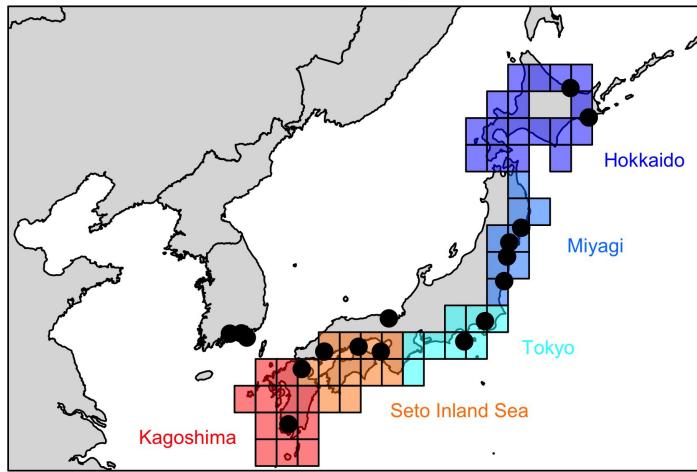
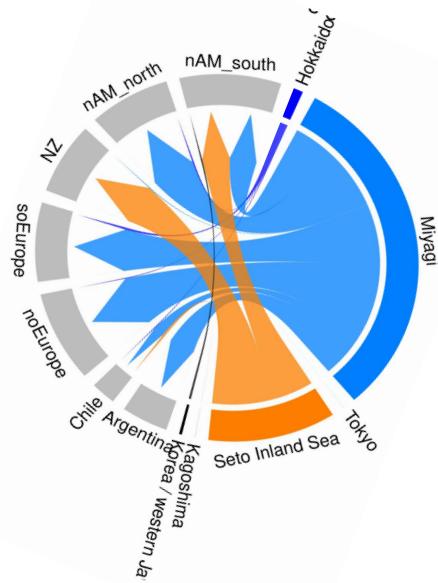
- a) Identify introduced species with publicly available genetic data
- b) Simulate genetic data for those species based on the two alternative vector models
- c) Use Approximate Bayesian Computation (ABC) to assign relative model fits

Oyster genetics

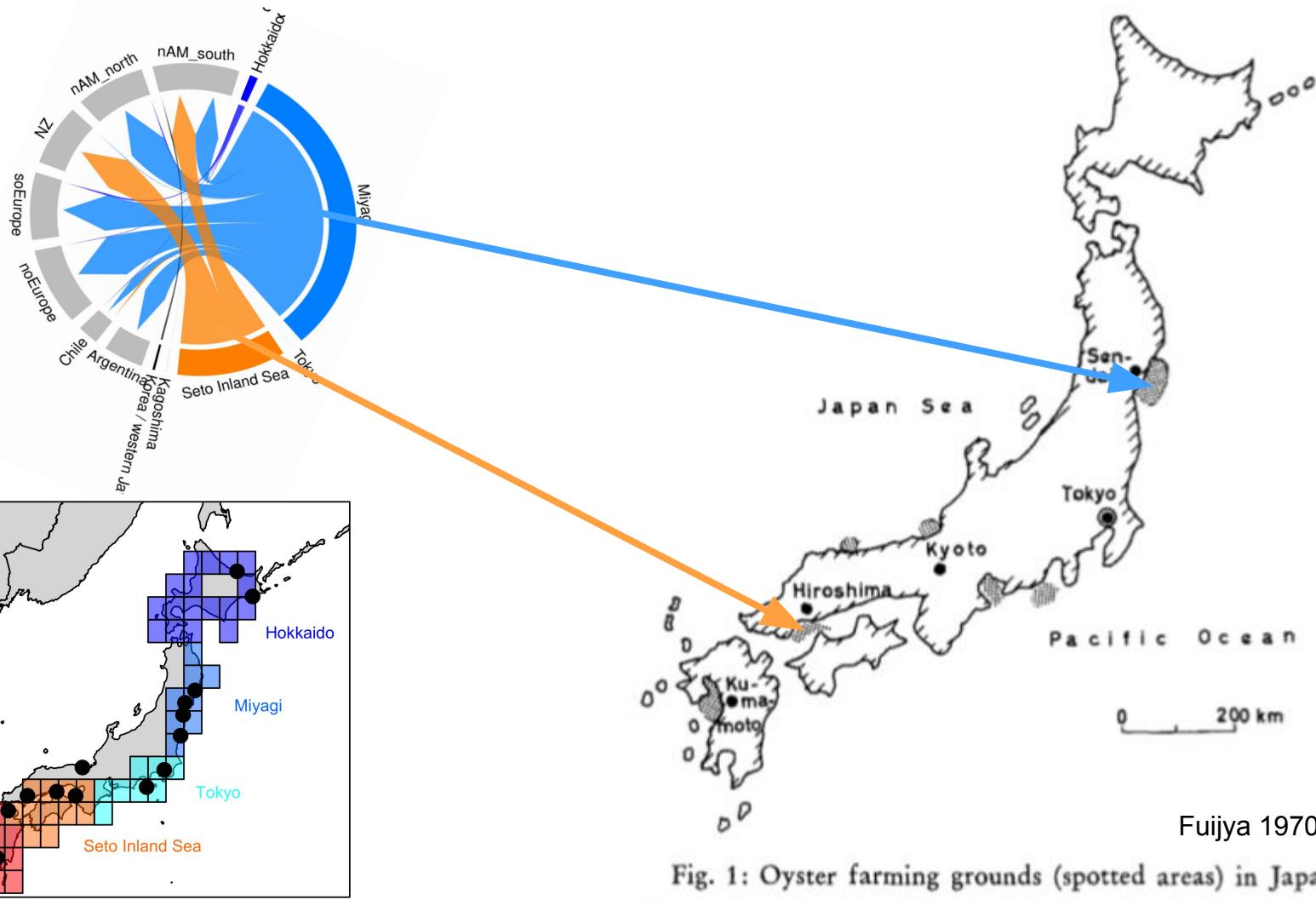
- 41 populations ($n \sim 20$)
 - 20 native (Korea, Japan)
 - 21 non-native (Europe, Western US, Chile, Argentina, NZ)
- Feral populations (on rocks, jetties, reefs, etc..)
- Genotype-by-sequencing
- Dataset: 726 individuals and 7046 SNPs (no missing data and at HWE)

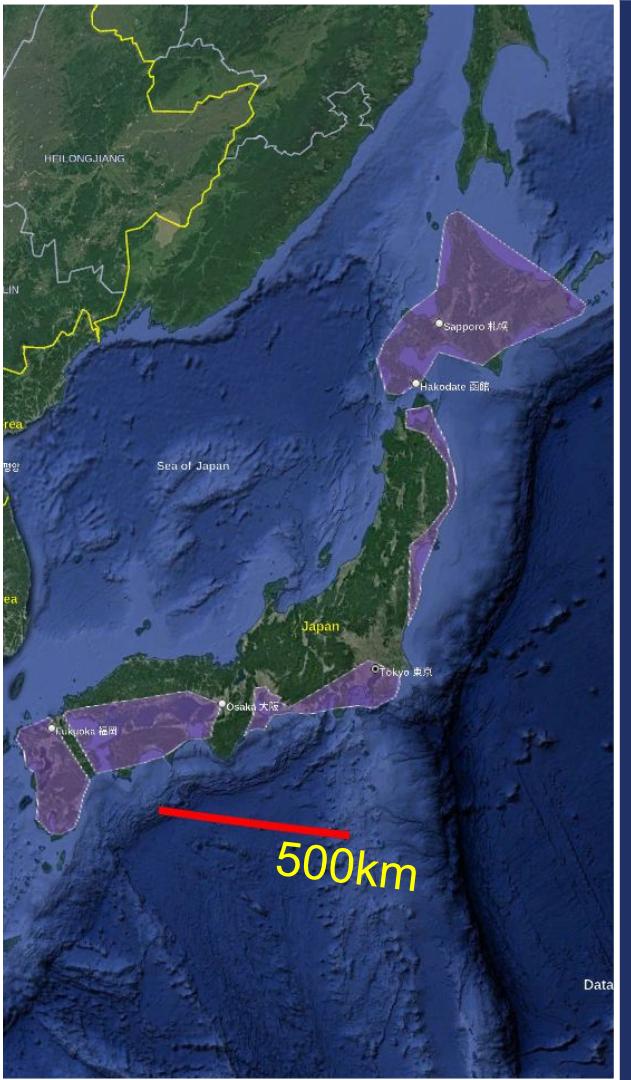


Random Forest assignment of (genetic) source to introduced regions



Random Forest assignment of (genetic) source to introduced regions





Creating the shipping introduction model

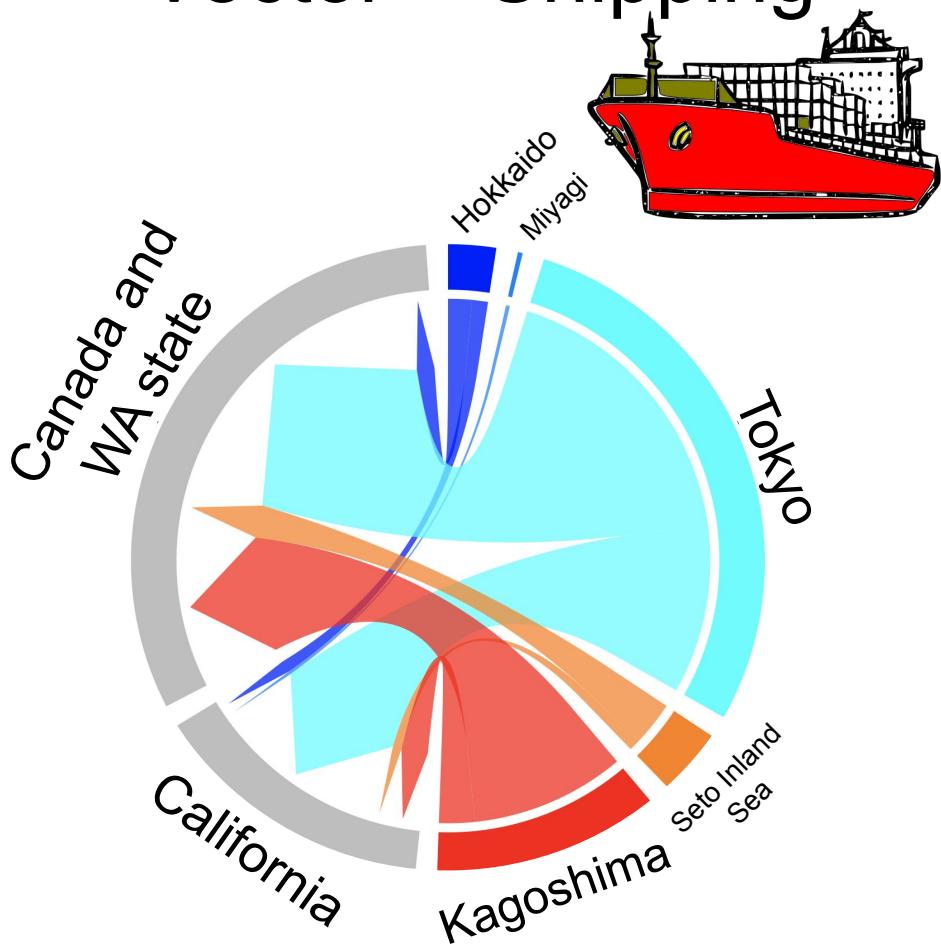
ICOADS data were used to identify voyages

- Voyages had to originate in Japan between 1950-2010
- Voyages arrived in introduced region in less than 60 days
- Origins and destinations were determined by passage of ships through predefined buffers

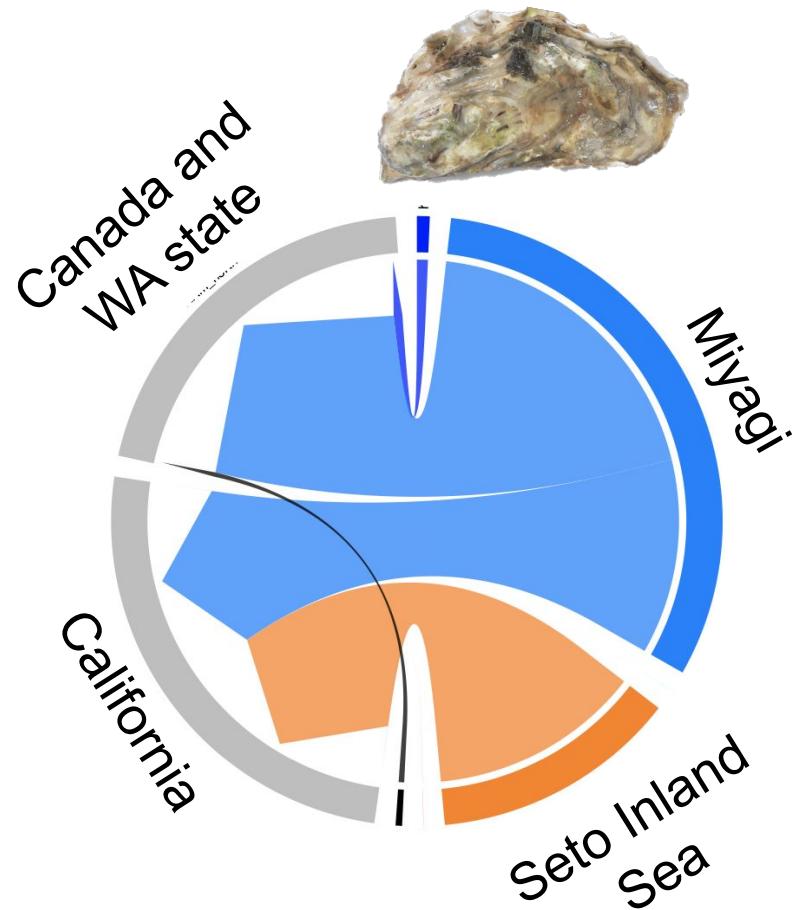
Relative (but not absolute!) measure of propagule pressure

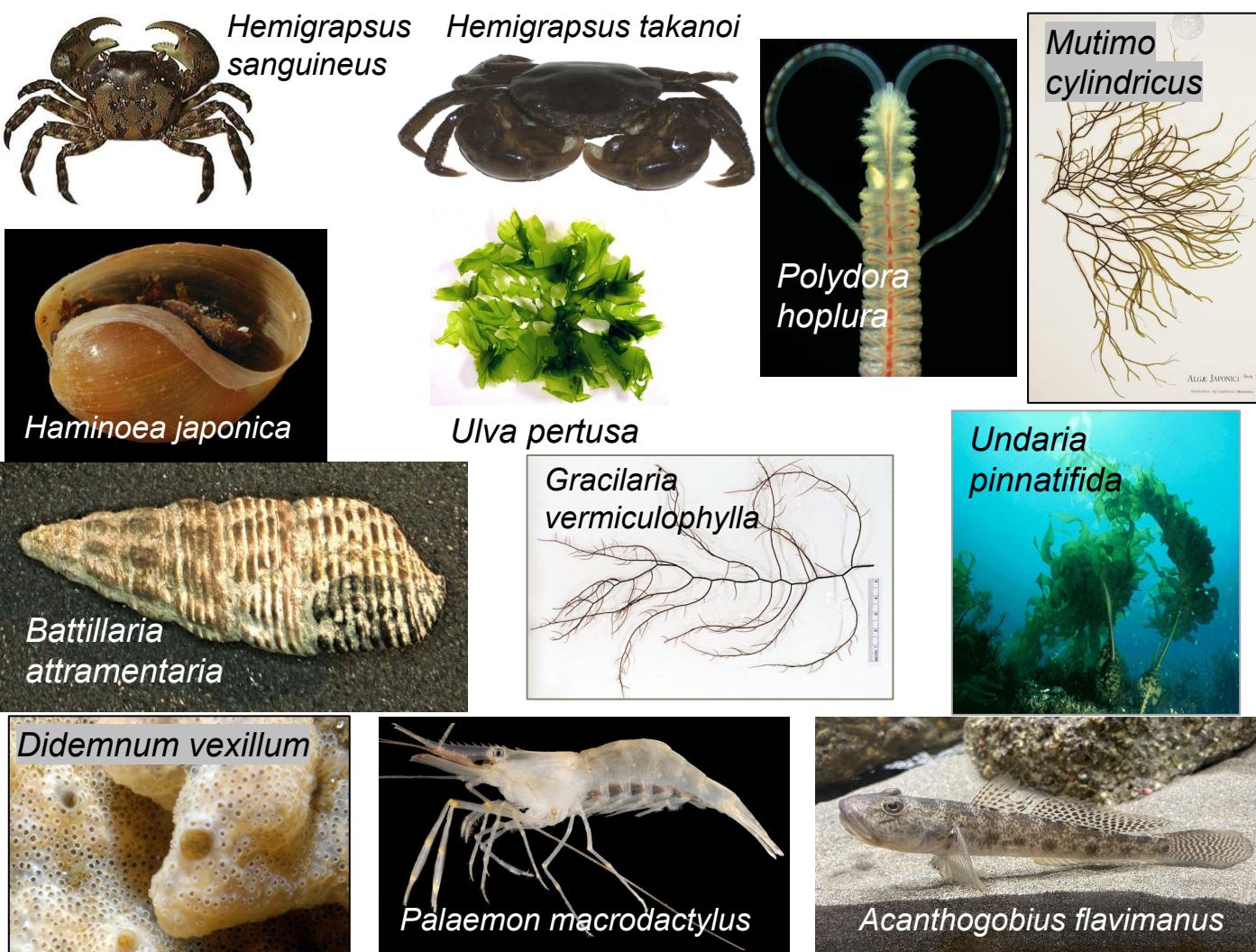


Vector = Shipping



Vector = Oysters





Criteria for inclusion

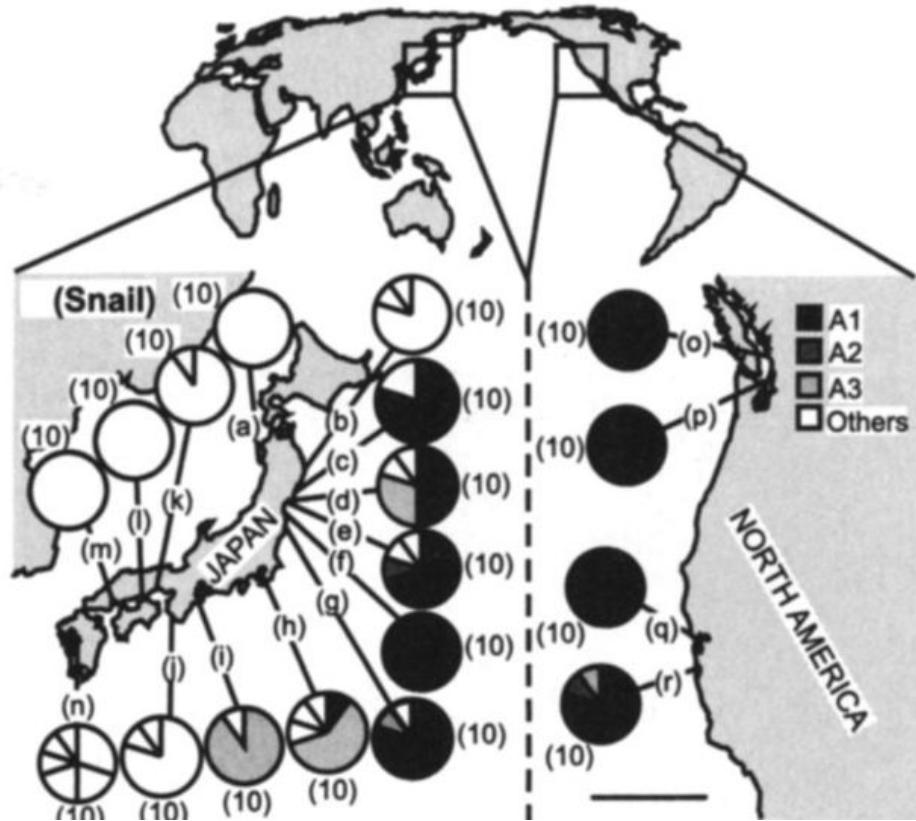
- Genetic data are publicly available
- 2+ regions in Japan
- Western NA, Europe or both

Genetic data

Primarily organelle*
Single gene

**G. vermiculophylla*
is the exception

Typical dataset: *Battillaria attramentaria*



Miura et al. 2005 PNAS

ABC: Simulations replace likelihoods

$$\Pr(\text{Inv. Model} \mid \text{Genetic data}) \propto \Pr(\text{Genetic data} \mid \text{Inv. Model}) \times \Pr(\text{Inv. Model})$$

Posterior Prob.

Likelihood

Prior Prob.
of Model

ABC: Simulations replace likelihoods

$$\Pr(\text{Inv. Model} \mid \text{Genetic data}) \propto \Pr(\text{Genetic data} \mid \text{Inv. Model}) \times \Pr(\text{Inv. Model})$$

Posterior Prob. Likelihood Prior Prob.
of Model

$$\Pr(\text{Inv. Model} \mid \text{Genetic data}) \propto (\text{Simulate genetics under model}) \times 0.5$$

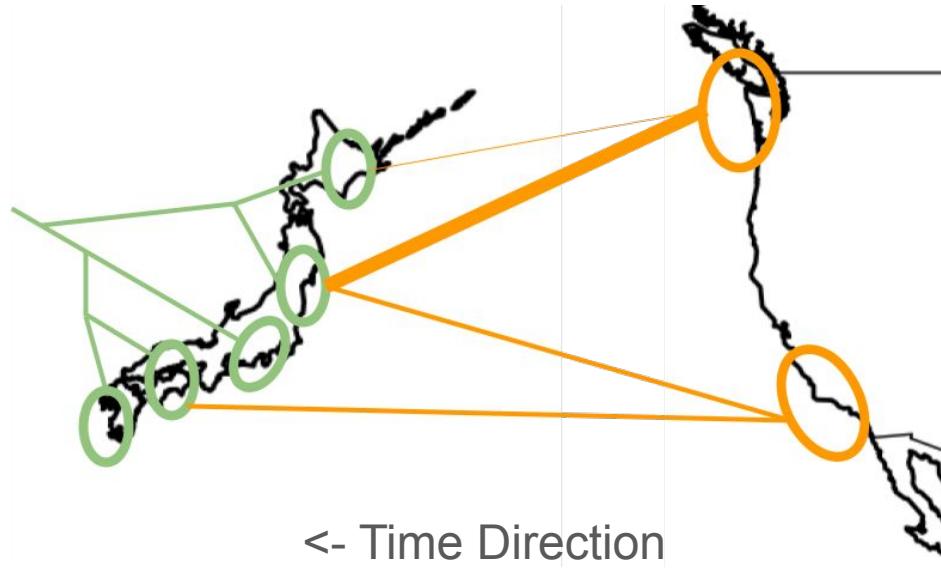
Posterior Prob. Likelihood substitute “flat” Prior

Simulations produce genetic summary statistics

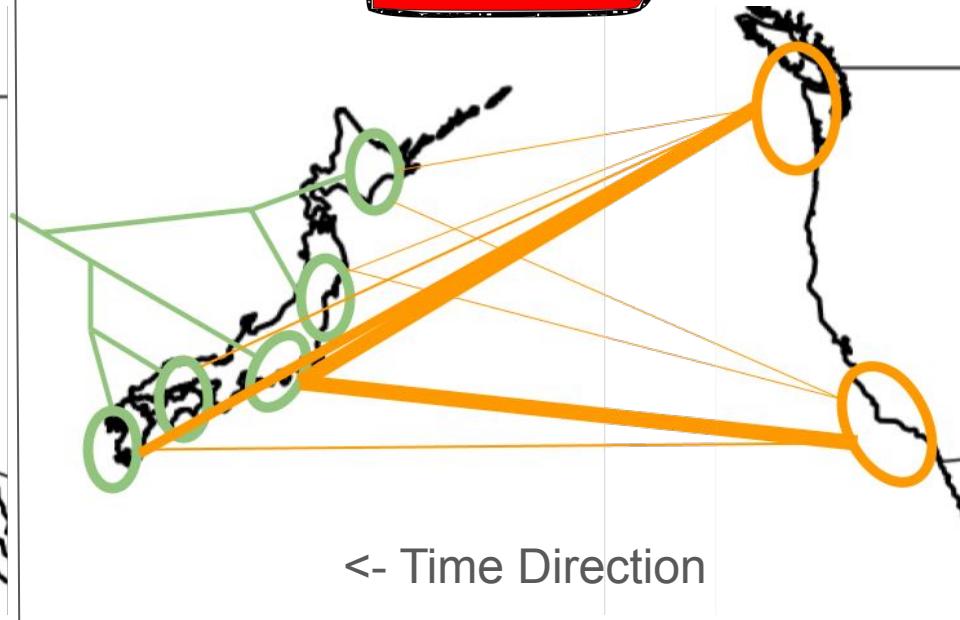
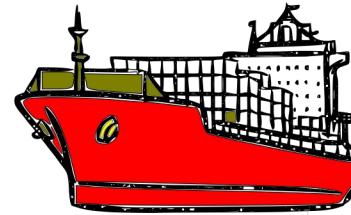
- mainly within/among population diversity

The closer a simulation outputs are to the actual data observed, the higher the “likelihood substitute” for that model

Coalescent trees simulated for each invasion model



<- Time Direction



<- Time Direction

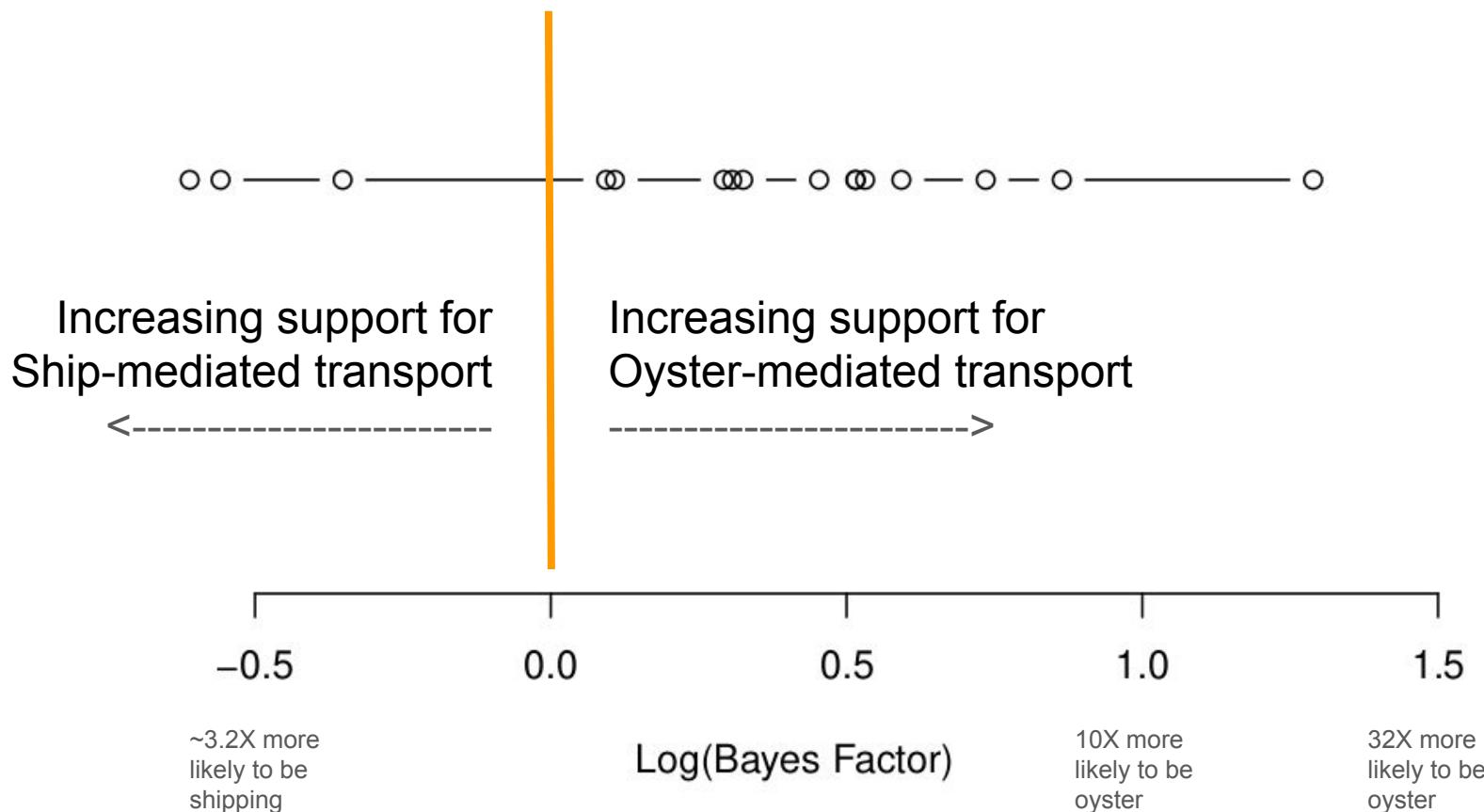
Coalescent trees simulated for each invasion model

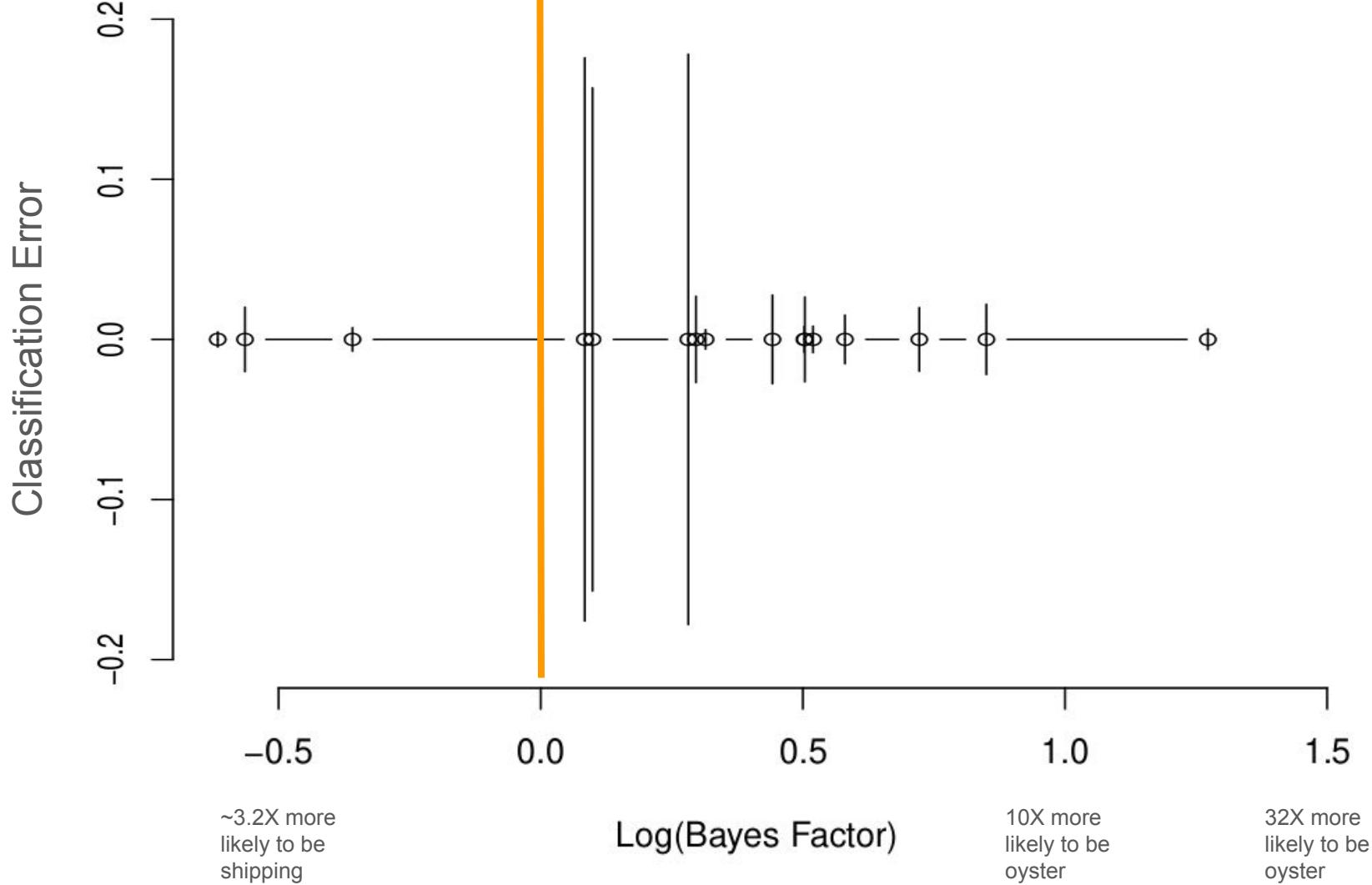
- 700K Simulations for each of 16 datasets
- ~200K hours compute time (Thanks OSG/CofC!)
- Simulation code available as an R package at <https://github.com/stranda/TestInvPath>

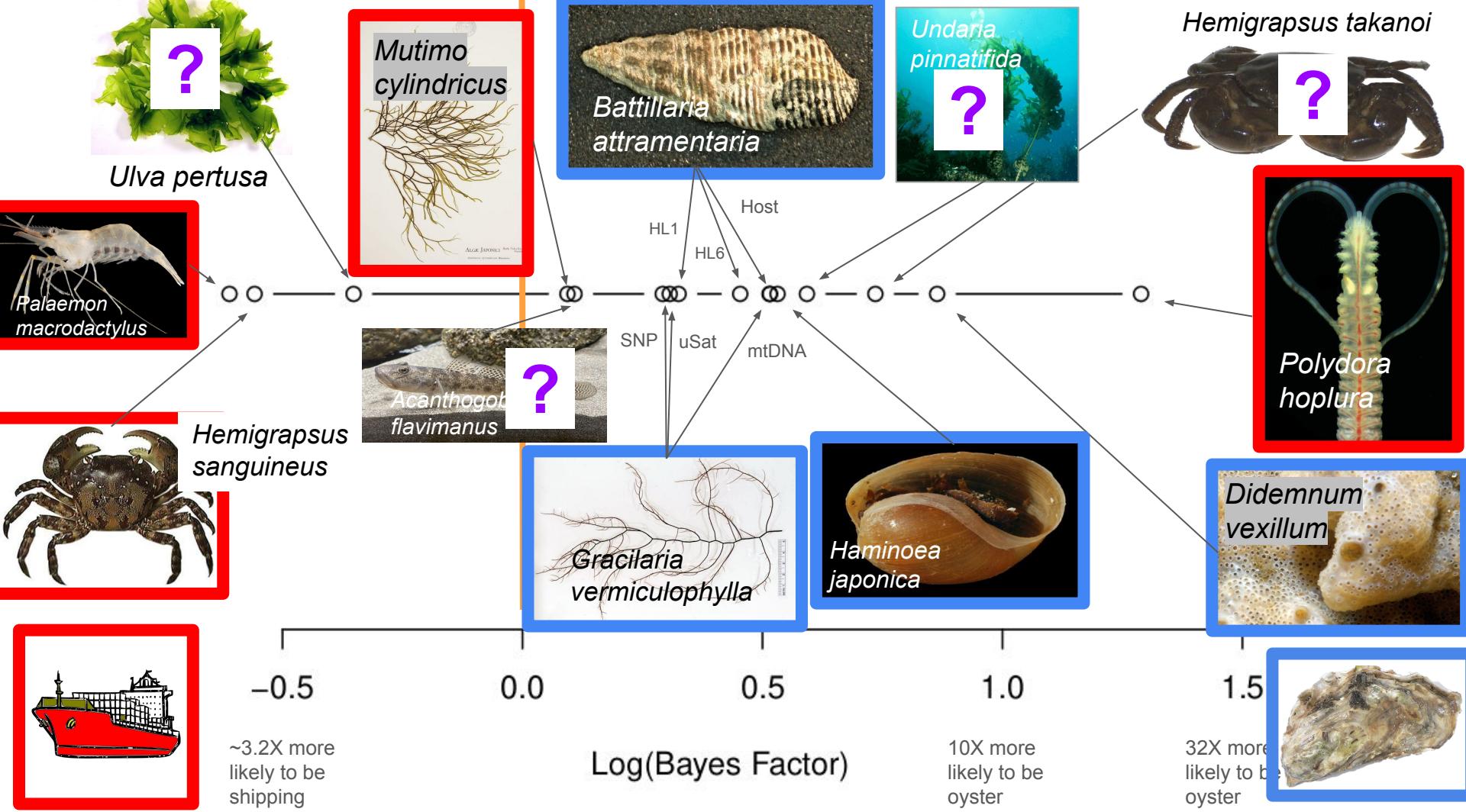
<- Time Direction

<- Time Direction

Species ranked based on relative support for Shipping versus Oysters as vectors for introductions







Conclusions

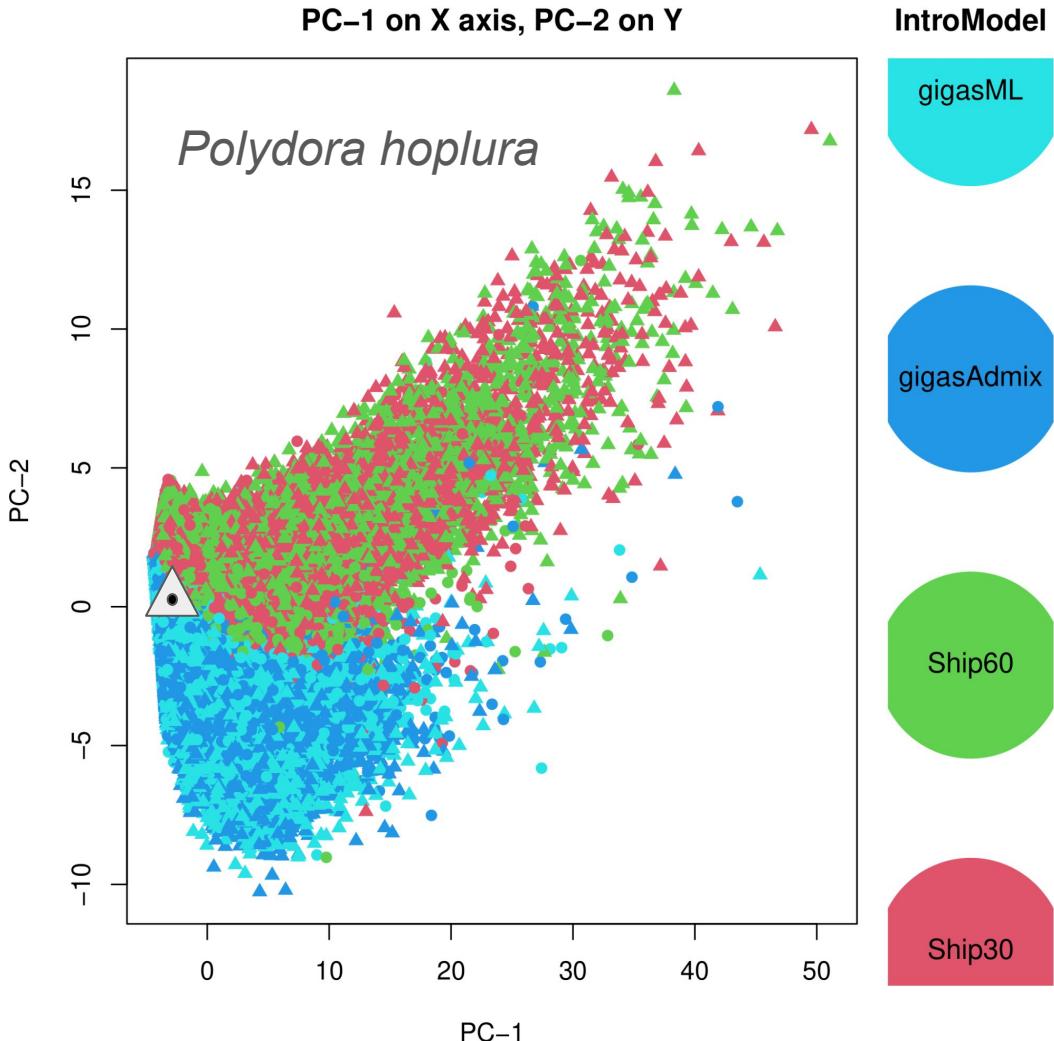
- Biological
 - Introduced Pacific oysters likely originated in historic aquaculture grounds
 - Oyster transport does appear to explain most (of these) invasions
 - Vector assignment possible in cases where we didn't know before
- Methodological
 - We can assign some measure of relative support to alternative invasion models.
 - Uncertainty can be estimated

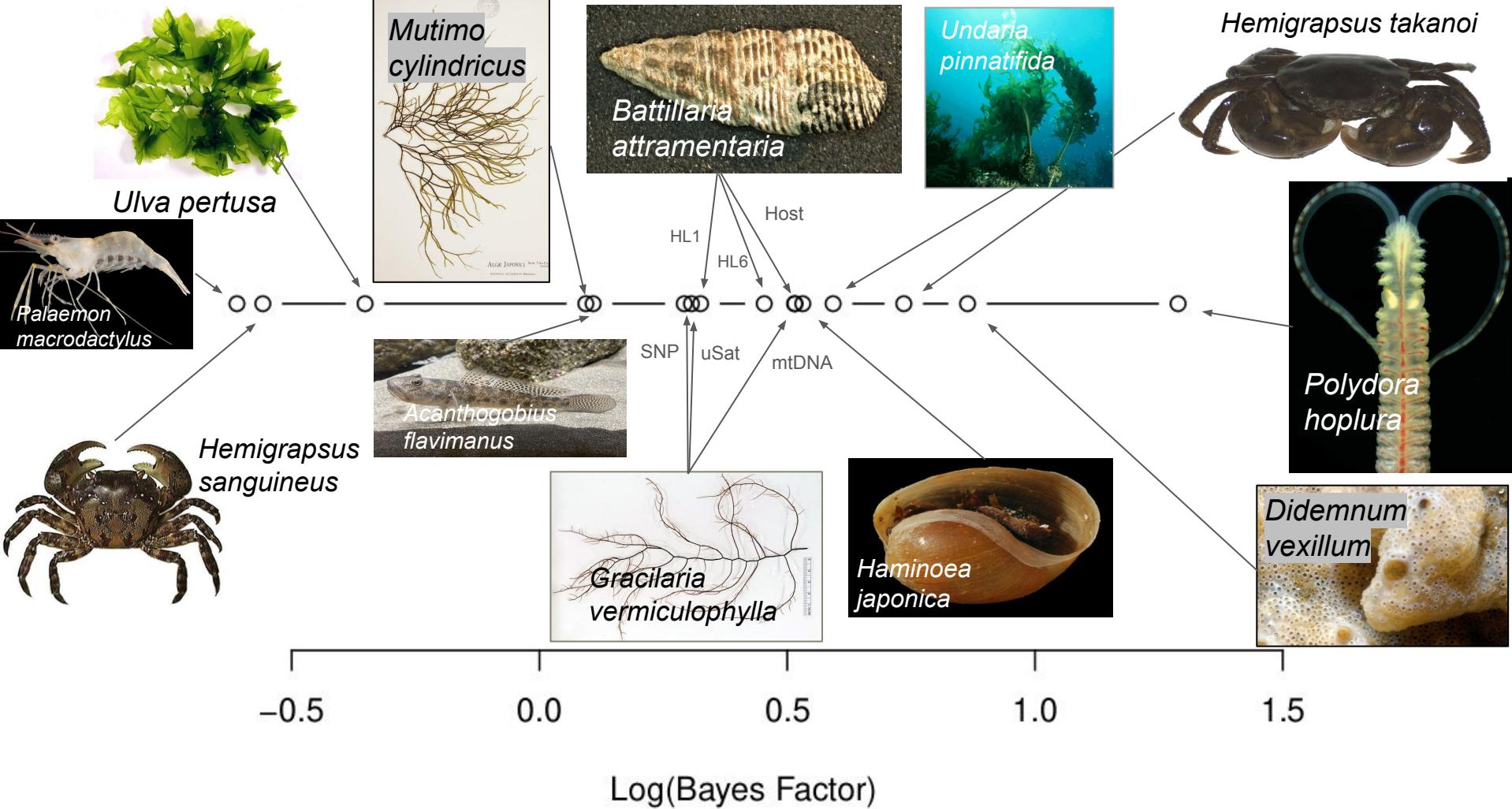
Thank you!

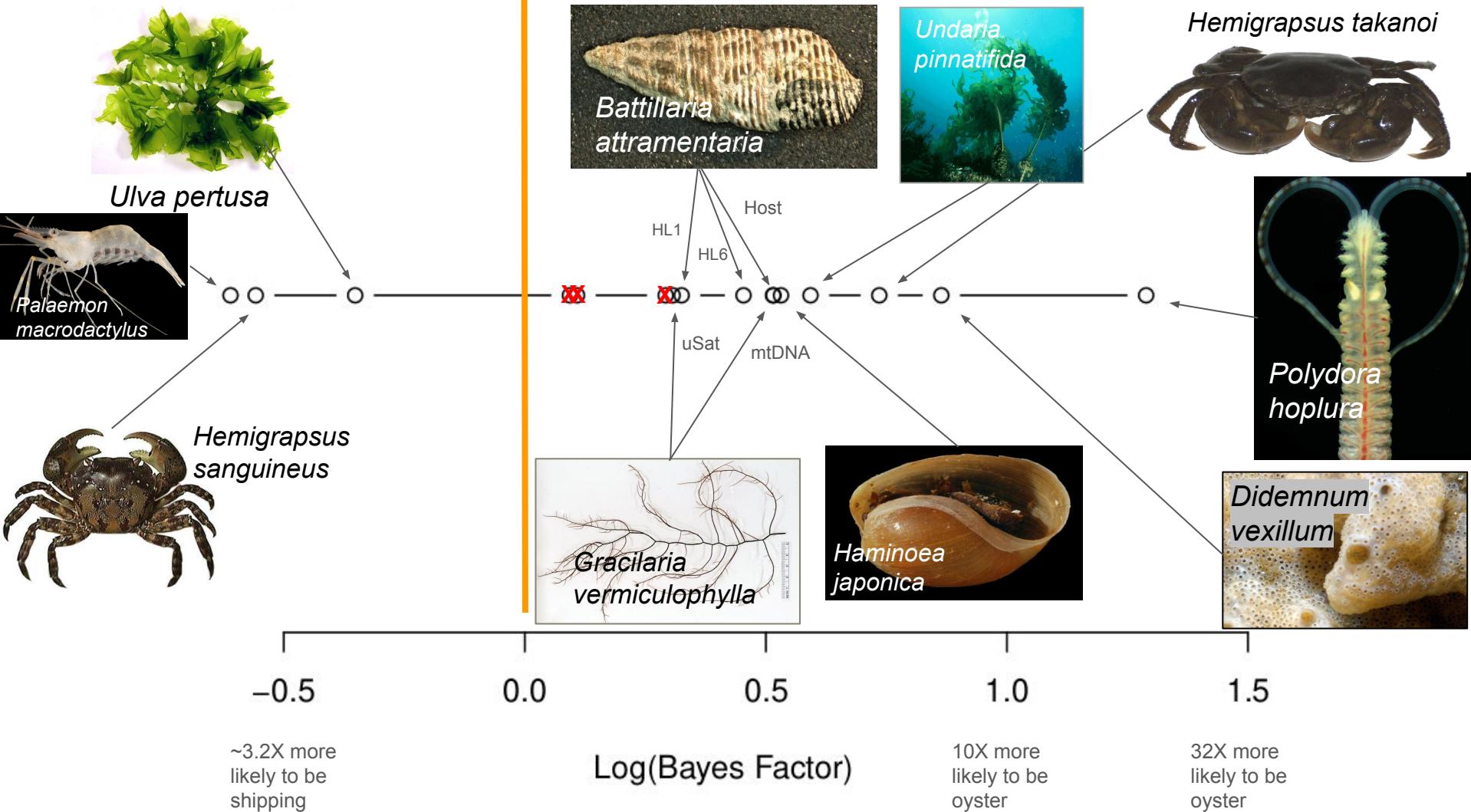
Do our simulations reflect the real world?

Probably not...

But ordinating the summary statistics from simulations shows correspondence between the observed data and simulated data







Voyages stopping or originating in Japan, 1978

Data from ICOADS

