# ### All the softwares we used are free and open source, and we have cited every software in our manuiscript.

# A README file gene annotation

## Inter-species Conserved or Specific TAD searching

1. Multi-species alignment was performed using cactus.
2. halLiftover was used for export alignment bed coordinate.
3. conserved\_TAD\_domain.sh : Personal shell pipeline combining

bedtools

1.split\_bed\_for\_liftover.pl,;

2.intersect\_bound\_pass.pl;

3.TAD\_body\_size\_pass.pl;

4.boundary\_overlap.pl for batch searching homologous TAD body.

(4) putative\_TAD\_boundary\_filter.sh: Very similar scripts pipe to the above but focus on TAD boundary

1.split\_bed\_for\_liftover.pl.wjl

4.boundary\_overlap.pl.wjl

mcscan\_boundary.pl

Other correlated script for cactus.maf