Heterogeneity and population dynamics

Olivier Gimenez

olivier.gimenez@cefe.cnrs.fr

http://www.cefe.cnrs.fr/olivier-gimenez

Population dynamics in the wild

Ecology: Impact of global change

Evolution: How to adapt when facing changing environments

Management : Propose and evaluate strategies


Faucon crécerelle


Manchot empereur


Saumon atlantique


Sanglier

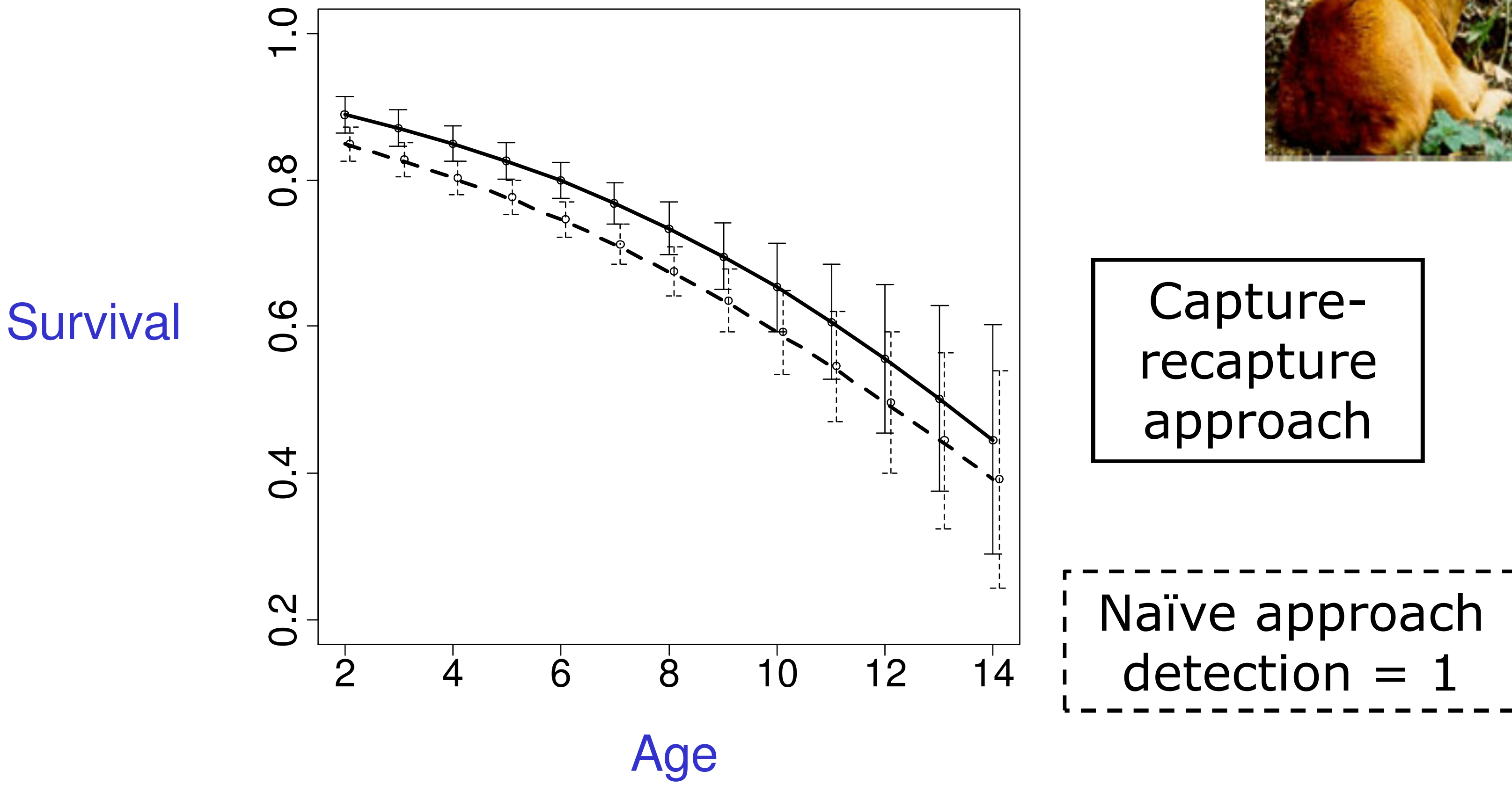
Population dynamics in the wild

- Investigating process in natural populations
- Long-term individual monitoring datasets
- Methodological issues when moving from lab to natural conditions
  - Issue 1: detectability < 1
  - Issue 2: individual heterogeneity (IH)

Issue of detectability < 1

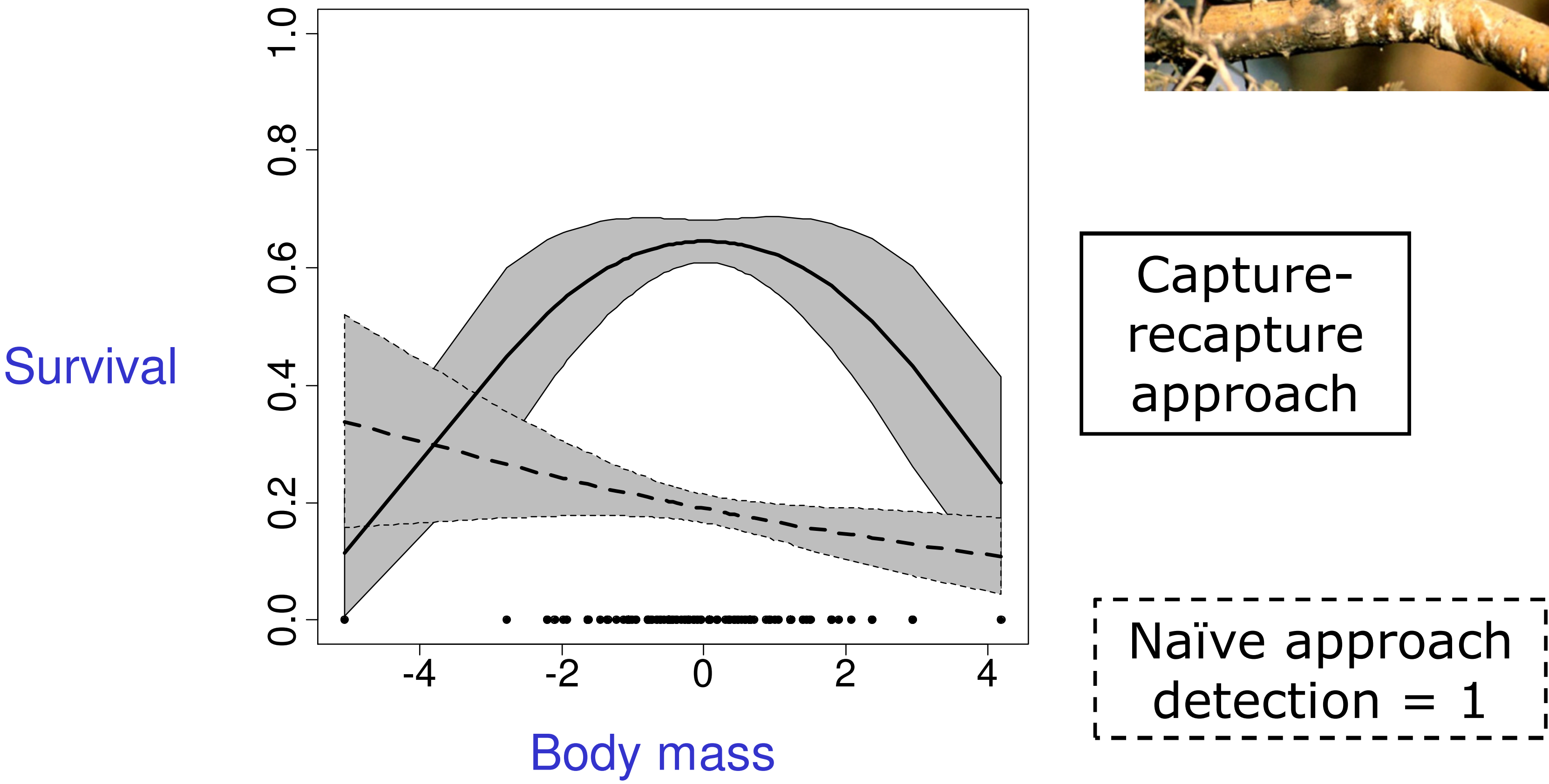
- How to reliably estimate demographic parameters in the wild?
- Individuals may be seen or not
- If they're not... Are they breeding? Are they on the study site? Are they dead?
- Individually mark and monitor individuals: capture-recapture (CR) data

Why bother with detection < 1?



Bias in survival and rate of senescence

Why bother with detection < 1?



Bias in shape of selection

Issue of individual heterogeneity (IH)

- Standard CR models assume homogeneity
- Inter-individual variation in demographic parameters = *individual heterogeneity* (IH)
- From a statistical point of view, IH can cause bias in parameter estimates
- From a biological point of view, IH is of interest – individual quality

Accounting for individual heterogeneity

- CR models do not cope that well with IH
- If you're a biologist, rely on empirical measures (mass, gender, age, experience, etc.)
  - How to incorporate this information?
- If you're a statistician, intrinsic property of individuals
  - How to filter out the signal from noisy observations?

Capture-recapture models

- Intro: CR data and state-space models
- How to account for individual variation?
  - Random-effect models
  - Non-parametric Bayesian approach
- Perspectives

Common marking methods

- Ear tags for mammals / leg bands for birds

- Passive integrated transponder (PIT) tags

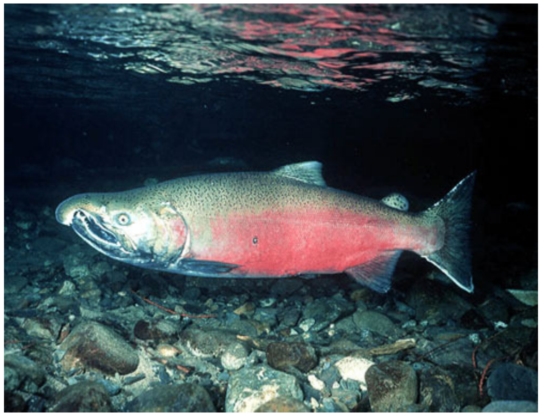
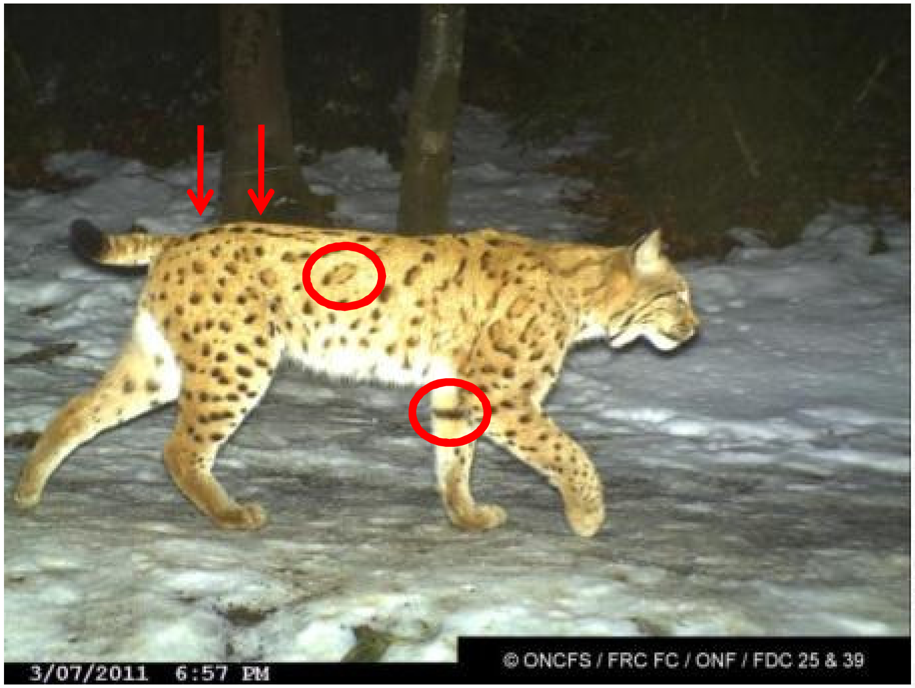
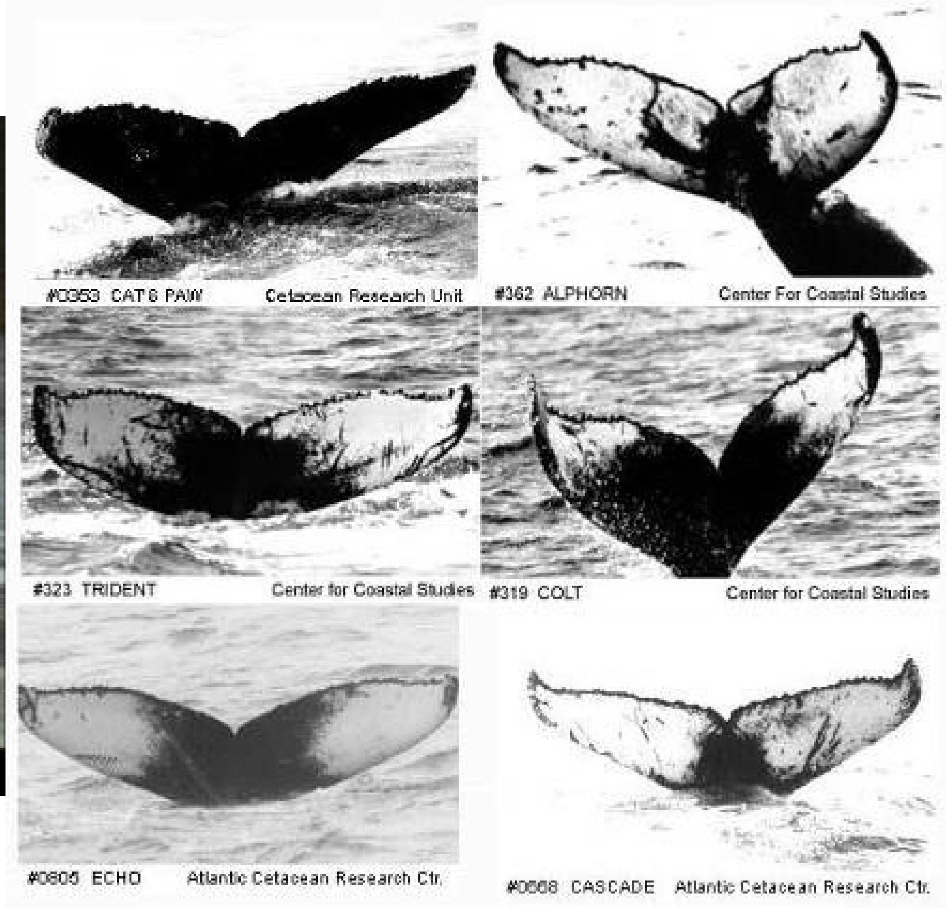


photo-identification

Whales

Lynx

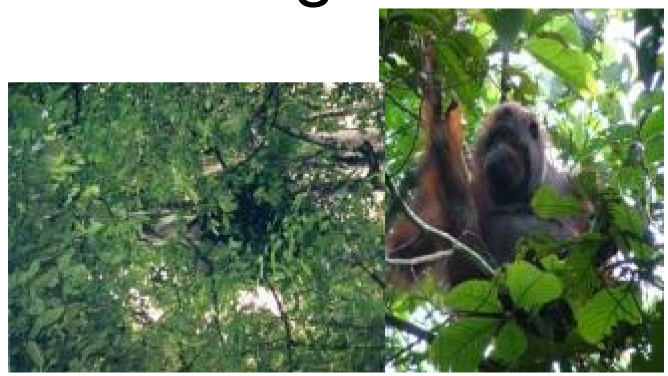




DNA identification

Bears

Orang-utans

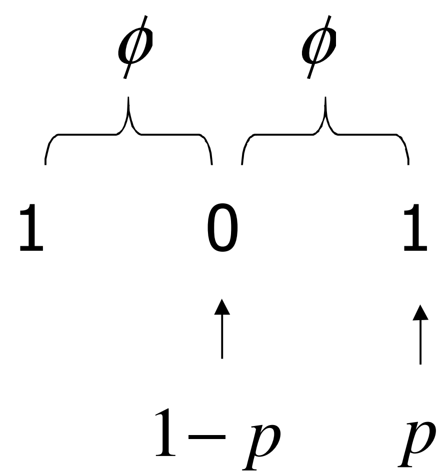


Wolves

Bats

Modelling CR data

- An encounter history: h_i = (1 0 1)



$$\Pr(h_i) = \phi\,(1-p)\,\phi\,p$$

- Survival probability ϕ
- Detection probability p

Modelling CR data

- A probabilistic framework developed in the 60s

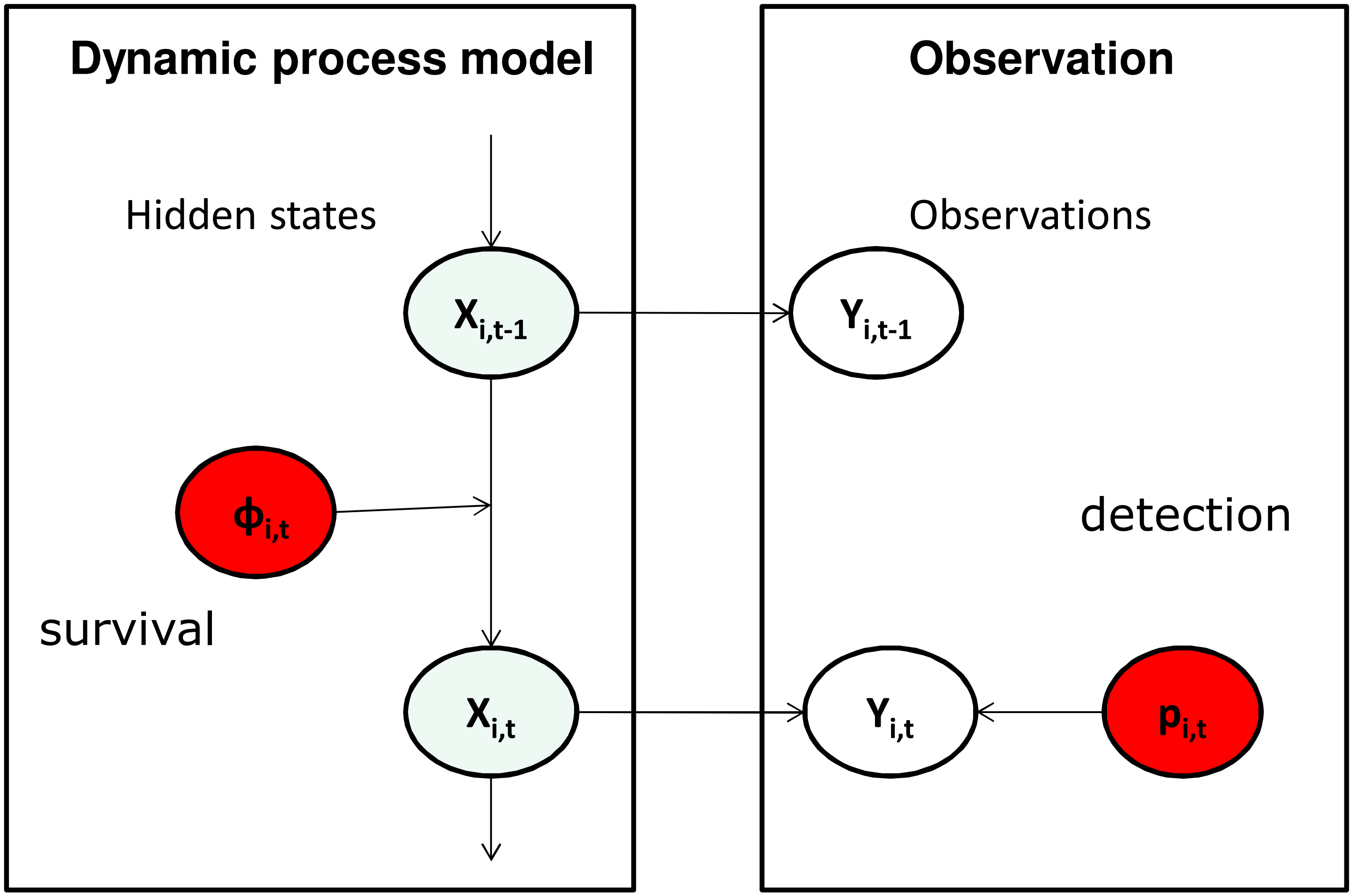
$$\Pr\left(h_i\right) = \phi\left(1 - p\right)\phi\, p$$

- Central role of likelihood (frequentist / bayesian)

$$L = \prod_i \Pr\left(h_i\right)$$

- How to deal with IH in survival and/or detection?

State-space modelling of CR data



State equation

$$X_{i,t} \mid X_{i,t-1} \sim \text{Bernoulli}\left(\phi_{i,t} X_{i,t-1}\right)$$

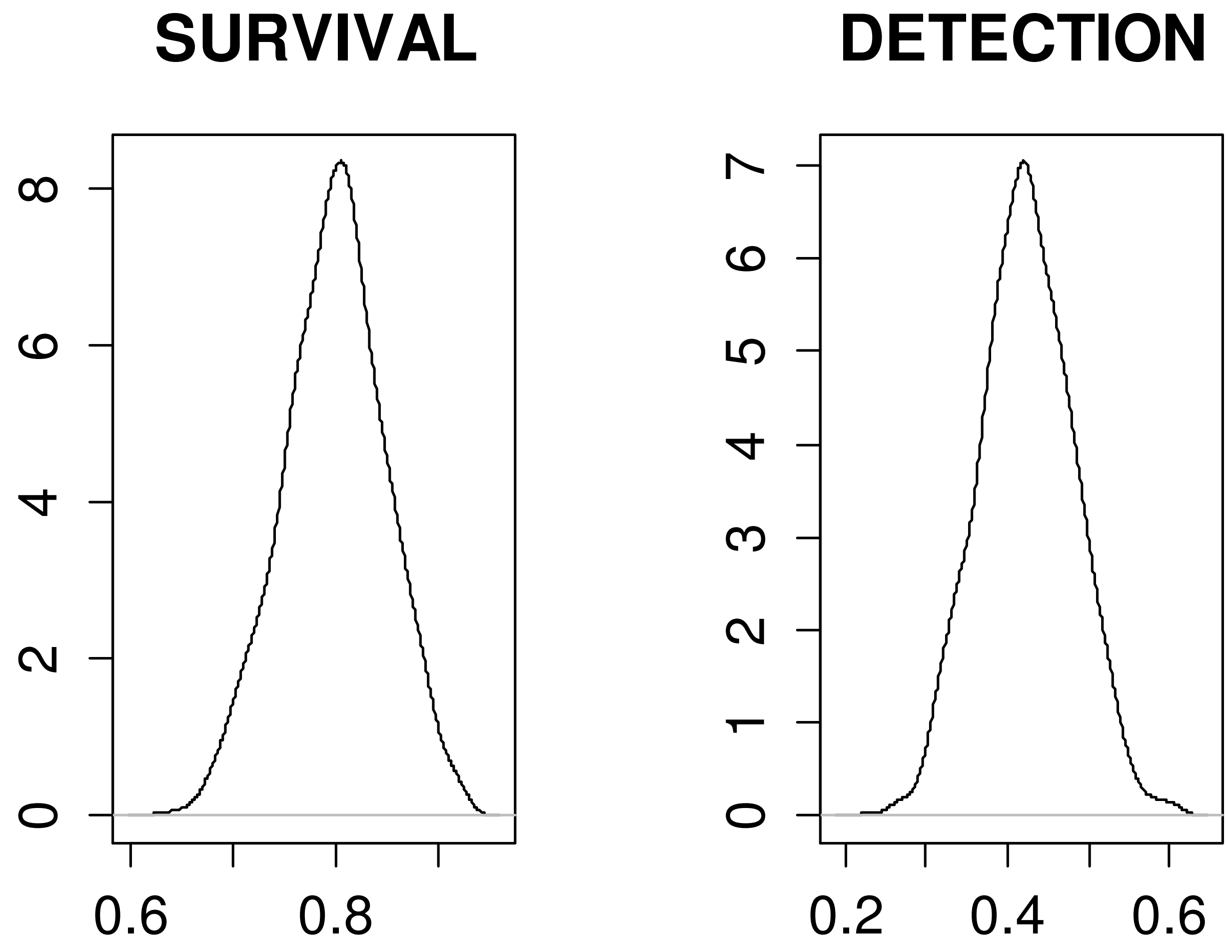
Observation equation

$$Y_{i,t} \mid X_{i,t} \sim \text{Bernoulli}\left(p_{i,t} X_{i,t}\right)$$

Case study in conservation biology

- Wolf is recolonizing France
- Problematic interactions with human activities
- Population dynamics as a tool for management and conservation

Results on wolves (1995-2003)



Sources of heterogeneity in wolves

Sampling

DNA sequencing

- Wide area and genetic CR data
- Social species

Random effect CR model

- On logit scale, detection probability is:

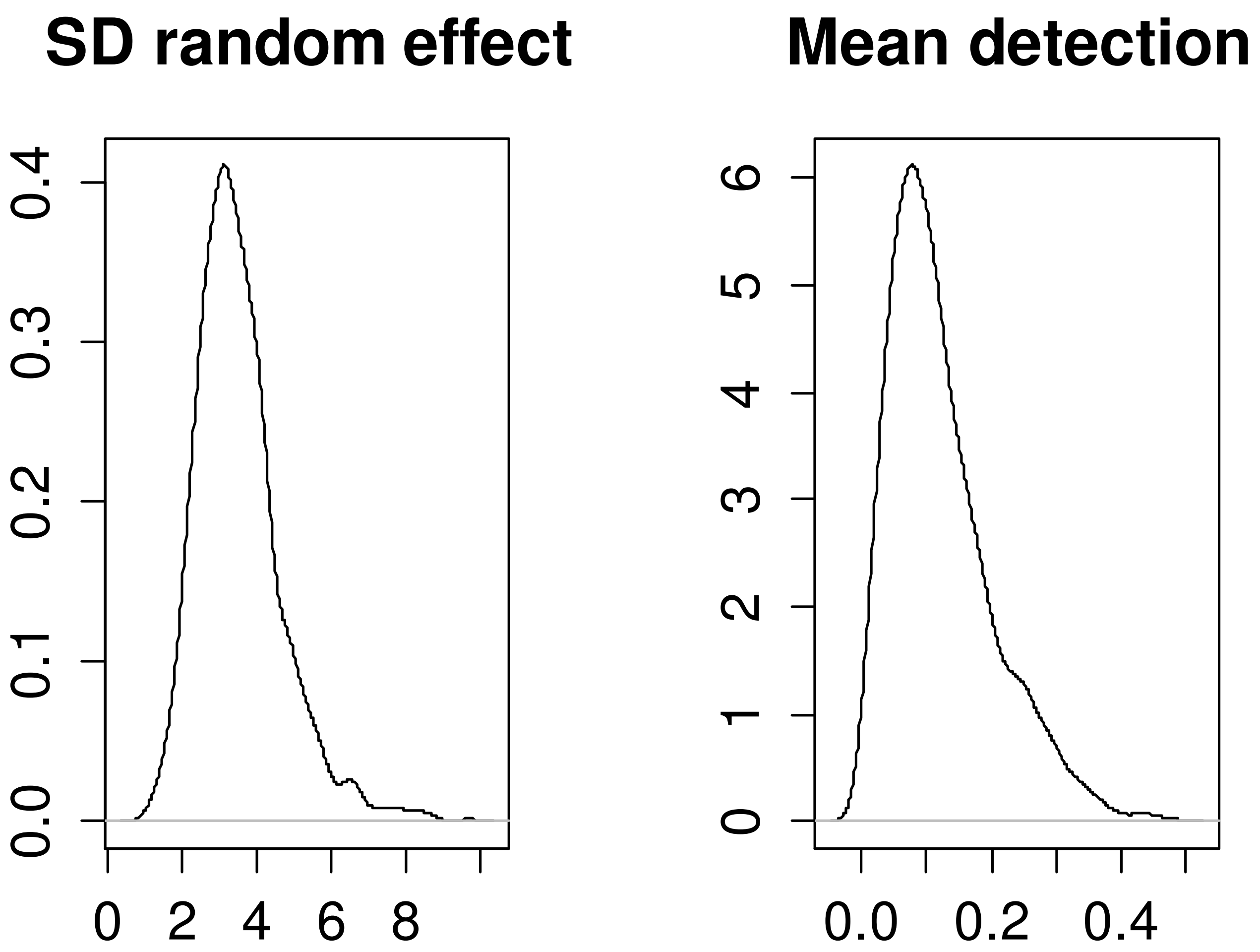
$$\text{logit}(p_i) = \mu + \varepsilon_i$$

- With random effect

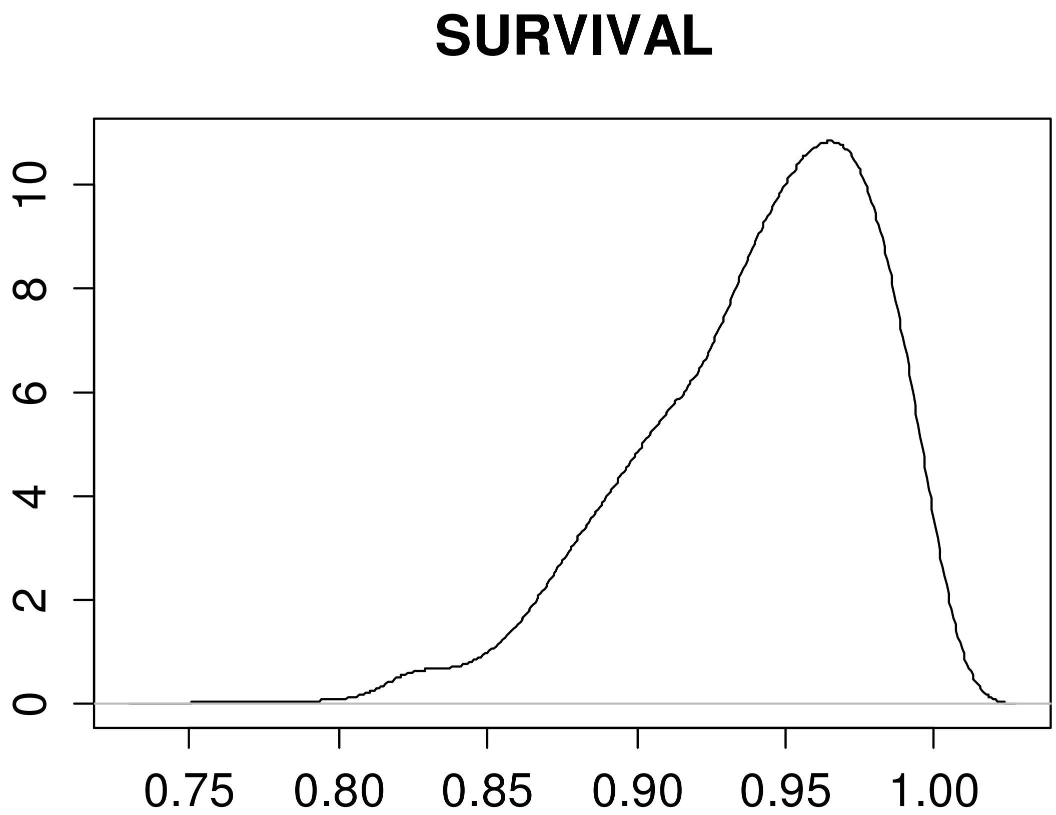
$$\varepsilon_i \sim N(0, \sigma^2)$$

- Uniform prior on SD σ of the random effect

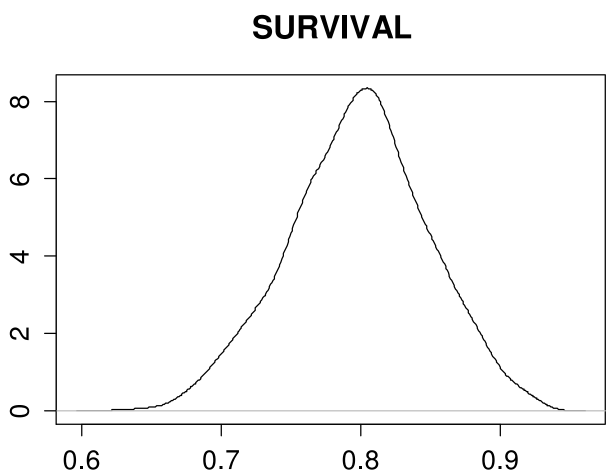
Results on wolves (1995-2003)

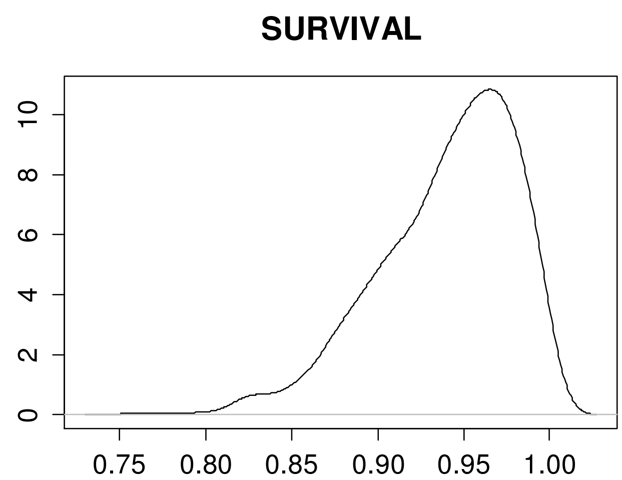


Results on wolves (1995-2003)



Results on wolves (1995-2003)





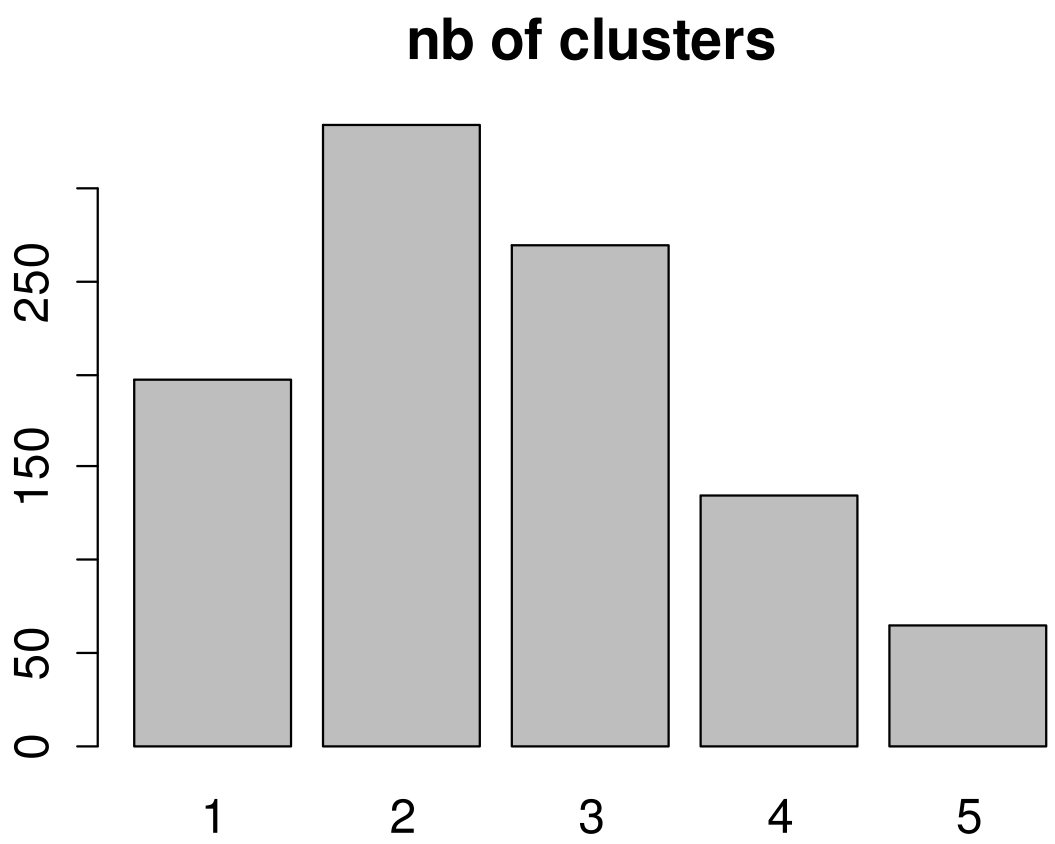
WITHOUT heterogeneity

WITH heterogeneity

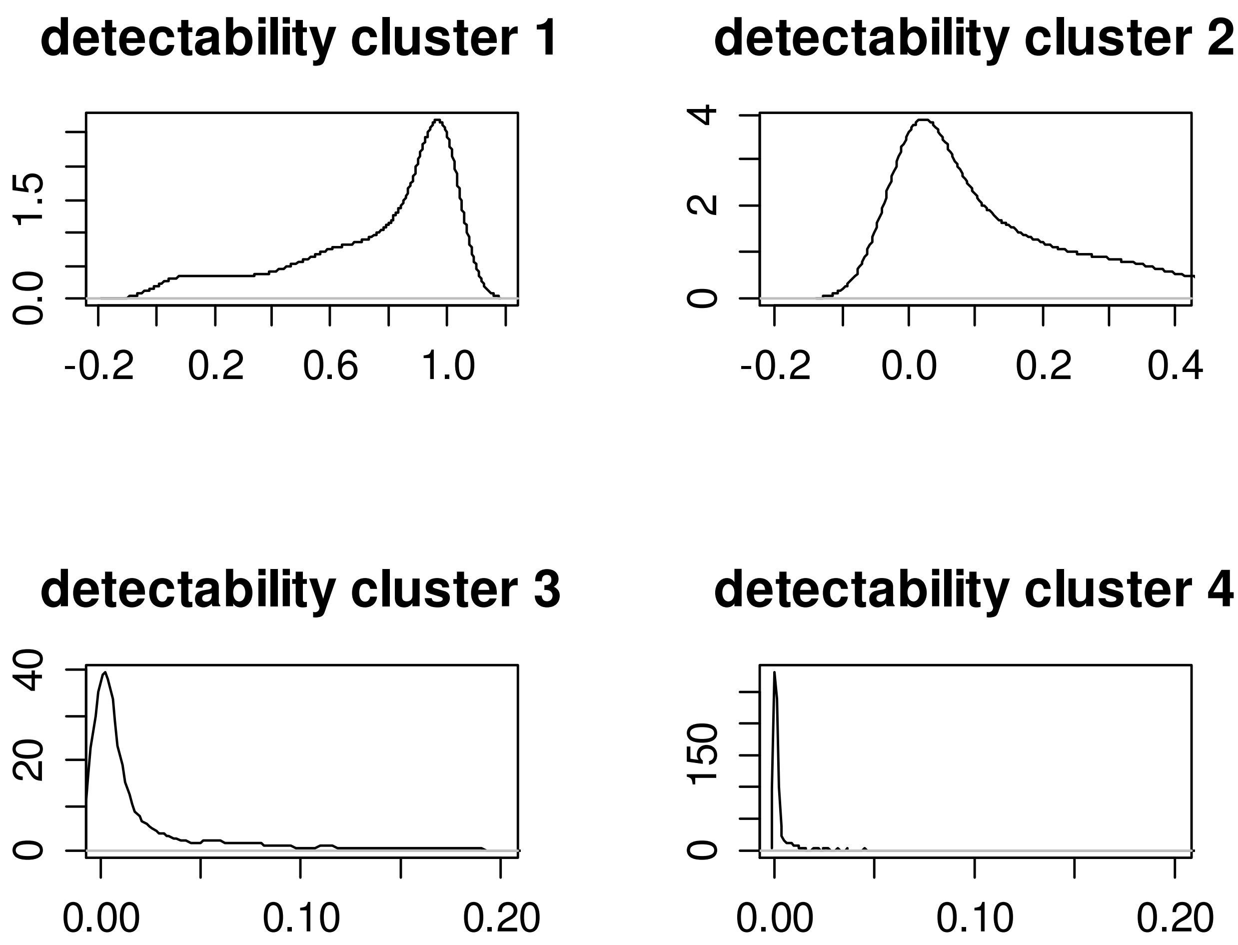
Non-parametric Bayesian approach

- $F(x) = \int N\left(x \middle| \theta, \sigma^2\right) Q(d\theta)$ where $Q(d\theta)$ is a discrete mixing distribution
- Dirichlet process as prior on $Q(d\theta)$
- On the logit scale: $\mathrm{logit}(p_i) = \mu + \varepsilon_i$
- With $\varepsilon_i \sim N\left(\theta_h, \sigma^2\right)$ with probability π_h
- π_h defined by stick-breaking prior

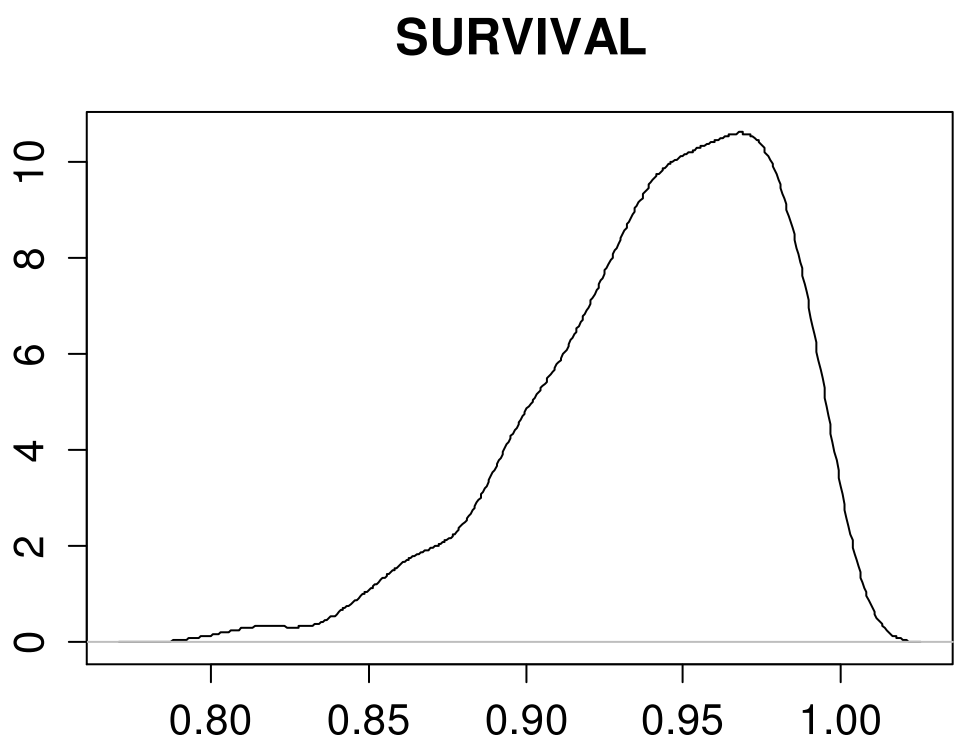
Results on wolves (1995-2003)



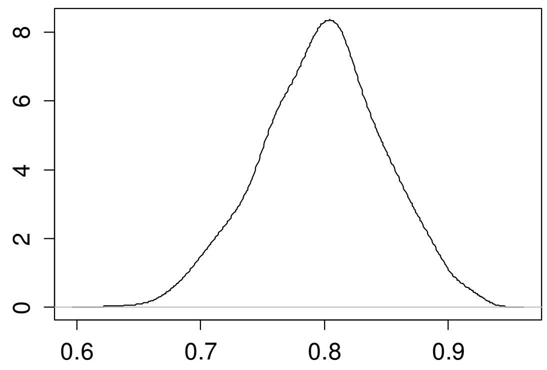
Results on wolves (1995-2003)



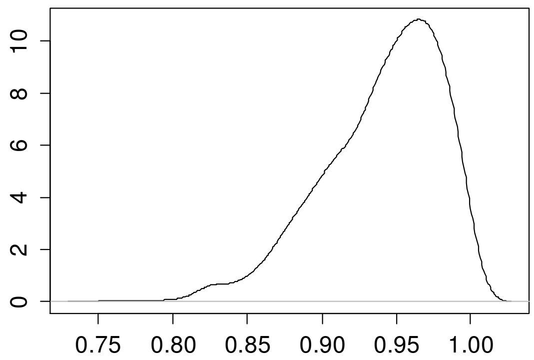
Results on wolves (1995-2003)



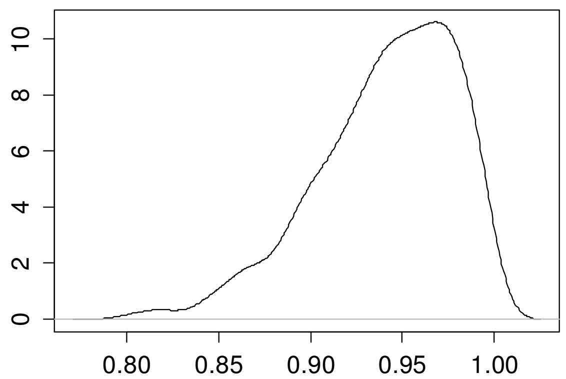
Wolf survival



homogeneity



random effect



mixture of normals

Conclusions

- CR methodology is catching up with ‘p=1’ world
- IH needs to be accounted for
- State-space models : IH as well as $p < 1$
- If possible, biological view – measure IH on the field

Perspectives

- Model selection?

Model	Dev	DIC	pD
homogeneous	174.9	273.6	98.5
(single) normal random effect	126.1	228.8	101.1
mixture of normal distributions	124.3	227.9	103.8

- Computational burden?

- User-friendly implementation?

Centre d'Ecologie Fonctionnelle & Evolutive
Centre National de la Recherche Scientifique

References

Dirichlet process

- Ferguson, T.S. (1973). A Bayesian analysis of some nonparametric problems. Ann. Stat. 1:209-230
- Ohlssen et al. (2007). Flexible random-effects models using Bayesian semi-parametric models: Applications to institutional comparisons. Statistics in Medicine 26:2088-2112
- Sethuraman, J. (1994). A constructive definition of Dirichlet priors. Stat Sin 4:639-650

Capture-recapture models

- Cubaynes et al. (2010). Importance of accounting for detection heterogeneity when estimating abundance: the case of French wolves. Conservation Biology 24:621-626
- Gimenez et al. (2007). State-space modelling of data on marked individuals. Ecological Modelling 206:431-438
- Gimenez et al. (2008). The risk of flawed inference in evolutionary studies when detectability is less than one. The American Naturalist. 172:441–448.
- Gimenez & Choquet (2010). Individual heterogeneity in studies on marked animals using numerical integration: capture-recapture mixed models. Ecology 91:951-957
- Gimenez et al. (2012). Estimating demographic parameters using hidden process dynamic models. Theoretical Population Biology *in press*