
Research Journal

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Contents

18 July 2016

18 July 2016

1 FONSE SEMPPR

Alan Dixon

Figures/2016/07/IMG_152.JPG

- Notes on board from our discussion.
- Still haven't solved drop in LLik
- Still don't have LLik plots on per AA basis

- Look MCMC at codon specific steps.
 - On first glance we thought the problem was a log comparison to a $U(0,1)$ RN, but we realize the comparison is to $-\exp(1)$ RN.
 - NB: Shared MCMC acceptance/rejection step pull and compares a random number even if the acceptance ratio is > 1 . – This seems inefficient.
 - Log Pr values are consistently 0. This caused the acceptance ratio to always be 1 and the model to drift off to bad values. Alan did often see acceptance rates of 1 which is consistent with this behavior.
 - Codon probability vector calculated on per amino acid and per position basis. Looking at an example of alanine he sees (1,0,0,0) for a particular instance. If a 0 pr codon is observed, the code ignores this fact and does not adjust the LLik. QUESTION: What we should we do in these instances? Throw an error? Throw a warning and add in a very large negative value to the LLik function? Does the other code take this same pathological approach.

2 RFP Data

Hollis Bui

- Thinks he's finished the unit testing for the small parts of ROC RFP but not the medium sized functions.
- Created benchmarks for larger model.
- Last meeting on or around July 12th we were
 - Looking how Pop et al data was processed by my Mathematica code.
 - Still haven't gotten code for running Mathematica.
 - Can see code via pdf file
- Went looking for Gabe's old code that compares estimates to those from Premal (NB, Hollis is comparing to those in Pop et al).
- Graphs λ and α' estimated vs. Pop don't look good but it turns out that he only ran the MCMC for 10 samples. Hollis will rerun for longer.