

# moult and moultmcmc: Inference for moult phenology models

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[title slide]

Hi I'm Philipp. I'm an Ecological Statistician at the British Trust for Ornithology and today I'll talk about estimating the phenology of avian moult.

[slide 1]

Studying phenology allows us to understand the processes governing the annual cycles of animals and plants, and how they change, for example under climate change. Phenological analyses focus on the timing of particular events, for example the laying dates of chaffinches in Britain.

[slide 2]

However, for many phenomena the dates of particular events are more difficult to observe than the state of the system itself. Avian moult is such a case, for example from mist net captures we can identify birds in active moult across a free living population, but determining the exact date of moult initiation and the pace of moult in individuals is usually not possible.

[slide 3]

Moult in birds can be described as a categorical state by classifying an individual into 'old plumage', 'active moult', or 'new plumage' and categorical regression models can then be used to make inference about the start date and duration of moult.

[slide 4]

For flight feather moult can we also score individual feathers based on how far they have regrown. For birds with complete wing moult we can sum individual feather scores to obtain an overall moult score.

[slide 5]

In many species weighting the feather scores by the relative mass of each feather gives a near linear indication of moult progress.

Moult scores hold a lot of information because they let us reconstruct how long a bird has been in active moult.

[slide 6]

However, because moult scores represent proportions simple linear regression applied to moult scores will yield biased estimates of start dates and duration, but we can use something akin to a hybrid of a linear regression model and a categorical model – the so called Underhill moult model - to model them accurately. All else equal using feather scores will result in better precision estimates than using categorical data alone.

[slide 7]

Maximum likelihood inference for moult models, both for categorical and moult score data were described by Les Underhill and colleagues some 30 years ago, and these models are implemented in the R package ‘moult’ which is available on CRAN<sup>1</sup> and described in detail in the companion paper by Birgit Erni and others<sup>2</sup>.

[slide 8]

However, inference for moult models can be challenging with real data, in particular when capture probabilities are not homogeneous across the moult cycle, and when only parts of the moult process can be observed. Bayesian inference can be more robust in some cases, and even where it fails it can make it easier to diagnose model or data pathologies.

Bayesian inference also allows us to open up moult models to include features that ecologists like– namely hierarchical model structures to account for individual heterogeneity in moult parameters and other random effects for multi-site or multi-year datasets.

For example, using a hierarchical moult model we were able to infer moult parameters for free living Eurasian Siskins using information from repeat captures. The classical moult model failed to provide sensible estimates this instance.

[slide 9]

Our R package `moultmcmc`<sup>3</sup> implements Bayesian inference for moult models. It uses Hamiltonian Monte Carlo samplers from `stan` as the backend, so typical moult data sets can be analysed in a matter of seconds to minutes.

The generic interface for random effects is still a work in progress but the package is available on github, so give it a try and let us know how you get on with it.

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<sup>1</sup> <https://cran.r-project.org/package=moult>

<sup>2</sup> <http://dx.doi.org/10.18637/jss.v052.i08>

<sup>3</sup> <https://github.com/pboesu/moultmcmc>