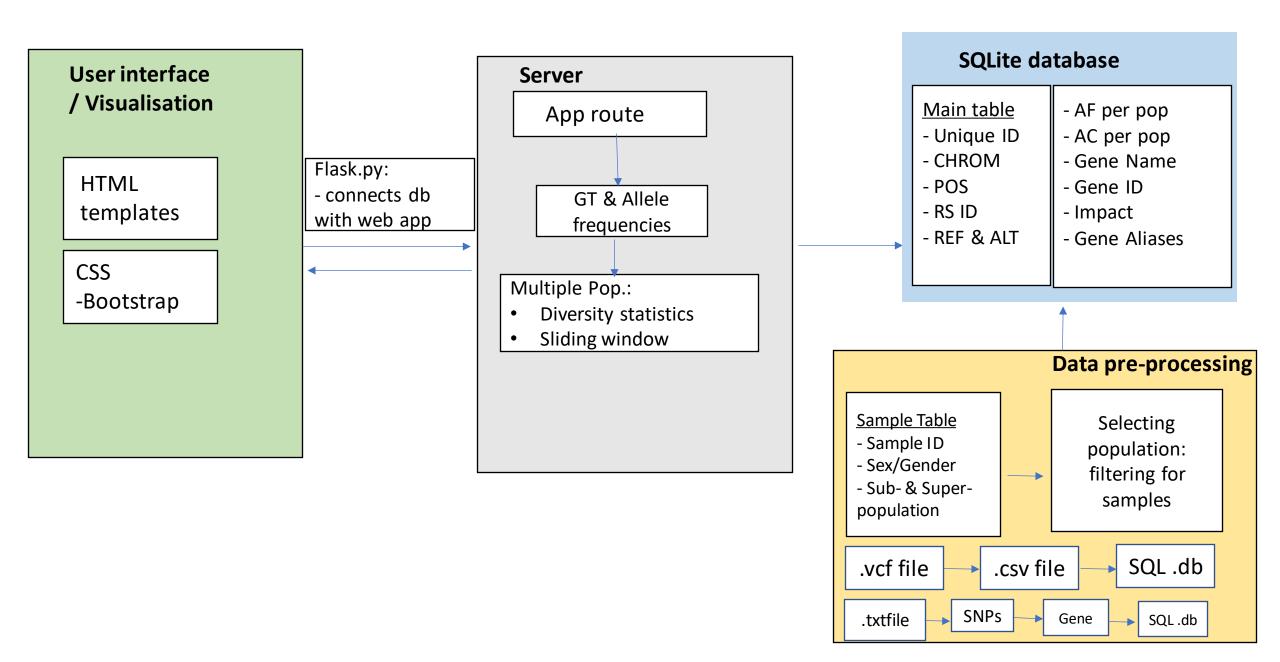
```
mirror_mod.mirror_object
 peration == "MIRROR_X":
 mirror_mod.use_x = True
mirror_mod.use_y = False
mlrror_mod.use_z = False
  _operation == "MIRROR_Y"
 irror_mod.use_x = False
 lrror_mod.use_y = True
 mirror_mod.use_z = False
   operation == "MIRROR Z"
  Lrror mod.use x = False
  irror mod.use_y = False
  BIO727P GROUP
SOFTWARE PROJECT
   ata.objects[one.name].se
   Int("please select exact)
   -- OPERATOR CLASSES ----
```

Team Celine
Celine, Amanah & Gracia
17.02.2021

x mirror to the select
iject.mirror\_mirror\_x"

#### SOFTWARE ARCHITECTURE

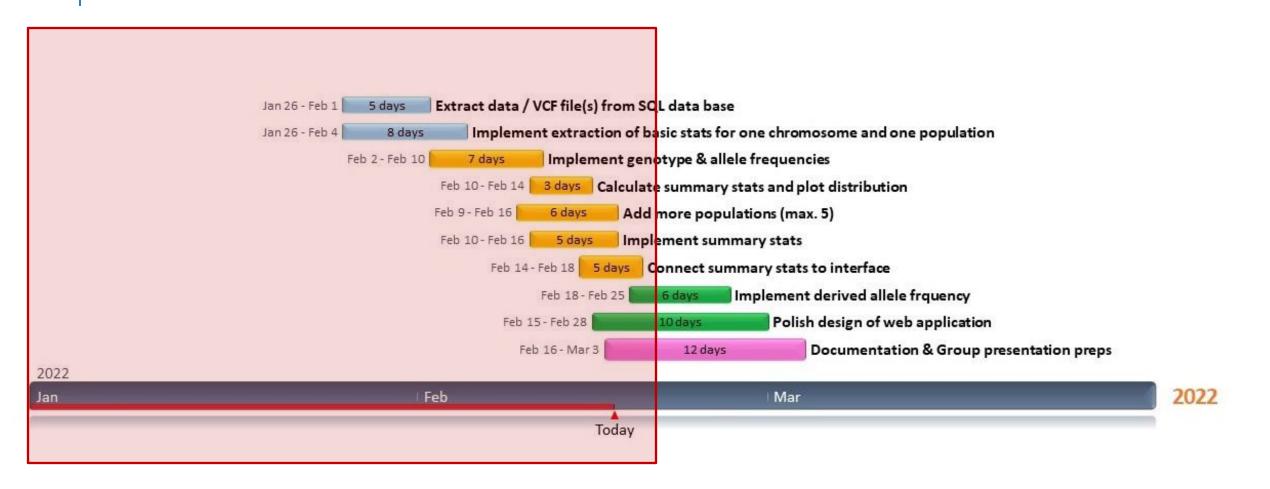




# COMPLETED TASKS (14/02 - 18/02/2022)

- Calculate summary statistics
  - ✓ Shannon Diversity, Tajima's D Celine
  - ✓ Heterozygosity Index Gracia
  - ✓ FST Amanah
  - ✓ Sliding window & plots Amanah & Gracia
- ✓ Gene Aliases added and combine data to one table Gracia
- ✓ Documentation Amanah
- ✓ Flask: added routes Celine
  - ✓ html pages (search results and statistics/population selection)
  - ✓ Statistics added: shannon
- ✓ Add more populations group decision
  - ✓ Extract population data and calculate gt & allele freqs Celine & Gracia

### GANTT CHART UPDATE





## NEXT WEEK'S MILESTONES (21/02 - 25/02/2022)

- Connect summary stats calculation and sliding window for a query to web app – Celine
- Download text file Celine
- Documentation Amanah & Gracia
- $\triangleright$  Polishing of web app (incl. Design  $\rightarrow$  HTML templates) Celine
- Derived chimpanzee allele frequency Amanah

==> making sure what we are producing makes sense!



### QUESTIONS

- Which types of genes should we keep? NcRNA (example: ENSG00000232073 \*\*\*), pseudogenes, or only DNA genes?
- 2. Derived allele frequency → theta threshold?
- 3. Is it a problem that no rsIDs for all SNPs?
- 4. Documentation structure?
- 5. Any questions for us?