**StringTie**

1. Page 2, 2nd to last paragraph on what was considered a ‘correctly identified’ transcript: Authors left a 100 bp window at the start and end of the transcript to ‘reflect the drop-off in coverage that often occurs near the ends of the transcript’ - these are 75 bp paired end reads, and ideally you would have forward & reverse reads (infact this data is generated by simulation, where you can lay stringency on the quality parameters, read pair distribution etc) that should nevertheless give you robust coverage at one/both termini. So I am not sure whether this was a valid reason for this approach, or if the deliberate addition of ambiguity around ‘what is a correctly identified transcript’ solely lends higher precision calls to the algorithm.
2. Wouldn’t the super-read synthesis lead to masking of low frequency isoforms, since one is just putting different pair reads in the same set based on a unique mapping in the longer super-read sequence (not based on coverage).

**MiRBooking**

1. The authors used m(i)RNA data from 41 different cell lines. The method for quantification of mRNAs that they used, however, does not seem justified properly. They look at the known absolute quantifications of 8 mRNAs (just 8!) in human CD4+ and CD8+ cells (their source data is from different cancer tissues, and NCI-60 cell lines!) to get a linear fit of the log transformed expression data – the approach appears to be spiking in a HUGE confounder, rather than correcting for batch effects/cell-line variances.
2. The paper is not clear on what happens by the Stable Marriage algorithm when the same seed has more than 1 optimal match. Would there be a subset of seed:MRE pairs that would constantly be in flux in this model, or would the algorithm automatically choose a random optimal MRE(y) for seed(x). I wonder if either of the approaches would lead to differences in prediction quality as well.