



Estimating life history parameters of European hake using Bayesian models

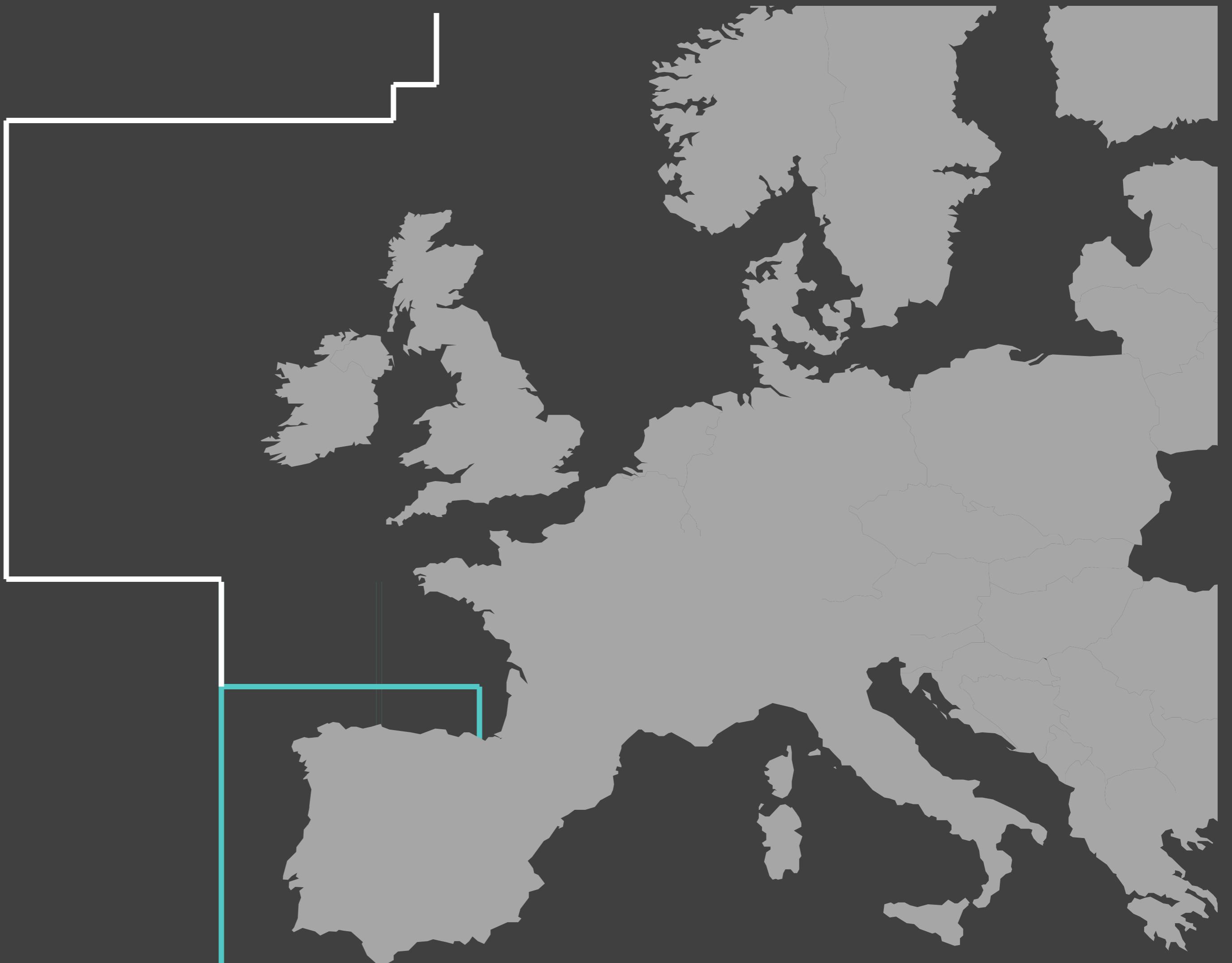
Francisco Izquierdo^{1*}, Santiago Cerviño¹, Catherine Michielsens², Massimiliano Cardinale³, Dorleta García⁴,
Maria Grazia Pennino¹

Motivation

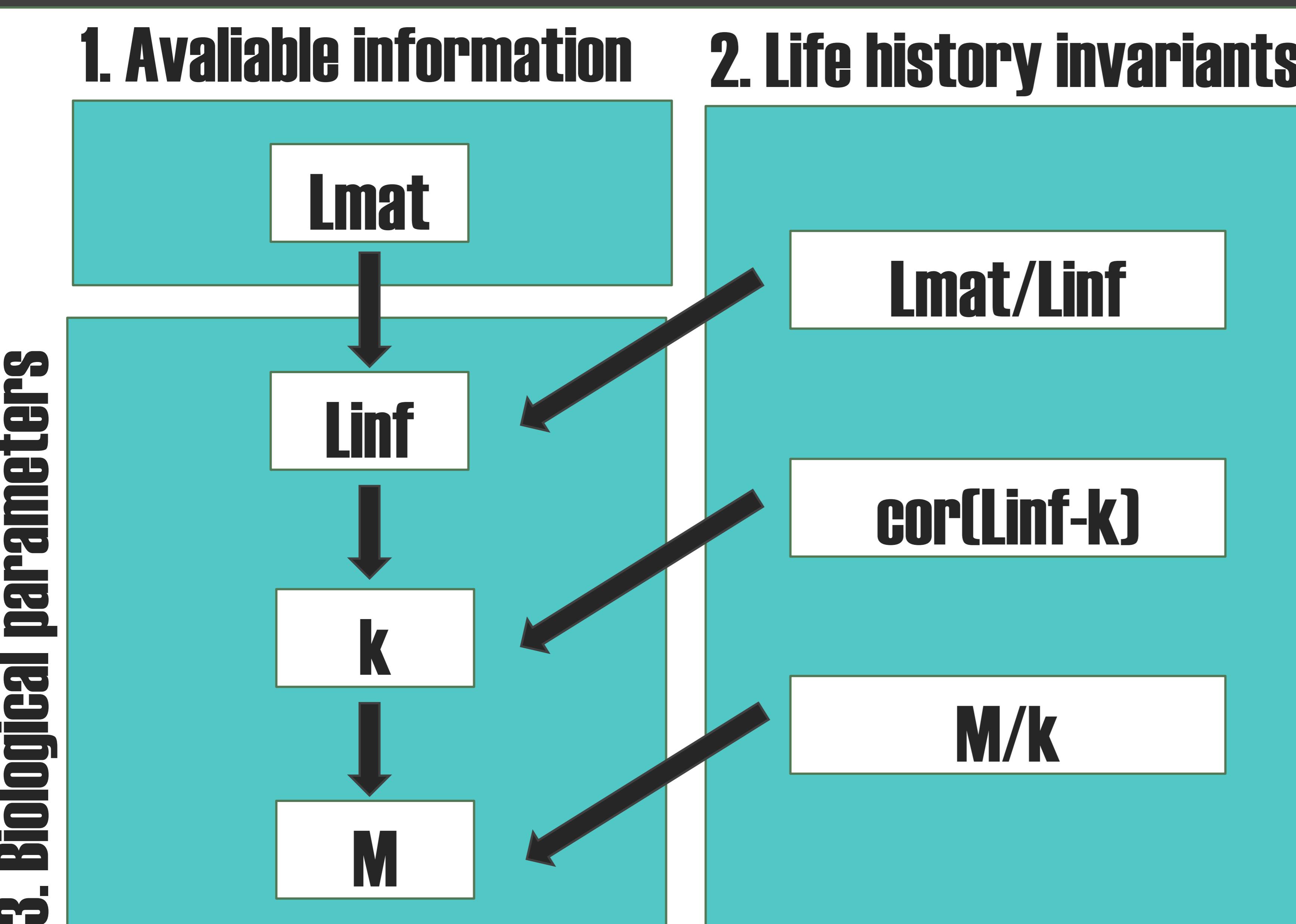
Biological parameters are one of the weakest areas in current stock assessment models.

Objective

Estimate biological parameters of the Atlantic European hake (*Merluccius merluccius*) **northern** and **southern** stocks from Lmat and bibliographic data of all hake species.



Methodology



LHI theory states that for a similar taxa, the relationship among some biological parameters are relatively constant (Charnov, 1993).

Meta analysis for all hakes biological parameters data by using [rfishbase + R2OpenBugs](#).

Bayesian hierarchical model by giving more weight to the European hake stock information.

Results

Parameter	Nhake	Shake
L_{inf} (Von Bert.)	mean=130.6 sd=21.91	mean=110.87 sd=18.93
K (Von Bert.)	median=0.14 cv=0.26	median=0.17 cv=0.27
M	median=0.30 cv=0.38	median=0.37 cv=0.39



Next

- Make an [R package](#)
- Estimate parameters by sex
- Inputs for stock assessment

¹Instituto Español de Oceanografía (IEO-CSIC), Centro Oceanográfico de Vigo, Vigo, Spain,

²Fisheries Management Division, Pacific Salmon Commission, Vancouver, Canada

³Department of Aquatic Resources, Institute of Marine Research, Swedish University of Agricultural Sciences, Lysekil, Sweden

⁴Azti-Tecnalia, Txatxarramendi ugartea z/g, Sukarrieta, Spain

Charnov, E. L. (1993). Life history invariants: some explorations of symmetry in evolutionary ecology (Vol. 6). Oxford University Press, USA.