* variant calling
  + align seqs to genome first, then correct them by doing a re-assembly to make sense of where reads are per site
  + can’t combine two separate vcf together since won’t share same sites
* N+1 problem: want to combine samples/data but can’t
  + solution: use gVCF files, “saves” work that caller has done (like caching)
  + combining gVCFs is comparatively short