# Model complexity and model choice for animal movement models

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# Outline

# Acknowledgements


| | |
|---|---|
| People | **Michael Li**, **Madelon van de Kerk**, Dave Onorato, Madan Oli; many unnamed field biologists |
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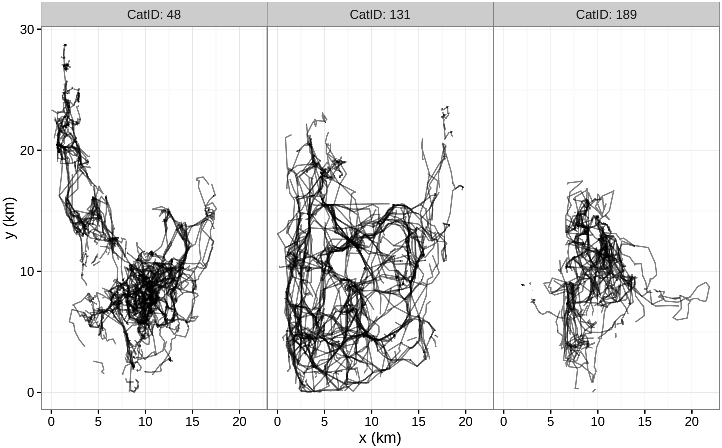
# Outline

# Florida panther movement

- endangered subspecies, *Puma concolor coryi*
- movement variation by sex and life history stage (juvenile, adult, mom with kittens . . . )
- effects of movement on threats
- predicting the effects of changes in habitat, etc.

# panther movement tracks

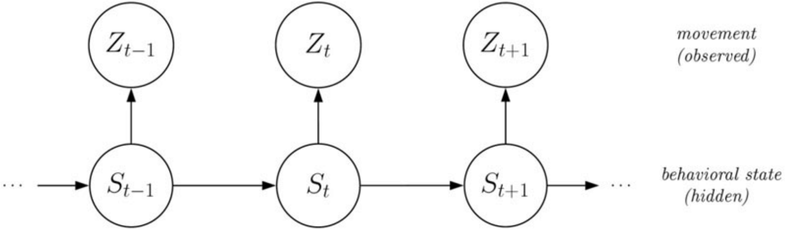
18 GPS-collared animals, 3200 panther days;
49000 locations (hourly); 1-15K observations per animal



# Outline

# Hidden Markov models

- finite mixture model with temporal dependence
- discrete time steps
- discrete latent state; *transition matrix*
- observations from *emission distributions* (continuous or discrete, univariate or multivariate)
- **multiphasic movement** (Fryxell et al., 2008; Langrock et al., 2012)



# Hidden Markov models (cont.)

**state:**

$$S_t \sim \mathrm{Multinomial}(S_{t-1}, \mu_{S,t})$$
$$\mu_{S,t} = \mathrm{multi\text{-}logistic}(\mathbf{X}_{S,t}\boldsymbol{\beta}_S)$$

**emission:**

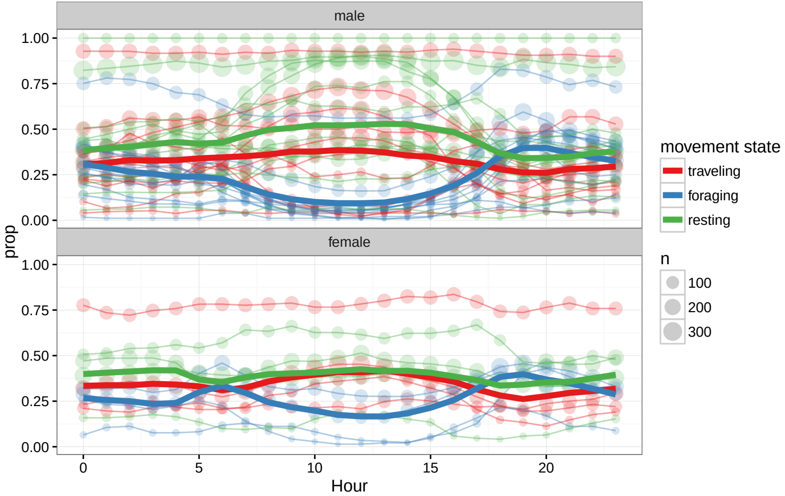
$$\mathbf{Z}_t \sim \{\mathrm{Dist}_1(\mu_{Z_1,S_t}), \ldots, \mathrm{Dist}_n(\mu_{Z_n,S_t})\}$$
$$\mu_{Z_i,S_t} = g^{-1}\left(\mathbf{X}_{Z_i,t}\boldsymbol{\beta}_{Z_i,S_t}\right)$$

# Hidden Markov models (part 3)

- *forward-backward algorithm* for estimating parameters
- *Viterbi algorithm* for estimating most probable state sequences
- `depmixS4` package (Visser and Speekenbrink, 2010) (also `moveHMM` (Michelot et al., 2016))
- hidden *semi-Markov* models: allow for non-geometric *dwell time distributions* (Langrock, 2011; Augustine, 2016): `move.HMM`

# Outline

# Diurnal variation



# what can we conclude so far?

**good news**

- basic biology: males move faster, farther
- three states are identifiable, sensible
- dwell distributions approximately geometric (HSMM $\rightarrow$ HMM)

bad news

- diurnal variation in Viterbi results - but it's not in the model!
- estimates of model complexity are too high

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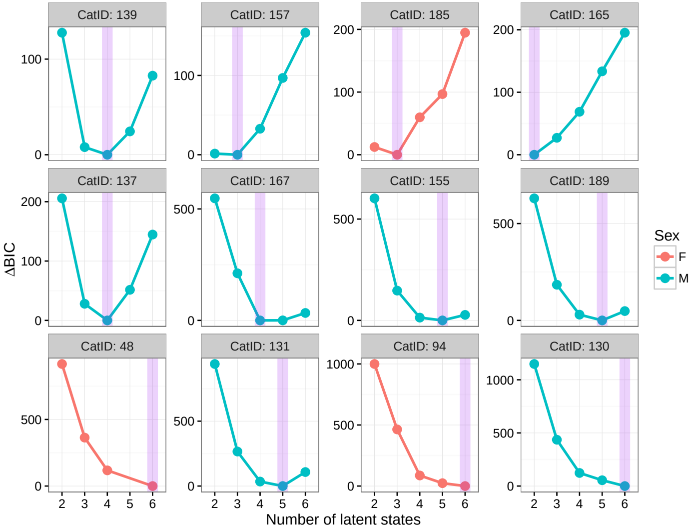
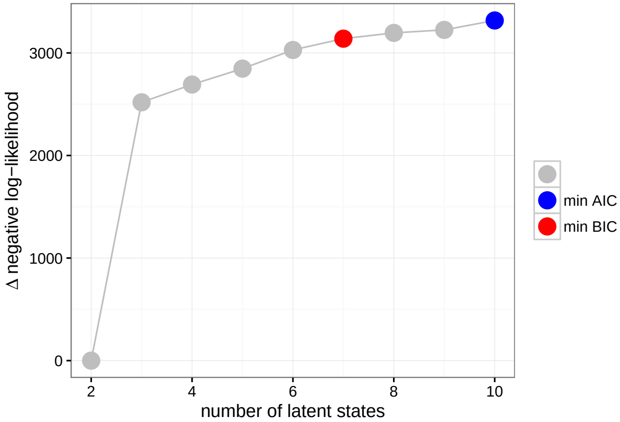
# Model complexity (bad news)



# Model complexity (Manx shearwaters, Dean et al. (2013))



# Outline

# Expanding the model

Attempting to fix these problems:

- extend the model to allow covariates
- specifically, allow for diurnal variation
    - simplify model (log-Normal step length only)
    - *fixed* state-specific emissions parameters (step length mean and std dev)
    - time-varying transition parameters
    - also try *finite mixture models* (independent occupancy)
- how much does this help?

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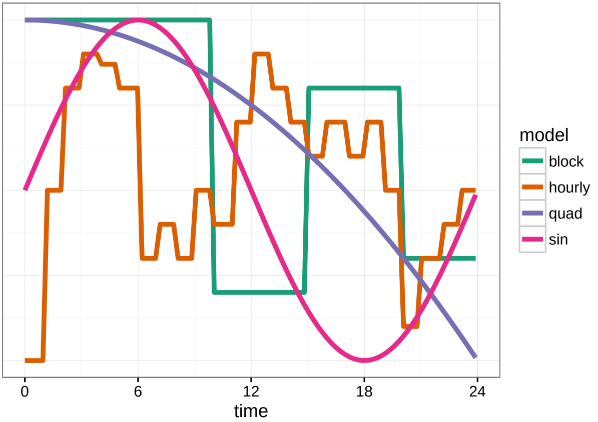
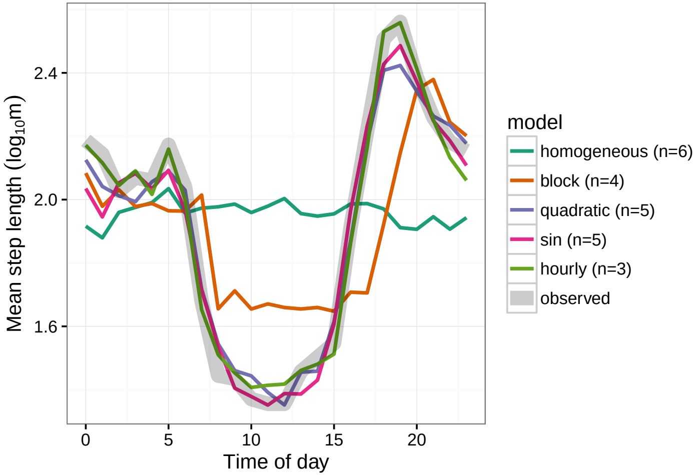
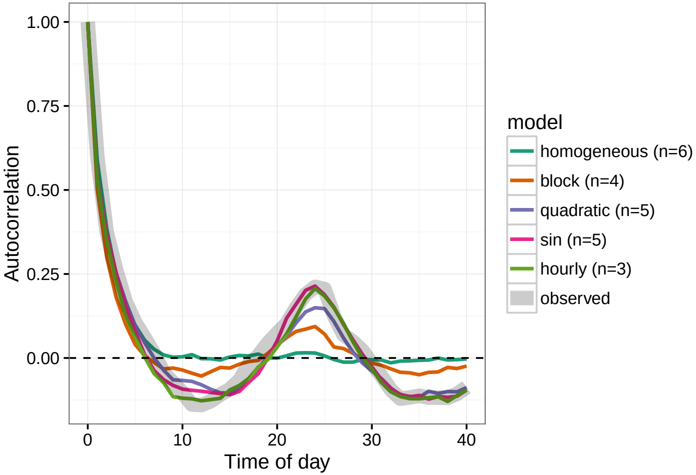
# Temporal models



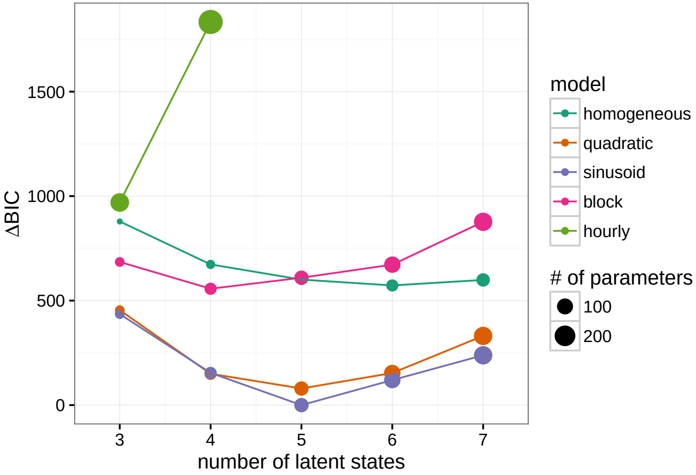
# Temporal patterns (step length)



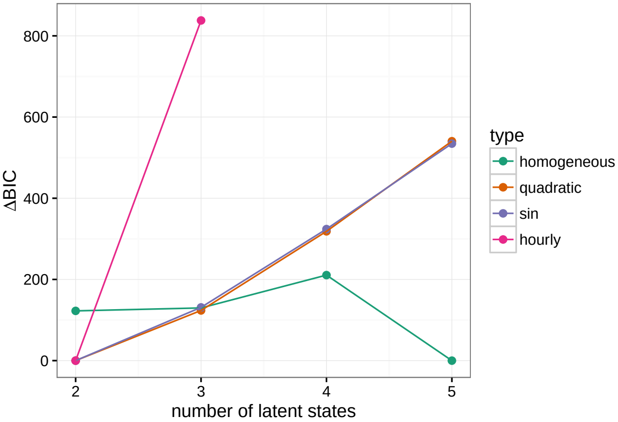
# Temporal patterns (autocorrelation)



# Goodness of fit/model complexity



# Model complexity: simulation



# Diurnal model: conclusions

- diurnal structure greatly improves fit ($\Delta\mathrm{BIC} \approx 500$)
- slightly improves latent-state issue ($n = 6 \to 5$)
- lots left to do!
  - seasonal variation
  - incorporate habitat, home range behaviour
  - etc. etc. etc.

# Outline

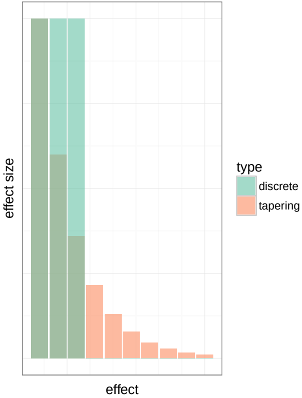
# Big data and small models

- simple model families + model misspecification → overparameterization
- Gelman: "Sample sizes are never large": (blog post)

> *N is never enough because if it were "enough" you'd already be on to the next problem for which you need more data.*

# An aside on AIC vs BIC

- "should I use AIC or BIC? I heard that AIC is inconsistent ..."
- complexity penalty = 2 (AIC) vs $\log(n)$ (BIC)
- best prediction vs. model identification (Yang, 2005)
- *effect size spectrum*: tapering or discrete?



# Tools needed

- cross-validation (Wenger and Olden, 2012)
- protocols and tools for model checking (Potts et al., 2014); score tests?
- flexible computational frameworks (ecologists can't afford consultants/ there are too many species out there)

# References

Augustine, B., 2016. Flexible, user-friendly hidden (semi) Markov models for animal movement data.

Dean, B., Freeman, R., et al., 2013. *Journal of The Royal Society Interface*, 10(78):20120570. ISSN 1742-5689, 1742-5662. doi:10.1098/rsif.2012.0570.

Fryxell, J.M., Hazell, M., et al., 2008. *Proceedings of the National Academy of Sciences*, 105(49):19114–19119. ISSN 0027-8424, 1091-6490. doi:10.1073/pnas.0801737105.

Langrock, R., 2011. *Computational Statistics and Data Analysis*, 55(1):715–724. ISSN 01679473.

Langrock, R., King, R., et al., 2012. *Ecology*, 93(11):2336–2342. ISSN 0012-9658. doi:10.1890/11-2241.1.

Li, M., 2015. *Incorporating Temporal Heterogeneity in Hidden Markov Models For Animal Movement*. Master's thesis.

Michelot, T., Langrock, R., and Patterson, T.A., 2016. *Methods in Ecology and Evolution*, in press. doi:10.1111/2041-210X.12578.

Potts, J.R., Auger-Méthé, M., et al., 2014. *Methods in Ecology and Evolution*, 5(10):1012–1022.

van de Kerk, M., Onorato, D.P., et al., 2015. *Journal of Animal Ecology*, 84(2):576–585.

Visser, I. and Speekenbrink, M., 2010. *Journal of Statistical Software*, 36(7):1–21.

Wenger, S.J. and Olden, J.D., 2012. *Methods in Ecology and Evolution*, 3(2):260–267. ISSN 2041210X. doi:10.1111/j.2041-210X.2011.00170.x.

Yang, Y., 2005. *Biometrika*, 92(4):937–950. doi:10.1093/biomet/92.4.937.