Peter's Practical	Data type	Command	Tree
1A_choose_model_paup	(iqtree preferred)		
1B_choose_model_iqtree (note: no partition, no tree search)	Nuc (ModelFinder will test 52 DNA models)	iqtree -s DataReferenceSuborders.fasta -pre Nuc -te BIONJ -mset JC,F81,HKY,GTR	1B_Nuc.treefile
	AA (ModelFinder will test 52 protein models TAKES TOO LONG, mtART chosen in the end)	iqtree -s DataReferenceSuborders.translated.fasta -pre AA -te BIONJ -mset DCMut,mtART	1B_AA.treefile
2A_jmodeltest	(iqtree preferred)		
2B_modeltest_iqtree (note: uses partition, no tree search)	Nuc (Can now see diff in codon positions in AIC)	iqtree -s DataReferenceSuborders.fasta -pre NucParts -te BIONJ -m TESTONLY -spp InitialPartitions.nex	2B_NucParts.treefile
	AA	n/a	
3_iqtree (note: uses partition, tree search) Have played with 3rd Codon here	Nuc (Cheat: partitions already have own model choice. Reused info. Did not do this again)	iqtree -s DataReferenceSuborders.fasta -bb 1000 -pre NucPartsWithSearch -spp NucParts.best_scheme.nex	3_NucPartsWithSearch.contree
		iqtree -s DataReferenceSuborders.fasta -bb 1000 -pre NucPartsWithSearchNo3rd -spp NucParts.best_scheme.No3rd.nex	3_NucPartsWithSearchNo3rd.contree
		iqtree -s DataReferenceSuborders.fasta -bb 1000 -pre NucPartsWithSearchOnly3rd -spp NucParts.best_scheme.Only3rd.nex	3_NucPartsWithSearchOnly3rd.contree

Peter's Practical	Data type	Command	Tree
	AA	n/a	

Note: could partition AA matrix into (1) sites exposed to mitochondrial matrix (2) sites wedged into mitochondrial inter-membrane space (3) sites exposed to cytoplasm. BUT: Already lots going on. This partitioning makes sense, but not sure what this will achieve.