**Session 5: Individual projects**

Main tasks for this session are:

1. Complete the lab exercise for your chosen study region and taxa.
2. Reading:
   * Focus on pages 28-39 (section 5) of the Pearson\_SDMGuide.PDF document
   * If you are interested in evaluating models built using very few occurrence records (e.g., <15) then you might also check out: Pearson et al. 2007
3. Continue to work on your individual projects. Please do get in touch with one of us if you have questions about your project.

Please email a single presentation slide with your Maxent model generated in R from this session’s lab to Pete before the next class, and be prepared to very briefly describe your results to the group next time.

Additional resources related to Session 5:

ENMEval R package: To conduct spatially independent evaluations and estimate optimal model complexity <http://cran.r-project.org/web/packages/ENMeval/index.html>

(Muscarella et al. 2014) <http://onlinelibrary.wiley.com/doi/10.1111/2041-210X.12261/abstract>

SpThin R package: for spatial thinning of species occurrence records

<https://cran.r-project.org/web/packages/spThin/index.html>

Wallace: a flexible software platform for reproducible modeling of species’ niches and distributions (incorporates ENMEval, SpThin, dismo, and other R packages into a shiny-based workflow)

<https://wallaceecomod.github.io/>

An R package to pinpoint positional error in species occurrence location and its impact on the performance of SDMs <http://r-gis.net/?q=positional_uncertainty2>

Running SDMs in QGIS:

QSDM: <https://conservationecology.wordpress.com/qgis-plugins-and-scripts/qsdm/>

Lifemapper tools and data management infrastructure: <http://lifemapper.org/?page_id=12>