

Fitting moult phenology models with `moult` and `moultmcmc`

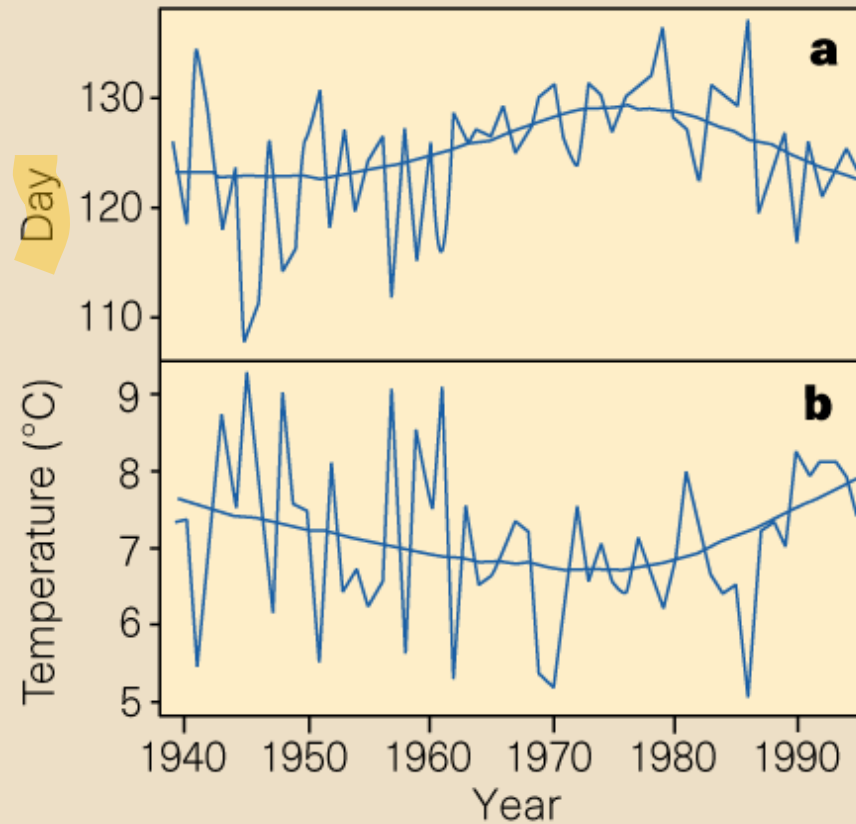
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British Trust for Ornithology @_BTO

Phenology can provide insight into ecosystem processes

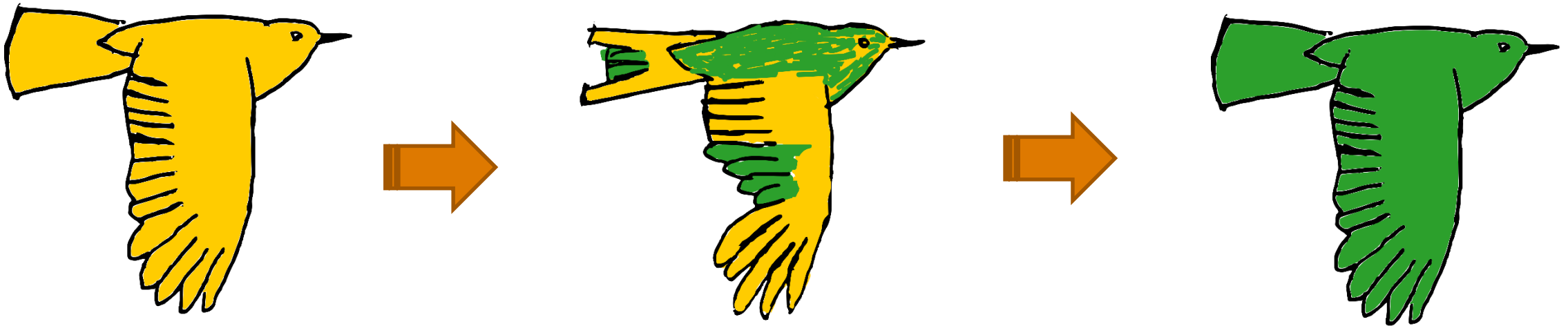


Chaffinch egg laying

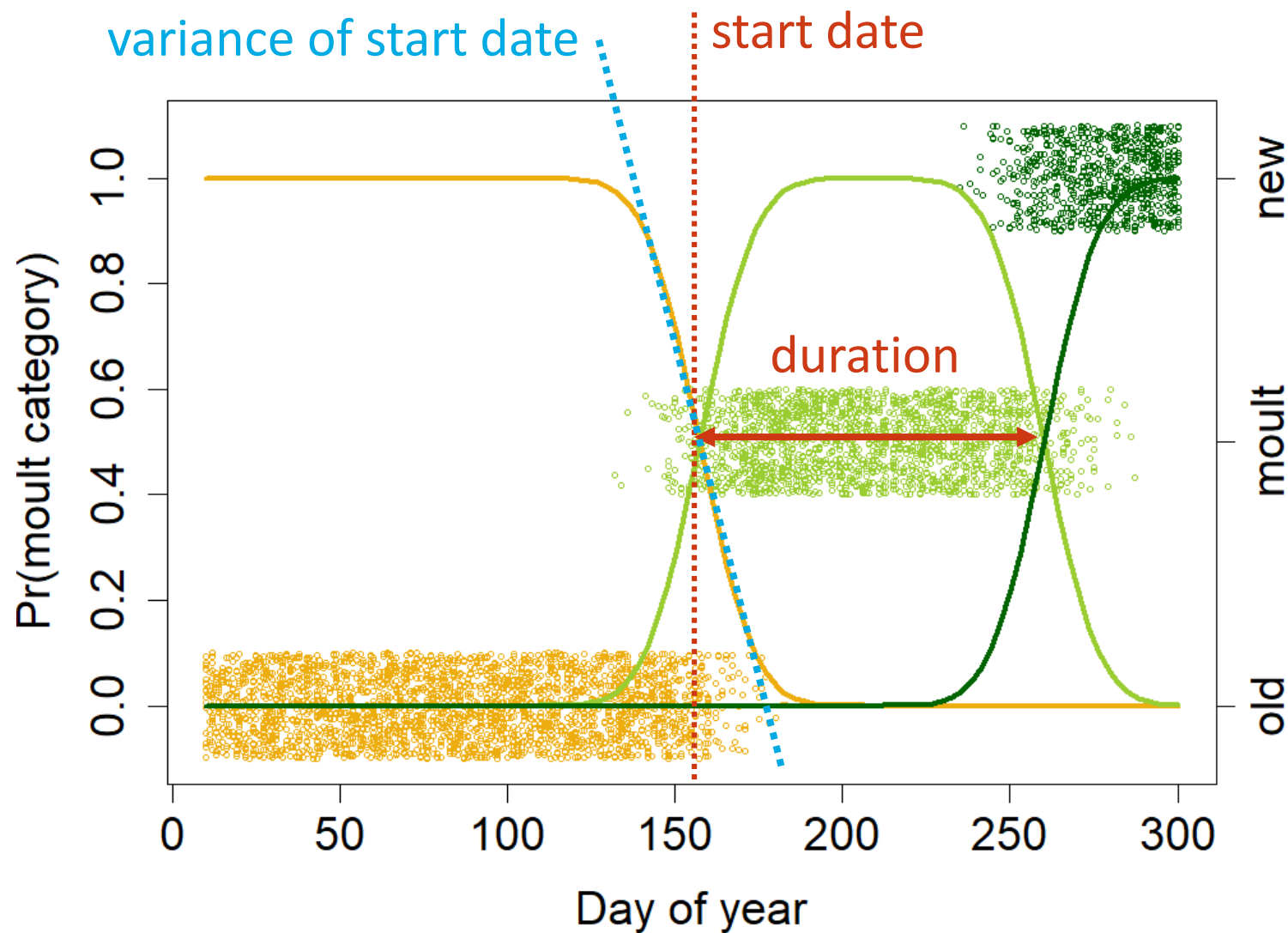
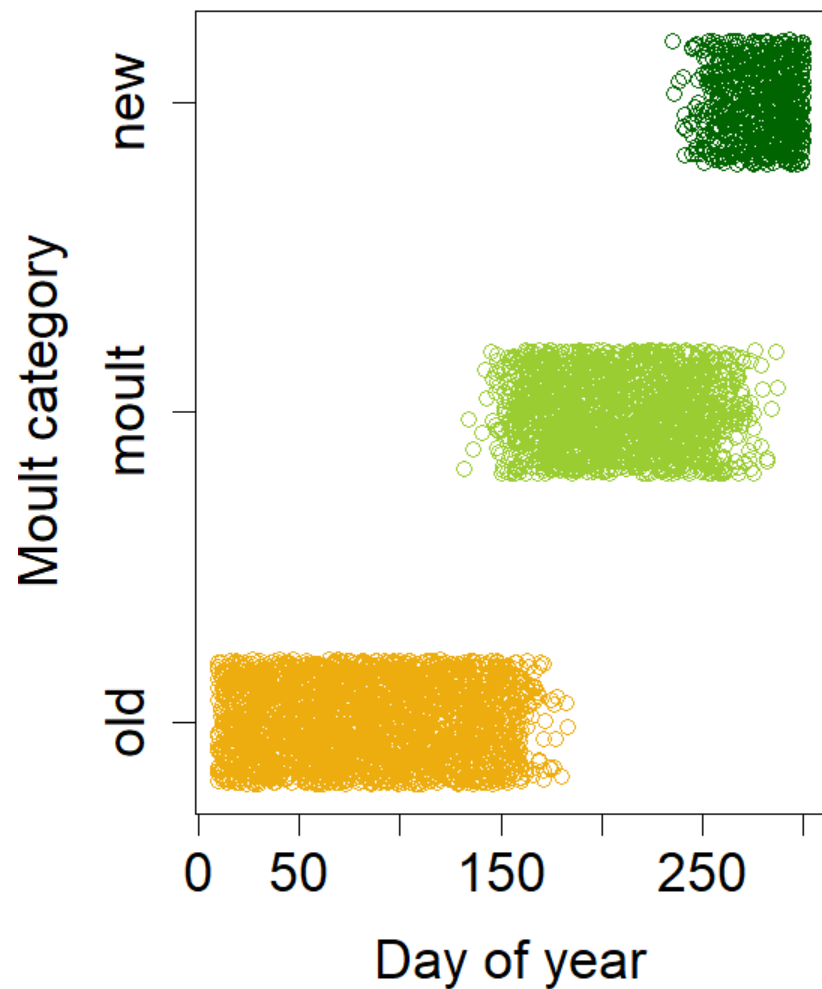


Moult cannot typically be observed fully in wild individuals

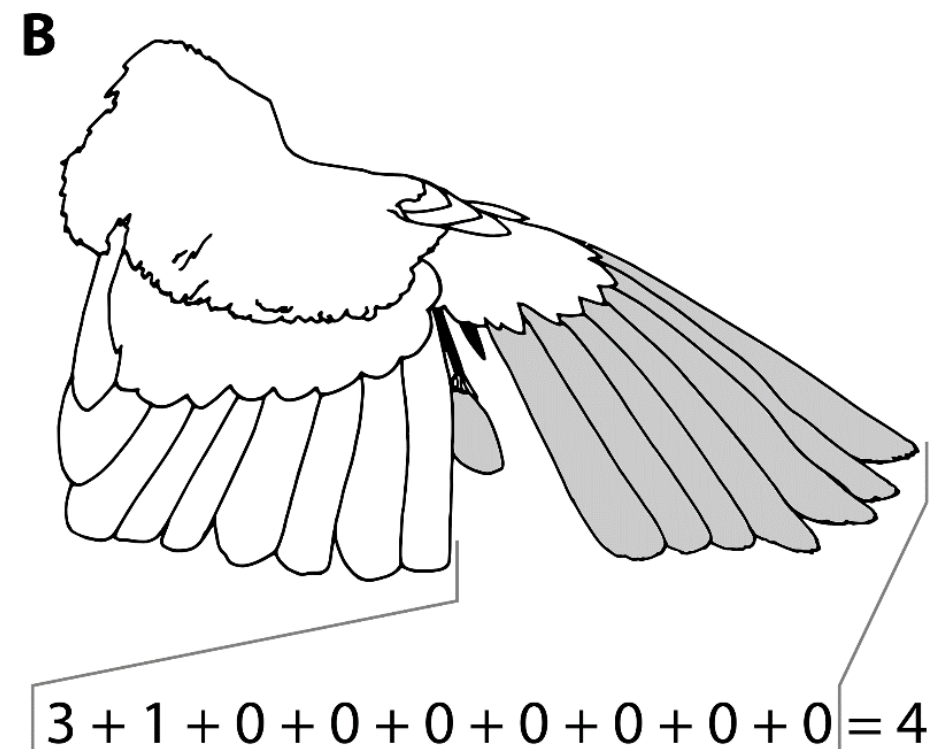
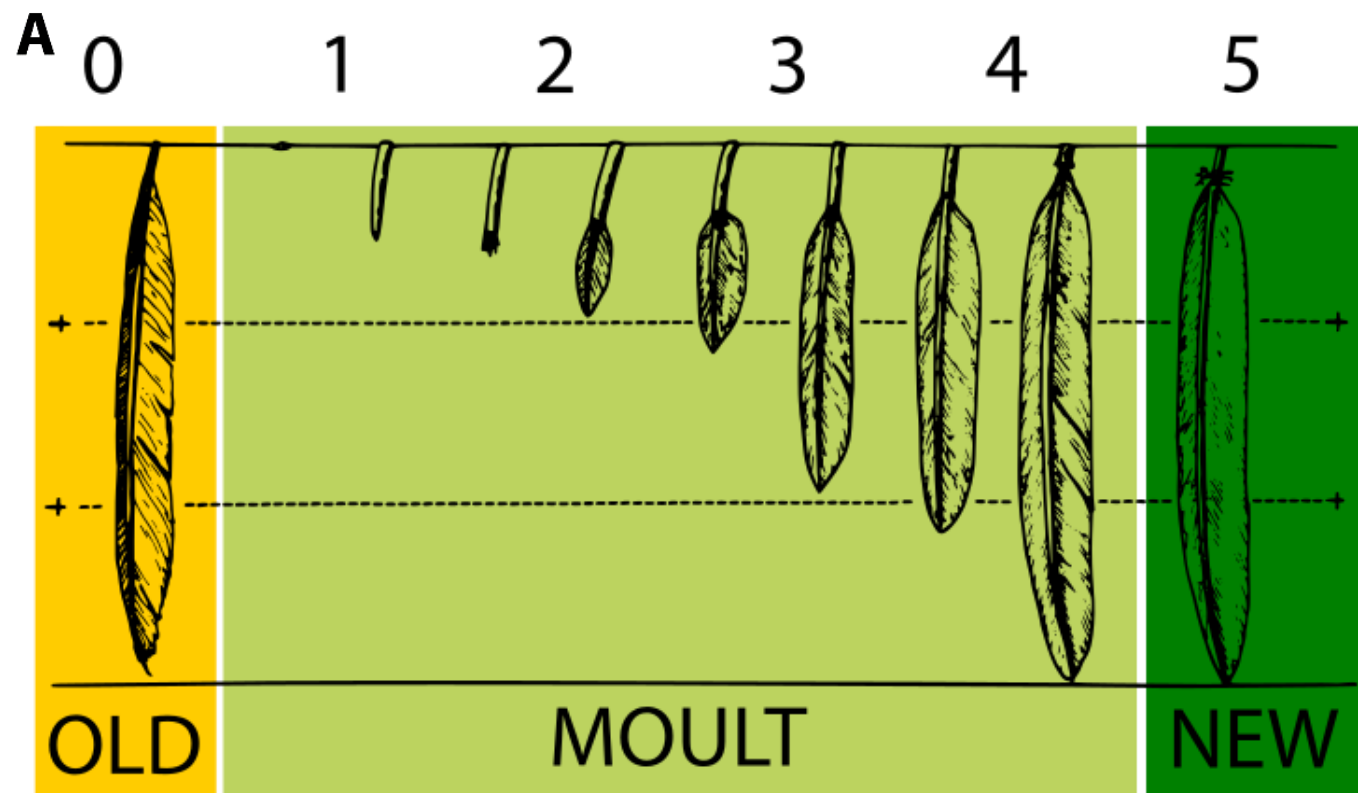
But we can e.g. count birds in old plumage, active moult, new plumage



Categorical moult models

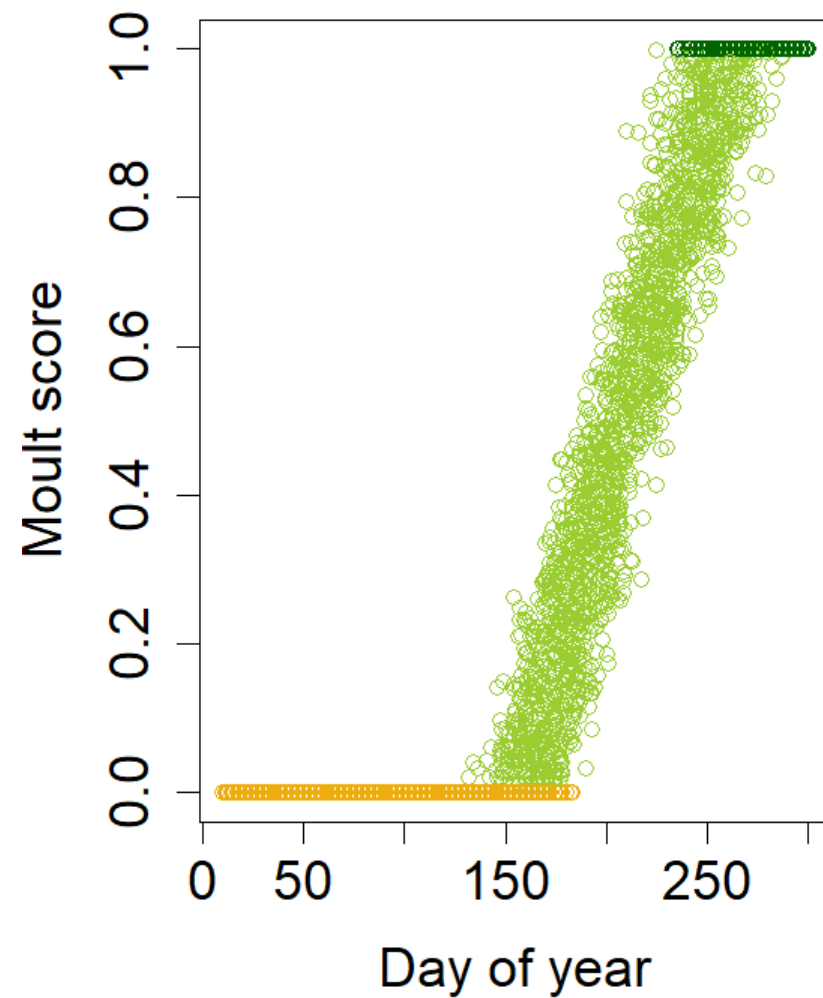
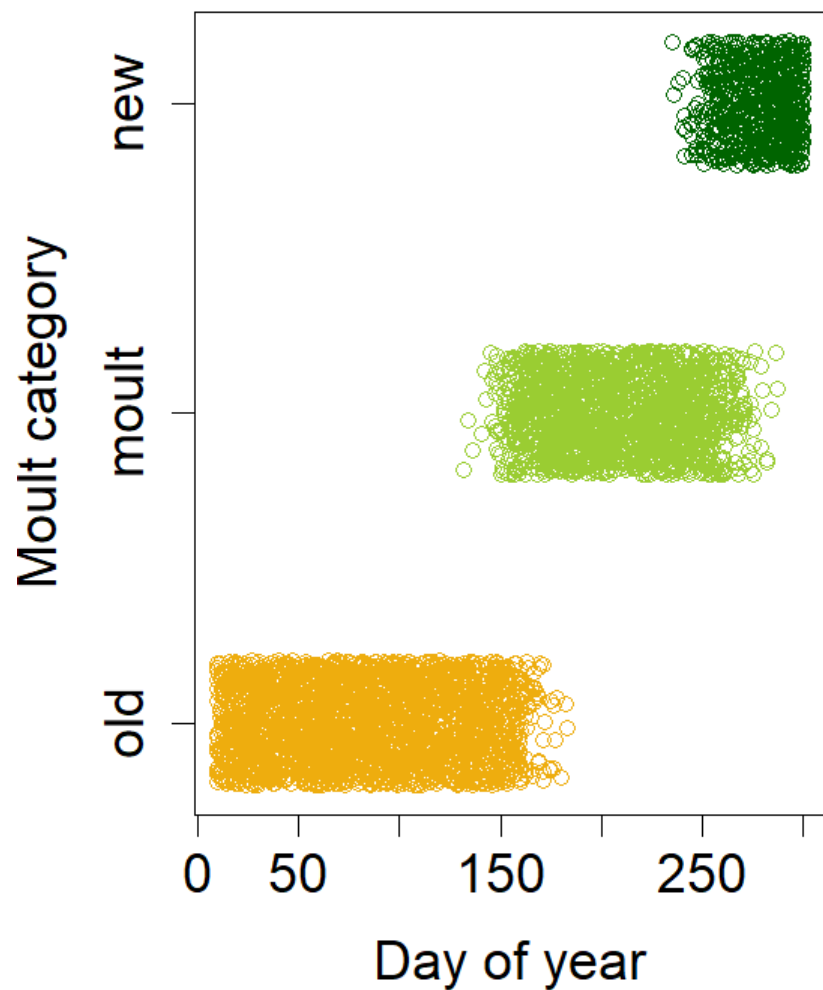


Flight feather moult data

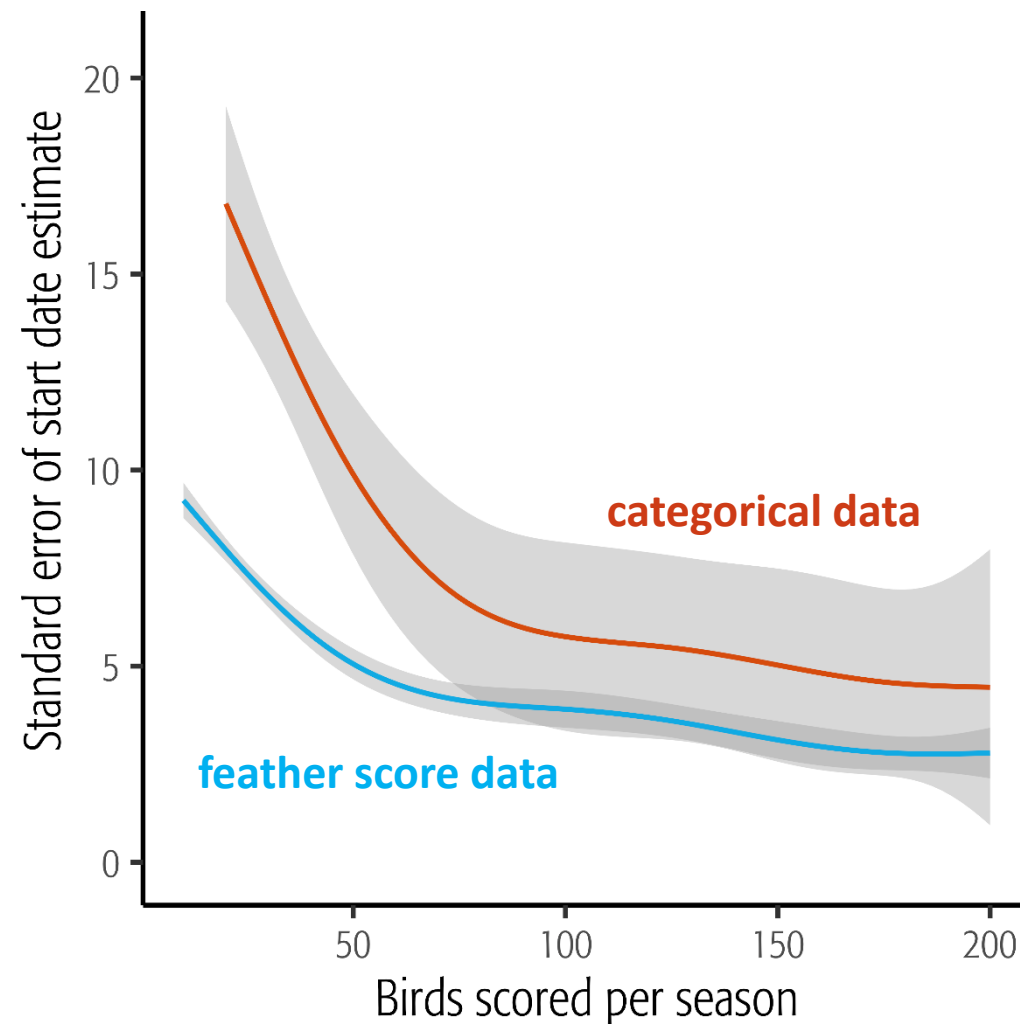
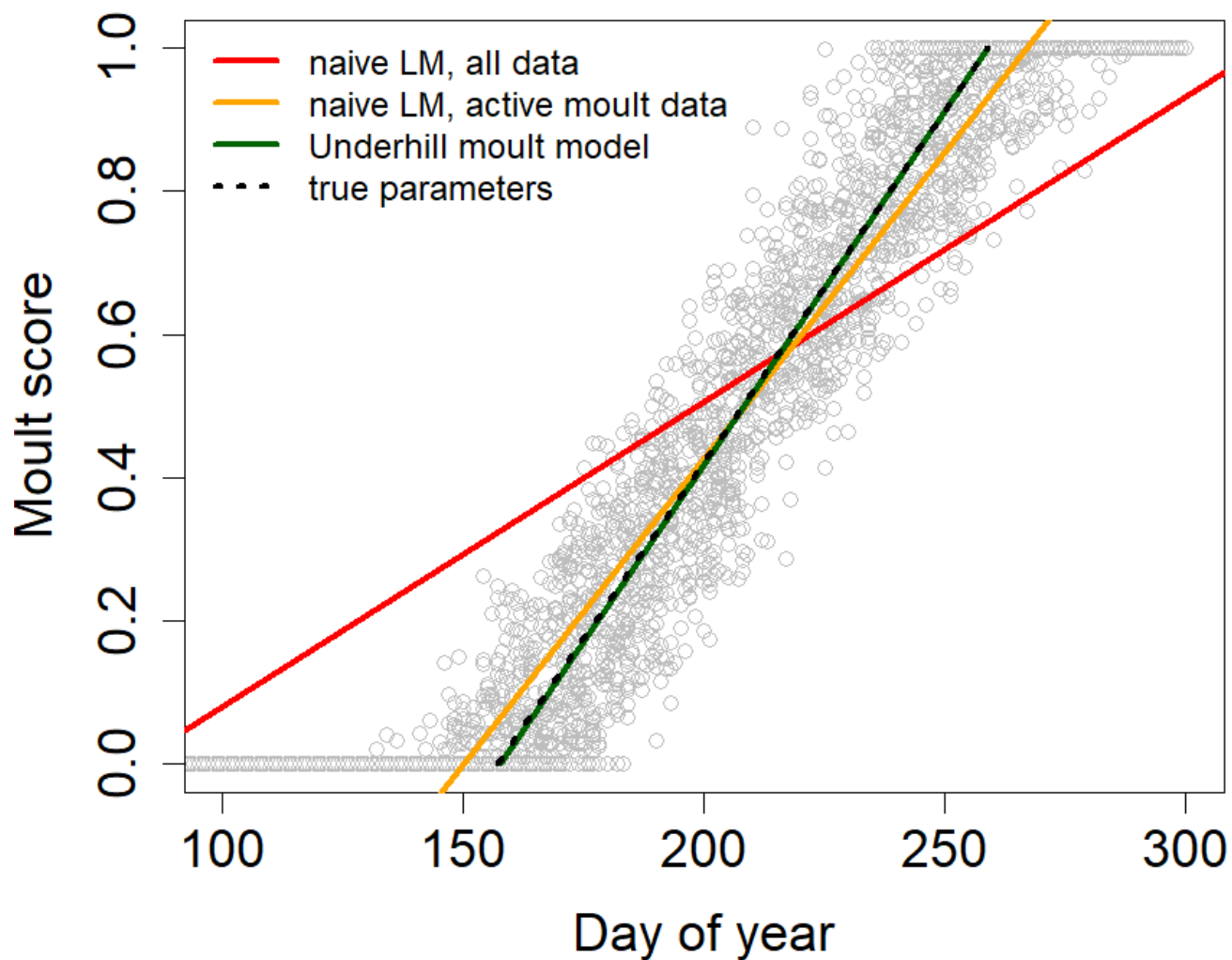


- data are partially continuous
- of biological interest are **start date** $T = \tau_1$ and **duration** $\tau = \tau_2 - \tau_1$

Feather score data is semi-categorical



Feather score moult models are more precise



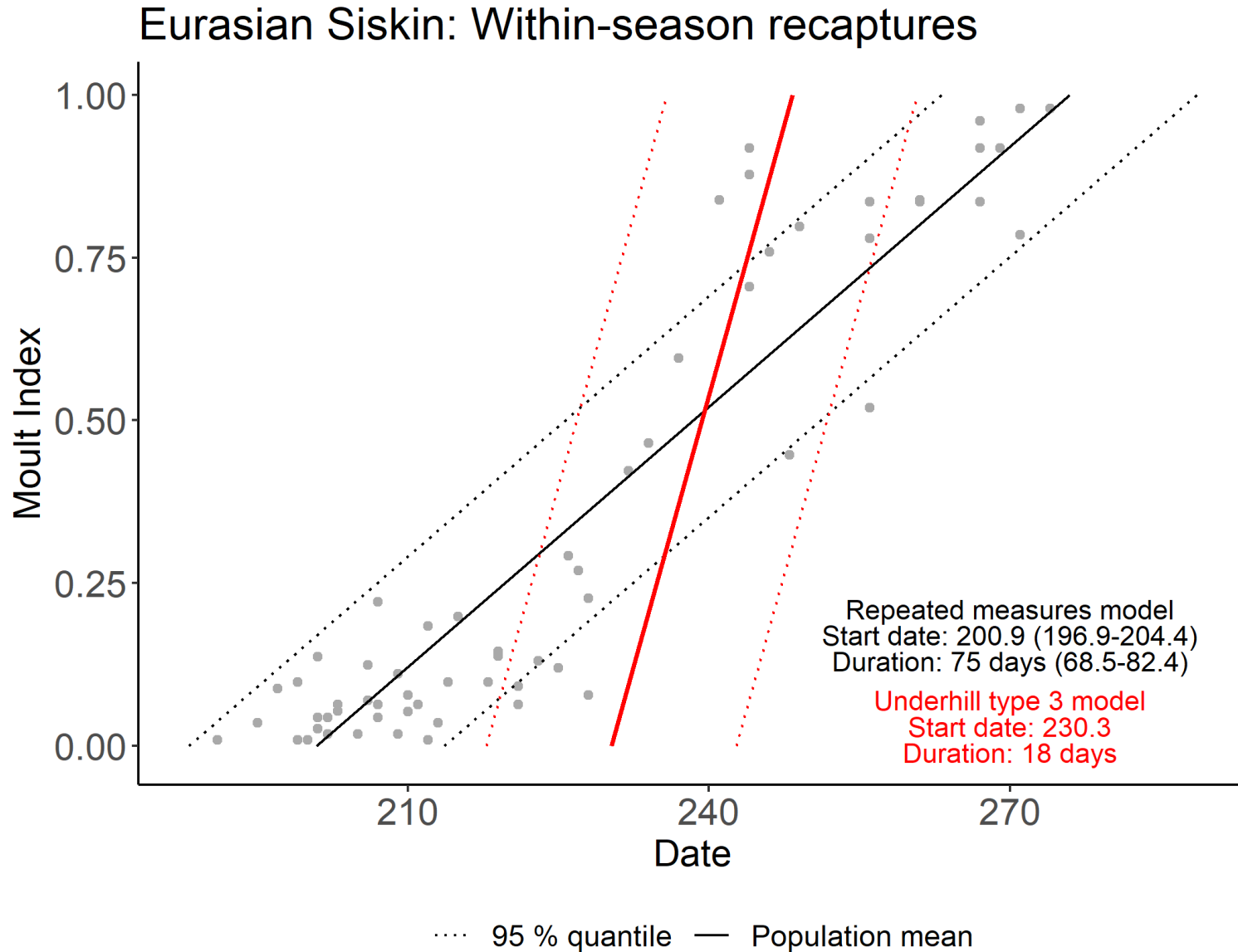
The `moult` package implements ML inference

- `moult` implements maximum likelihood inference for moult models
- Moulting data can be categorical classes or continuous moulting scores
- Linear predictors can be added for each parameter (moult start, moult duration, population variance of start date)
- Inference is very fast for realistic sample sizes (seconds).

`moult` is freely available on CRAN: <https://cran.r-project.org/package=moult>

It can be installed in R with the command
`install.packages("moult")`

Hierarchical moult models with moultmcmc



The `moultmcmc` package implements Bayesian inference



- `moultmcmc` implements full Bayesian inference for moult models.
- complements ML inference in package `moult`
- Models are fitted using HMC samplers from Stan
- Inference is fast for realistic sample sizes (seconds to minutes)
- Generic interface for hierarchical model structures in work

`moultmcmc` is freely available on github: <https://github.com/pboesu/moultmcmc>

It can be installed in R with the command
`devtools::install_github("pboesu/moultmcmc")`



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ACKNOWLEDGEMENTS

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