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| |  | | --- | | **Devin Molnau** | | Wed, Apr 24, 11:03 PM |  | https://mail.google.com/mail/u/2/images/cleardot.gif  https://mail.google.com/mail/u/2/images/cleardot.gif |
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Sorry for the late reply, your paper looks awesome! As to being behind on analysis, I think everyone is in that boat. You are just fine. Your topic looks very reasonable and ~250 sequences should be aligned and built by Sunday for sure. I am excited to see what you come up with. The only thing I can think of reading you paper, I am not sure if you specified what alignment program that you are using ( MAFFT, versus MUSCLE etc) and how are you comparing the trees (maximum likelihood, visually)? Honestly, you paper looks pretty darn good and there isn't much to say. Awesome work!

Sincerely,

Devin