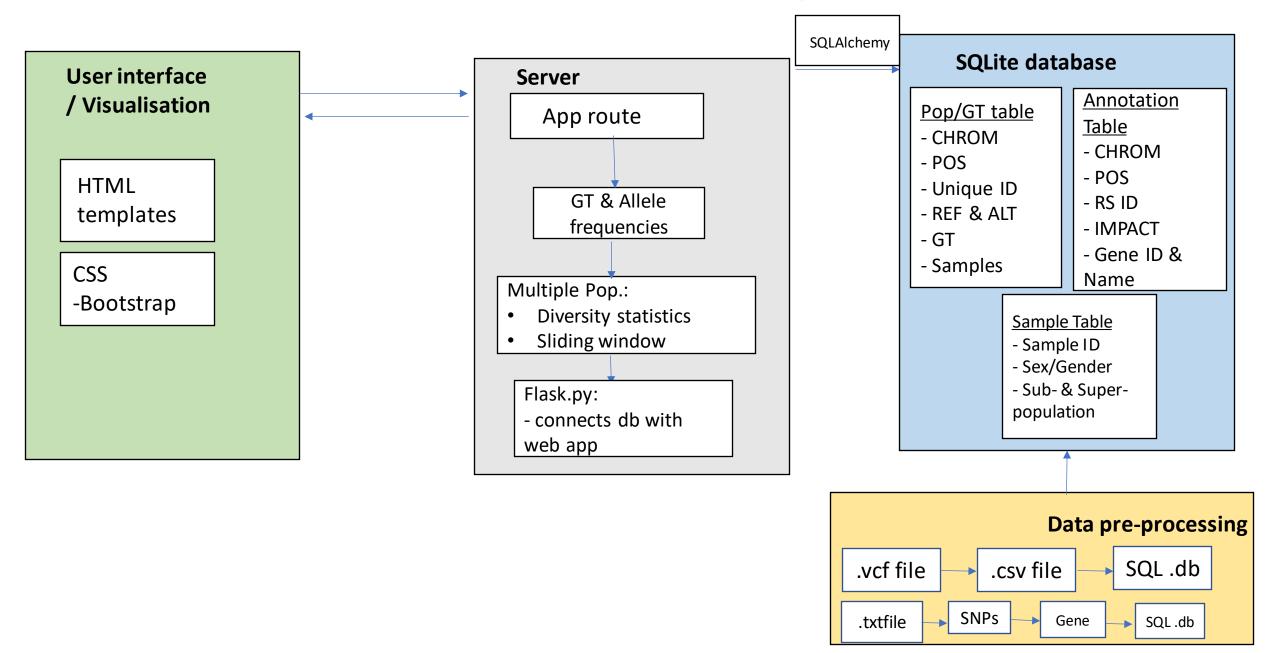
```
mirror_mod.mirror_object
 peration == "MIRROR_X":
 mirror_mod.use_x = True
mirror_mod.use_y = False
mlrror_mod.use_z = False
  _operation == "MIRROR_Y"
 irror_mod.use_x = False
 mirror_mod.use_y = True
 marror_mod.use_z = False
   operation == "MIRROR Z"
  Irror mod.use x = False
  irror mod.use_y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

Team Celine Celine, Amanah, Gracia & Pavan 03.02.2021

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

SOFTWARE ARCHITECTURE



Celine's Workspace – pls ignore

- need to refine indels and connect GBR table after frequencies are calculated

<u>Genotype table – phased.vcf</u>

- CHROM
- POS
- Unique ID {{PK}}

22:10519265:CA:C

- REF & ALT (multiple ALTs)
- GT/sample

Gene names table

- CHROM
- POS
- RS ID
- Unique ID {{FK}} need this
- REF & ALT <delete later>
- IMPACT
- GENE name
- GENEID

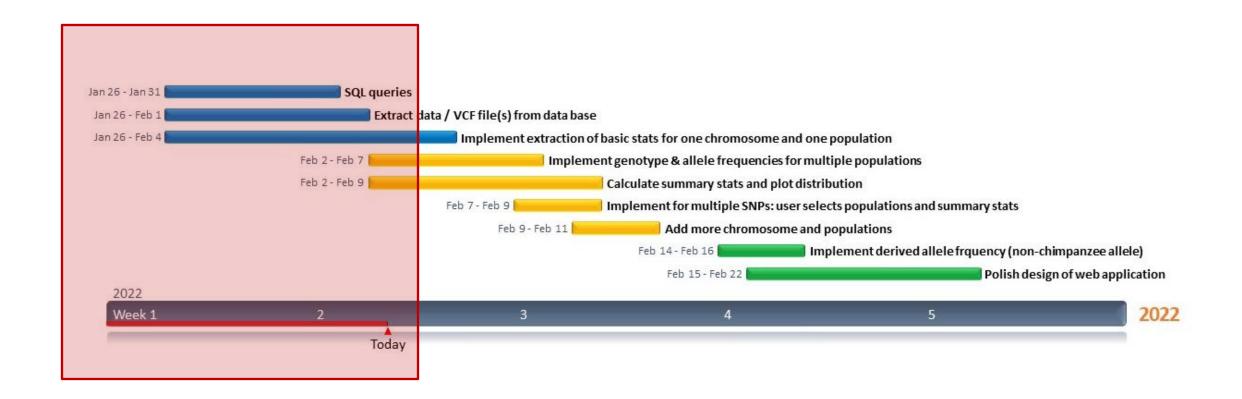
Population-sample table

- SAMPLE ID {{PK}}
- Sex
- Biosample ID
- Population code & name
- Superpopulation code % name
- DATA

COMPLETED TASKS

- ✓ Extraction of VCF files
- ✓ Building SQL database
- \checkmark Filter for one population using bcftools \Rightarrow focused on GBR for now
- ✓ Researched on summary statistics

GANTT CHART UPDATE



NEXT WEEK'S MILESTONES

- Properly research summary stats / inputs Amanah & Pavan
- ►Implement genotype frequencies → Amanah
- Calculate allele frequencies Pavan
- Connect flask and SQL database Celine
- >Setting up query function to search the DB -> Celine
- ➢ Build very basic web app template → Celine/Gracia
- Derive summary statistics from successful GT & allele frequencies (incl. Sliding window) Tracia



QUESTIONS

- Just SNPs? Or also indels
- Do indels count as SNPs
- •Who picks the 5 populations? User or us as developers?
- Do you have any questions for us?