**FloReMi**

1. When the authors use ‘median(ratioall cells) + 2 stdev (ratioall cells) as a filter step, do they really mean the Median Absolute Deviation? Otherwise, what is the point of using the *positive* interval of 2 stdev about the median as a filter, when the stdev is actually being calculated relative to the mean? Even if they were using the median absolute deviation, why then would they want to remove the ‘margin events’ before applying this method on the data (from what I understand, MAD is supposed to be a robust measure of the centrality of the data, and presumably a MAD based filter will remove outliers automatically).
2. It is intriguing that despite choosing a 13 feature space of features that were strongly correlated with survival, the Cox regression did not do as well on the test dataset as the random survival forest that used the same set of features. Does the main difference simply lie in the inherent iterativeness of the random forest approach? What is the iterativeness enriching for if not the individual significance / contribution of each factor in differentiating two sample (sets)?

**FERRET**

1. How would this method account for different associations between concepts that are co-occuring across species? For example, it is not clear how a negative association between a gene and drug in humans, and a positive association between the same in mice, will influence the enrichment calculation, especially since they just use the fisher exact test to assess the increase in co-occurrence of terms across literature.
2. Why did this method need to be gene-centric? Based on how they describe the method for building the relationships and parsing sentences, it seems that it could easily have been expanded to add support for just pathways, or just medical terms in general. Would making this tool non-gene-centric take it away from the multi-species perspective?