Projects:

1. CloneFinder:
   1. Status: algorithm is currently capable of accurately φ values given the correct number of clones, and also therefore accurately assigns aberrations to clones.
   2. Issues:
      1. The algorithm is still not great at inferring the number of clones.
         1. Auer-Gervini method: seems conservative, underestimates n more and more as n increases.
      2. The algorithm has not been written to infer the phylogenetic trees; this is partly because the number of possible trees is prohibitively large for many cases: we need to find a way to narrow down number of trees to consider.
      3. Also, the utilization of co-occurrence information is difficult to implement…
   3. Clinical associations…
2. H&N:
   1. Status: the algorithm effectively infers the normal cell proportion.
   2. Issues:
      1. In order to infer sizes of multiple subclones, we need to find a way to tailor the prior distribution on copy number to the sample, since it appears that the prior which leads to the most accurate estimate varies from sample to sample.
3. TCGA/Simon & Youn
   1. To do:
      1. Procure mutation data from all cancers using firebrowser
      2. Modify Simon and Youn’s model to utilize allele fraction information.
4. DeepCNV
   1. To do: Develop effective ‘simulation’ of targeted gene sequencing from whole genome/exome data for which we know what the copy numbers are.