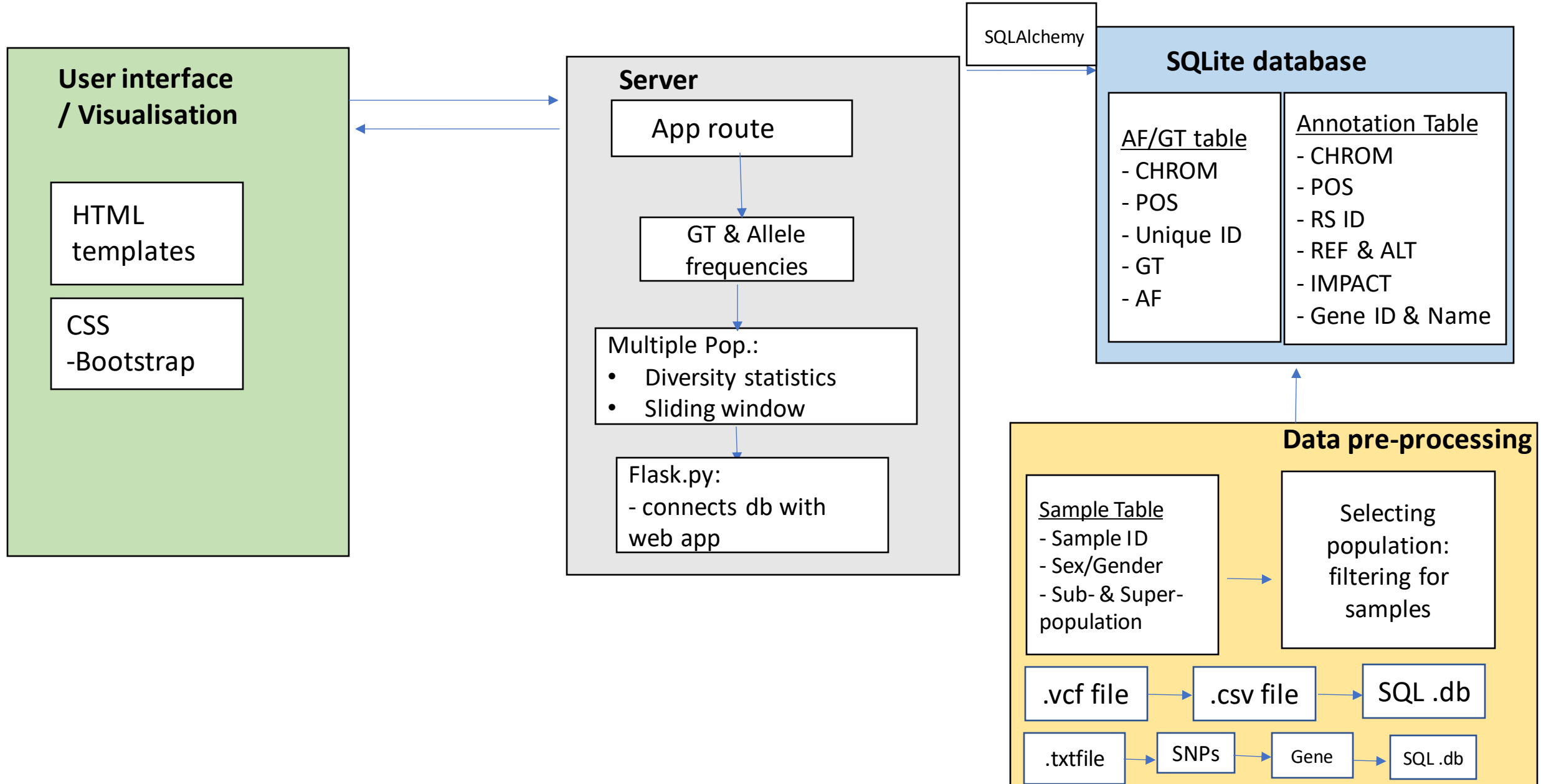# BIO727P GROUP SOFTWARE PROJECT

Team Celine
Celine, Amanah, Gracia & Pavan
10.02.2021

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
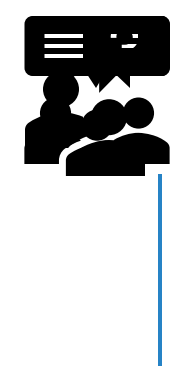
✓ Prepare project update PPT ➔ Gracia

GANTT CHART UPDATE
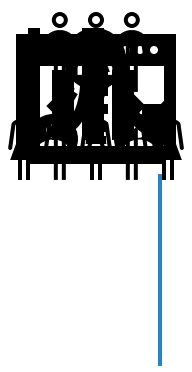
NEXT WEEK'S MILESTONES (14/02 – 18/02/2022)

➢ **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

1. 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)

5. Share data base via some online cloud (link) probably

6. Do you have any questions for us?