**main local folder: Joseph BBtree**

**Remote REPOSITORY:** Bitbucket. Alignment not there yet.

**User: s.claramunttammaro@utoronto.ca**

**Password: Ph@cellodomus1**

**Backbone tree still has some issues:**

backbone\_53genes\_SC\_cleaned\_iqtree\_partfind\_rooted.tre

backbone\_53genes\_SC\_cleaned\_iqtree\_partitioned-ML\_aLRT\_rooted.tre

Psittaciformes and Passeriformes are not sister! (Falconiformes and Cariamiformes are closer to Passeriformes)

Coliiformes and Strigiformes are sister (this may be ok as it is uncertain)

Phaethontiformes not sister to Eurypygiformes, which are sister to Strisores!

Delete Puffinus yelkovan which appears sister to pterocliformes

**Serious problems in Aquaernithia, see polyphyly of Ardeidae and the inclusion of Vultur**

**Add samples to complete recently proposed families:**

add platylophidae (but sister to Corvidae)

add Paradoxornithidae (but sister to Sylvidae)

add Alcippedidae (but sister to Leiothrichidae)

**Constrain:**

The seven magnificent but see

**Clade trees**

**Missing:**

**Otidiformes**

**Mesitornithiformes**

Many major passerine clades: Acanthisitti, suboscines (but can use the Harvey et al tree), **Corvides** (missing, maybe use published tree?), **Muscicapida, Sylvida, basal Passerides and basal Passerida.**

**Other notes:**

The Pelecaniformes tree includes Phaethontiformes and Suliformes

Eurypygiformes (but they are in the backbone tree)

Ciconiformes tree includes Pterocliformes, Thinocoridae, Balaenecipitidae and Scopdiae!

After eliminating redundant trees, only 5556 species are covered.

**Burleigh et al. Big Tree**

6714 species using the Clements taxonomy!

Calibrate in TreePL using a combination of fixed (for calibrations with fossil sets >= 5) and intervals (for calibrations with fewer than 5 fossils?).

Maybe substitute incomplete clades with complete clades (Tyranni, Emberizoidea, Alcedinidae?)

**Big Bird Tree:**

Join clades to backbone.

Complete missing species with random refoliation (at the genus level?).

**Pipeline:**

Calibrate

Prune extra terminals

Repopulate genera based on taxonomy, producing a pseudosample.

Estimate diversification rates: tip rates and rates through time.

**Papers:**

Bird diversification through time.

Dispersal ability and speciation rates.

**Strategy A: single big matrix**

Joseph has a sparse matrix of 8.1 Gb including about 11 thousand taxa (species and subspecies).

He is going to try to obtain a RAxML tree with it. If it works, we can use complete the project using this single big matrix.

Calibrations can be done with TreePL:

Obtain a bootstrap sample of trees (with branch lengths) But bootstrap is not good in sparse matrices.

Generate Monte Carlo calibration for TreePL incorporating fossil age and clade age uncertainty.

Run TreePL over a sample of trees and calibrations.

**Strategy B: backbone + clade trees**

Send Joseph a list of genes or alignments for building a backbone tree:

mtDNA: ND2, cytb, COI

exons: RAG1 and 2 (chromosome 5)

Introns: ALDOB, ACO1, CLTC, HMGN2, FGB, RHO

With a dense alignment of “good genes” we will obtain a backbone tree with basal relationships and incorporating topological uncertainty.

The tree will be calibrated with the best deep time calibrations to obtain a robust backbone calibrated tree.

Clade tree will be attached to those trees to obtain comprehensive molecular tree.