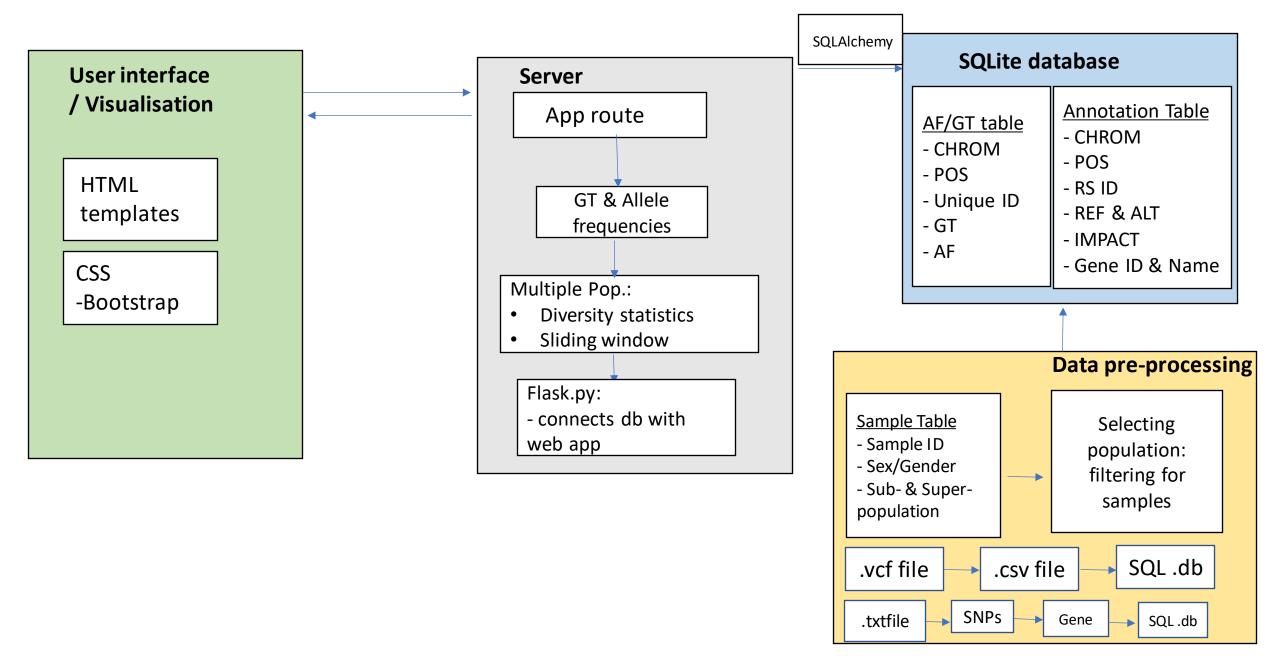
```
mirror_mod.mirror_object
 peration == "MIRROR_X":
 mirror_mod.use_x = True
mirror_mod.use_y = False
mlrror_mod.use_z = False
  _operation == "MIRROR_Y"
 irror_mod.use_x = False
 mirror_mod.use_y = True
 marror_mod.use_z = False
   operation == "MIRROR Z"
  Irror mod.use x = False
  irror mod.use_y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

Team Celine Celine, Amanah, Gracia & Pavan 10.02.2021

x mirror to the select
iect.mirror_mirror_x"
ror X"

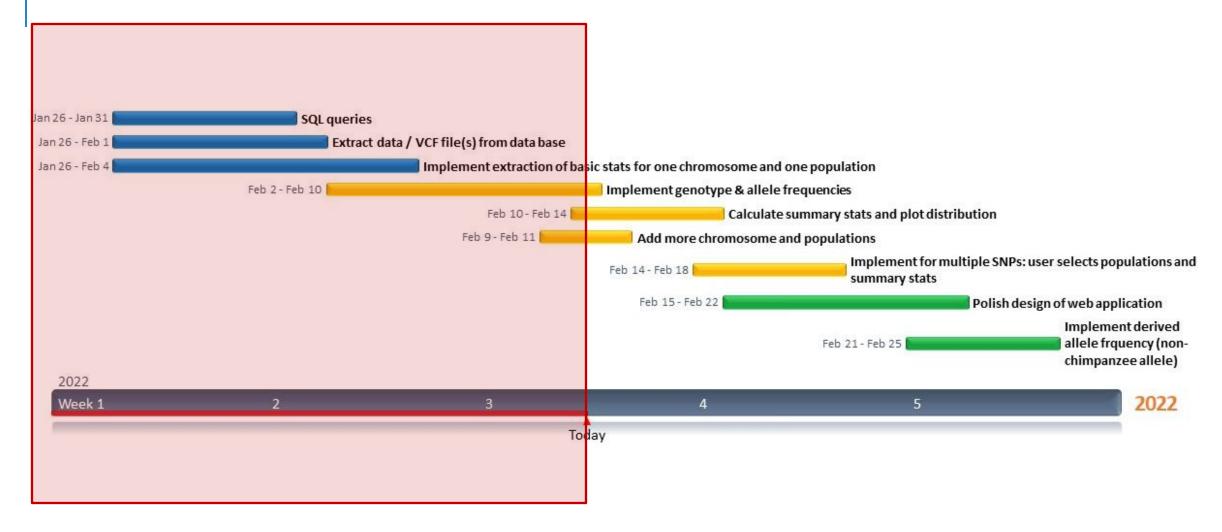
SOFTWARE ARCHITECTURE



COMPLETED TASKS (07/02 - 11/02/2022)

- ✓ Refined data base (removed indels) and connect GBR table after frequencies are calculated → Celine
- ✓ Connect flask and SQL database → Celine
- ✓ Setting up query function to search the DB → Celine
- ✓ Build very basic web app template → Celine
- ✓ Properly research summary stats and how to visualise them → Amanah & Pavan
- ✓ Calculate genotype frequencies → Gracia & Amanah
- ✓ Calculate allele frequencies → Gracia
- ✓ Prepare project update PPT → Gracia

GANTT CHART UPDATE





NEXT WEEK'S MILESTONES (14/02 - 18/02/2022)

- Derive summary statistics from GT & allele frequencies
- Connect R Script to flask /web app / data base
- ➤ Sliding window & plots
- ➤ Web application: HTML templates & result pages
- Add more populations
- ➤ Optional: add more chromosomes



QUESTIONS

- Do indels count as SNPs?
- 2. Who picks the 5 populations? User or us as developers?
- 3. Genotypes: 0/0, 0/1, 1/0?
- 4. Visualisation of GT frequencies → on summary stats! (if any additional visualisation that might be useful, that's fine too)
- Share data base via some online cloud (link) probably
- Do you have any questions for us?