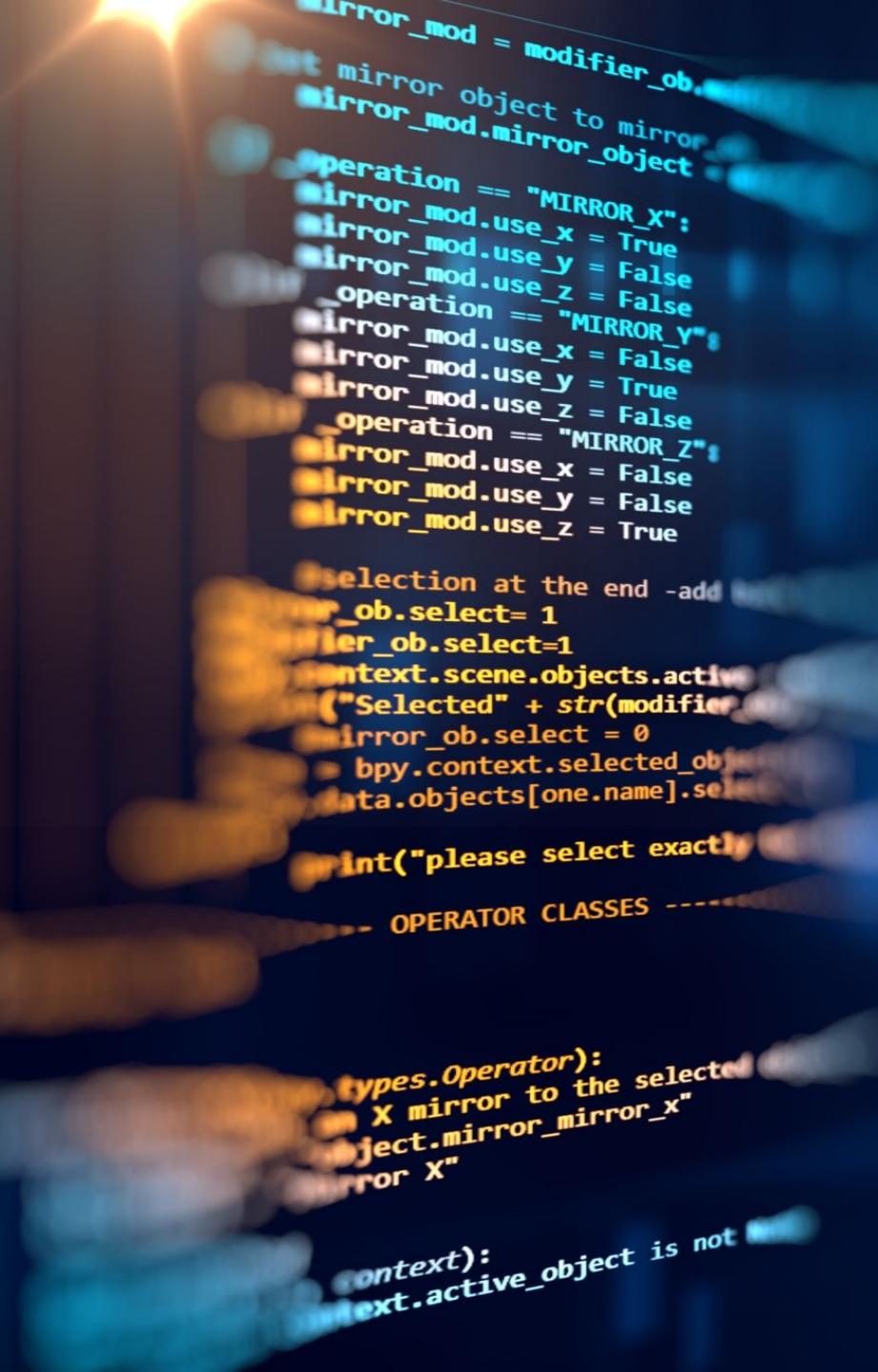


# DEEPIN GENETICS HUB

By: Shakkthi, Harry, Lydia

A close-up photograph of a person's hands holding a smartphone horizontally. The screen of the phone displays a block of Python code. The code appears to be a script for Blender, specifically for creating a mirror modifier. It includes logic for selecting objects, setting up a mirror modifier, and handling different mirroring operations (X, Y, Z) based on user input. The background is dark, making the bright screen of the phone stand out.

```
mirror_mod = modifier_obj
# Set mirror object to mirror
mirror_mod.mirror_object = mirror_obj
if operation == "MIRROR_X":
    mirror_mod.use_x = True
    mirror_mod.use_y = False
    mirror_mod.use_z = False
elif operation == "MIRROR_Y":
    mirror_mod.use_x = False
    mirror_mod.use_y = True
    mirror_mod.use_z = False
elif operation == "MIRROR_Z":
    mirror_mod.use_x = False
    mirror_mod.use_y = False
    mirror_mod.use_z = True

# Selection at the end - add
modifier_obj.select = 1
mirror_obj.select = 1
bpy.context.scene.objects.active = bpy.context.selected_objects[-1]
print("Selected" + str(modifier_obj))
mirror_obj.select = 0
bpy.context.selected_objects.append(data.objects[one.name].select)

print("please select exactly one object")
print("- OPERATOR CLASSES ---")

# Operator classes
class MirrorOperator(bpy.types.Operator):
    bl_idname = "object.mirror"
    bl_label = "X mirror to the selected object.mirror_mirror_x"
    bl_options = {'REGISTER', 'UNDO'}

    def execute(self, context):
        if context.object is None or context.object.type != 'MESH' or context.object.data is None:
            return {'FINISHED'}
```



# DESIGN PHILOSOPHY

# TARGET

Clinicians

Geneticists

Students

# SNP DATA AND POPULATIONS

## SINGLE NUCLEOTIDE POLYMORPHISM (SNP)

- ❖ Widespread type of genetic variation in humans
- ❖ Predisposition to various diseases

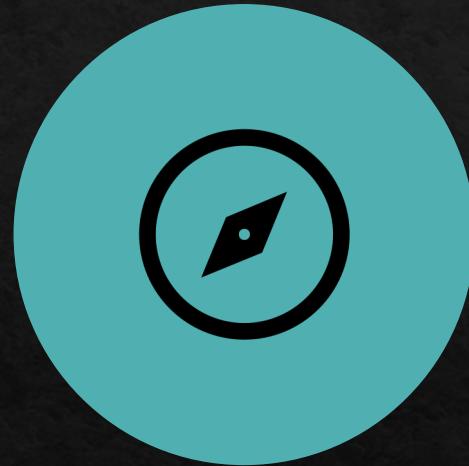
## POPULATIONS

- ❖ 27 populations (including Siberian)
- ❖ 5 superpopulations
- ❖ Siberian dataset (European superpopulation)

# USAGE



## SIMPLICITY



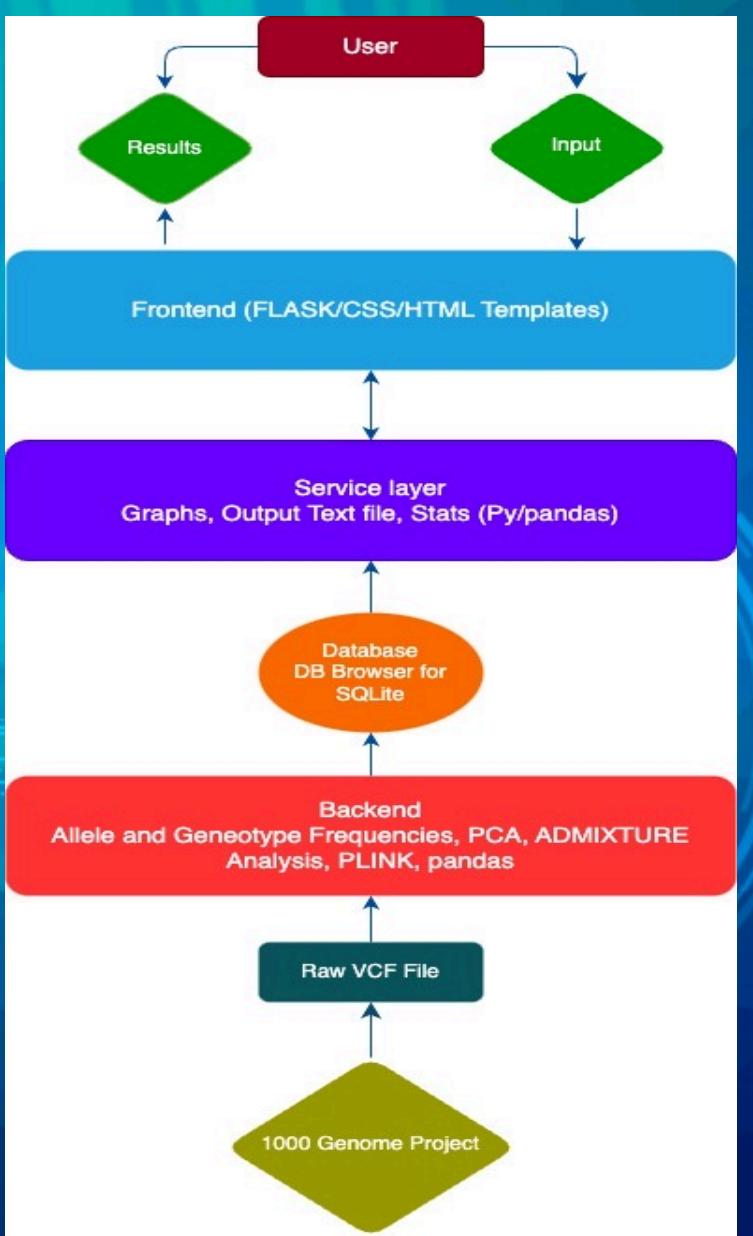
## NAVIGATION

# FRONT-END

Deepin Genetic Analysis Hub   [Home](#)   [Clustering Analysis](#)   [Admixture Analysis](#)   [SNP Search](#)   [About Us](#)

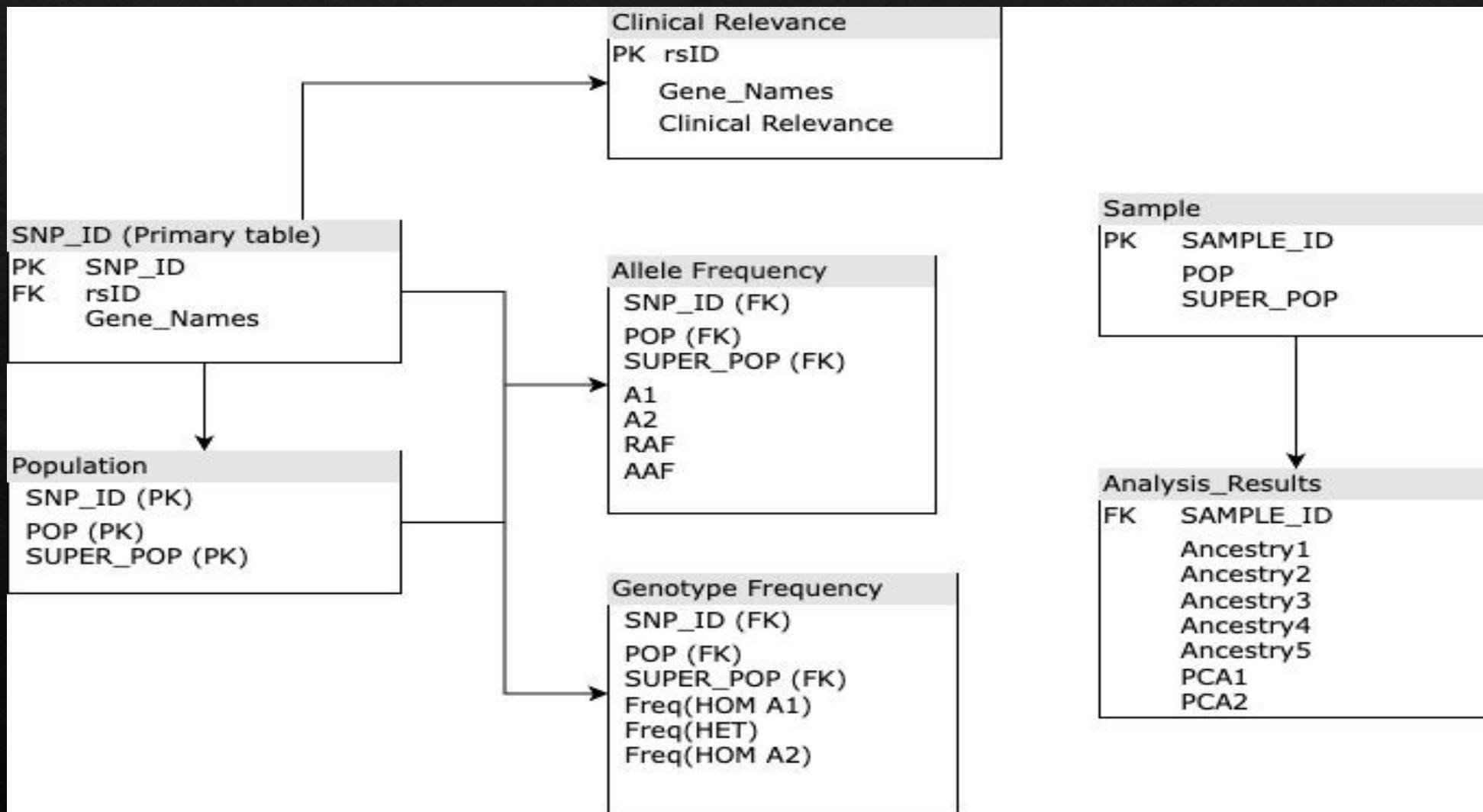


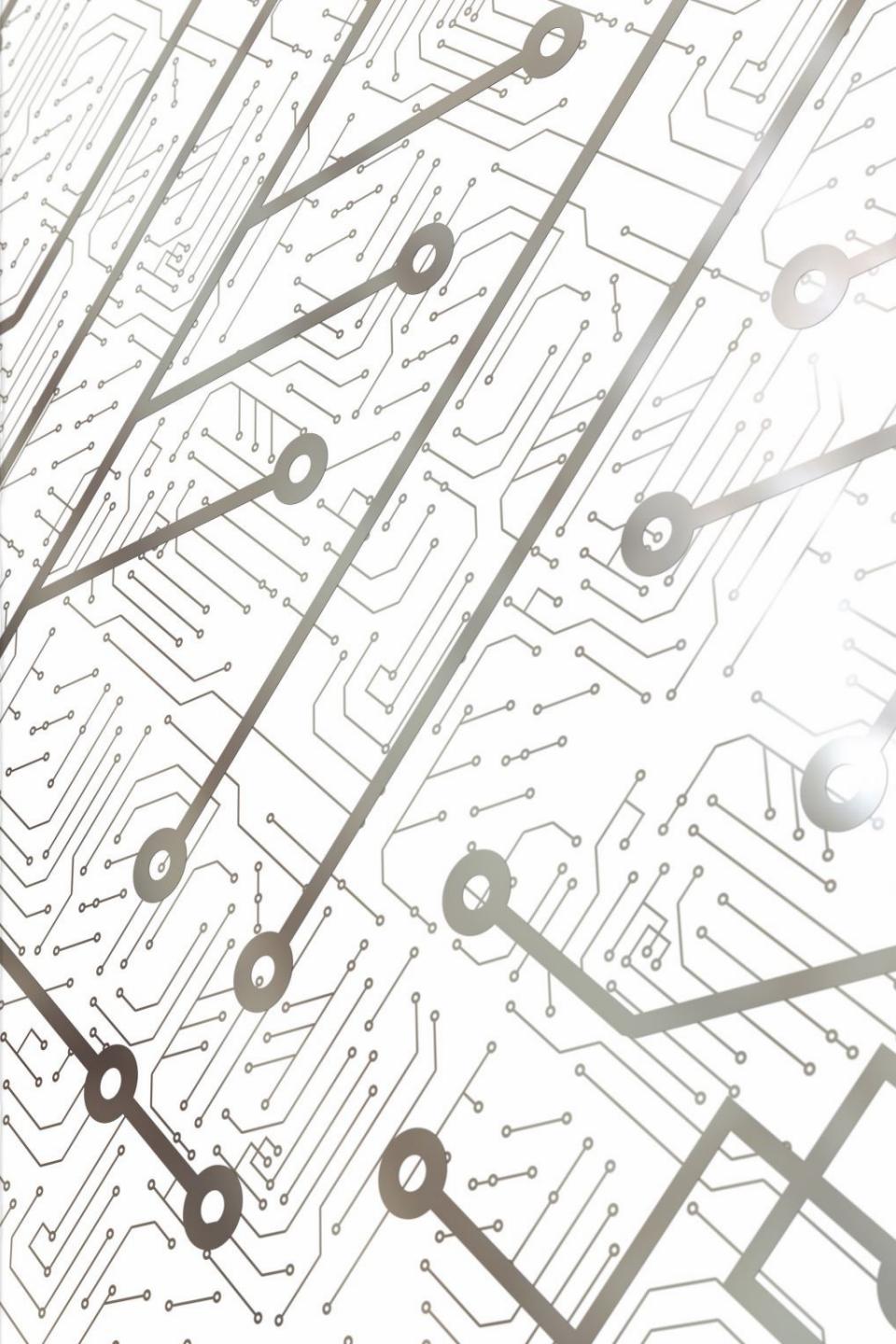
Choose an analysis:



# Software Architecture

# Data Schema

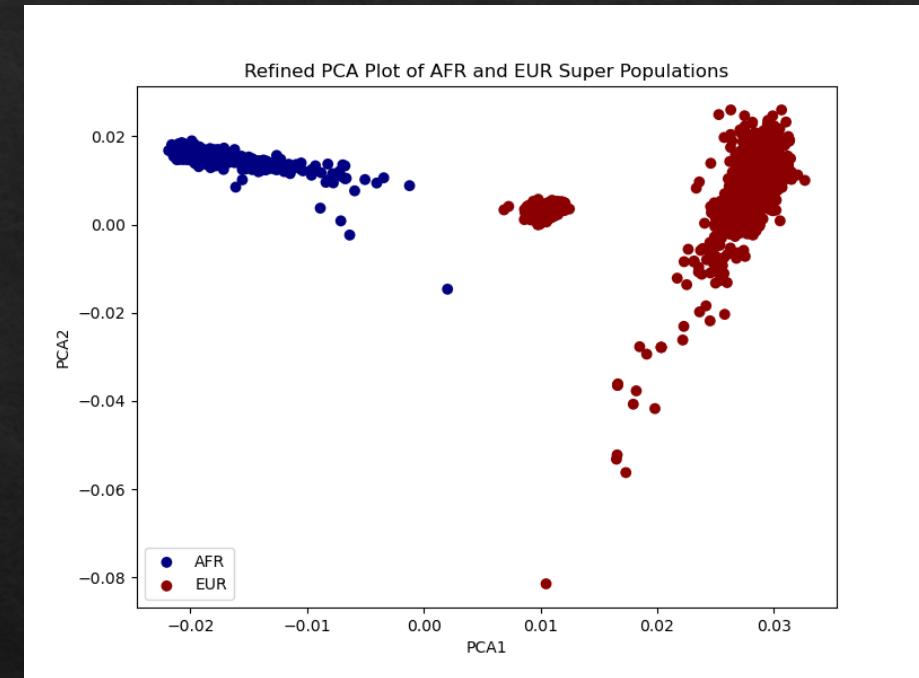
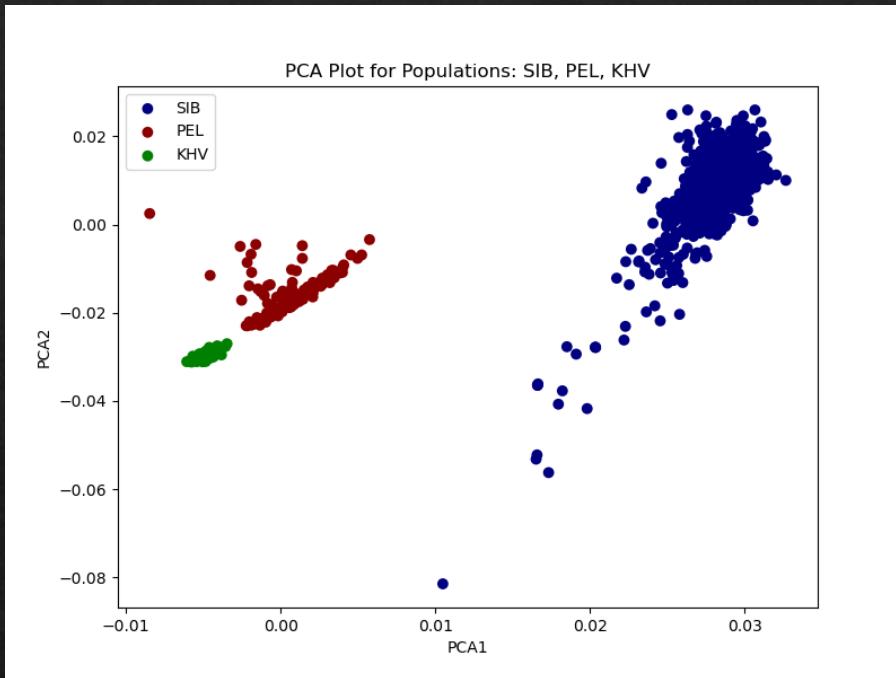


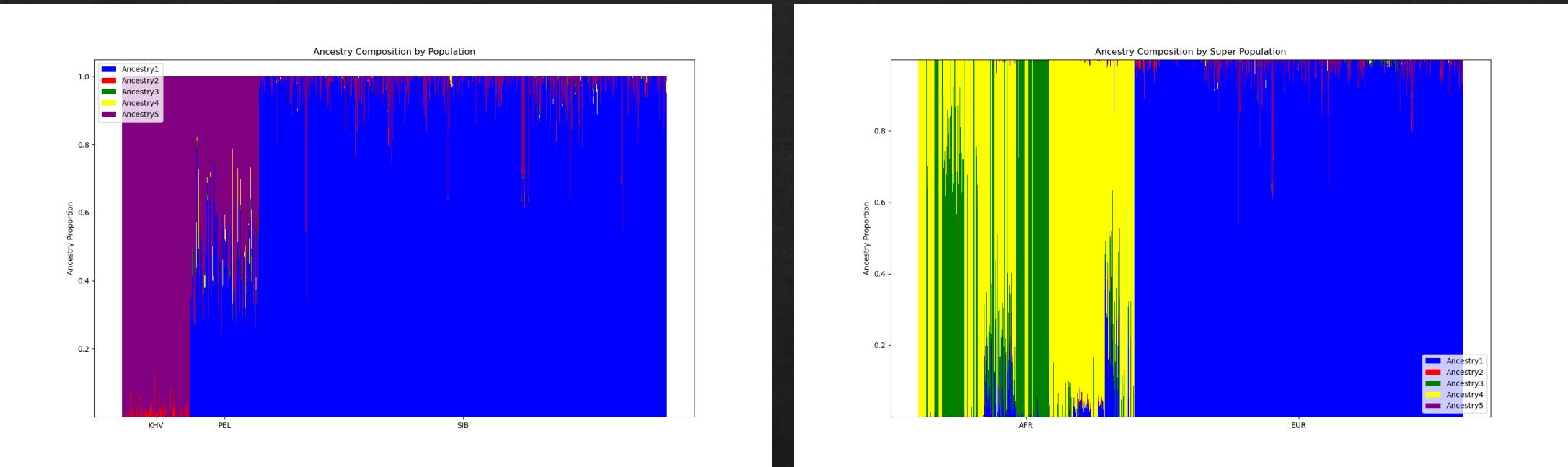


# Analysis

- ❖ PCA
- ❖ ADMIXTURE
- ❖ FISHERS EXACT TEST
- ❖ FST

# PCA

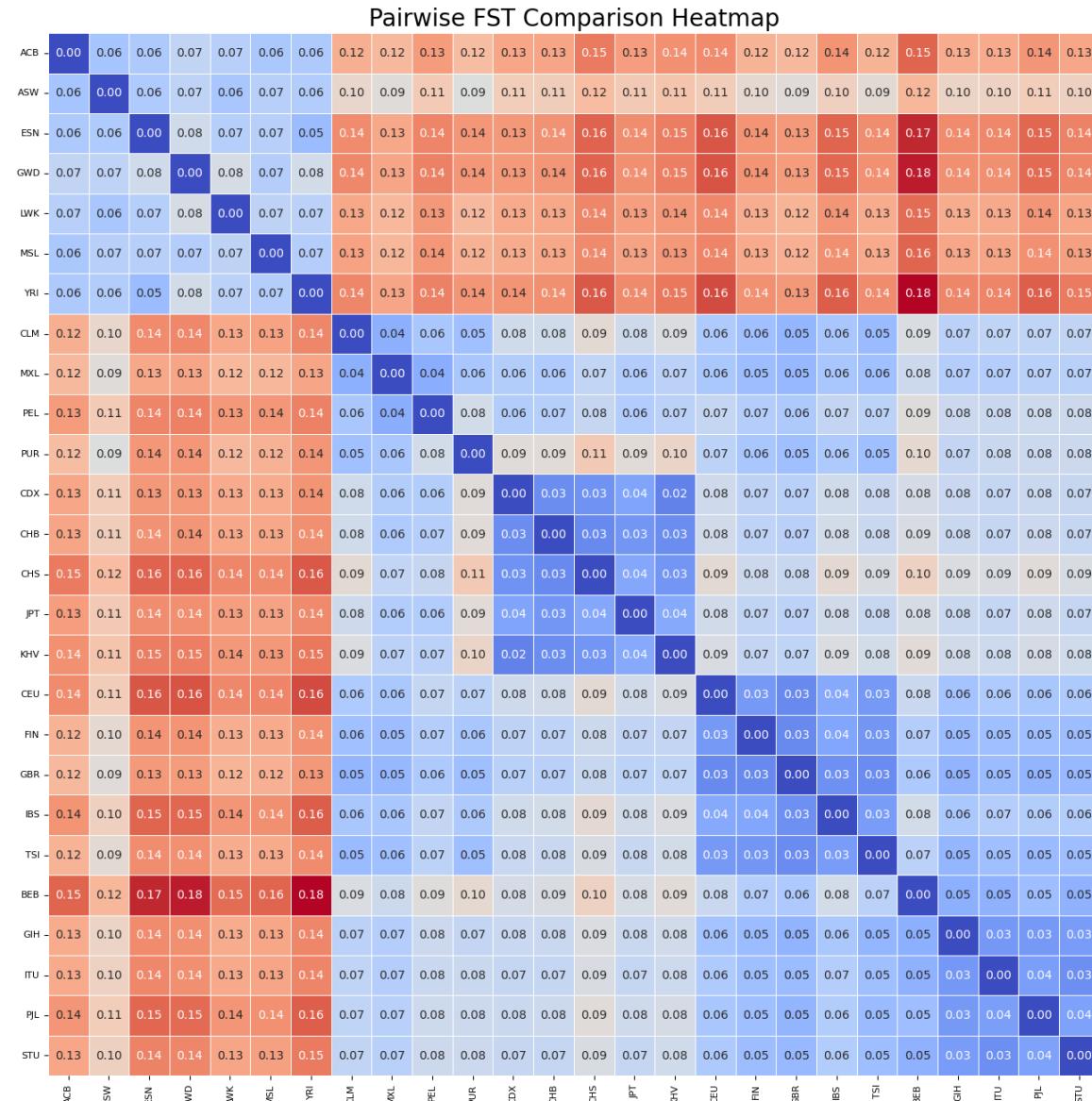




# ADMIXTURE

# FST

(Weir Cockerham)



# Fishers Exact Test

- ❖ To check for statistical significance between allele and genotype frequencies
- ❖ Super population allele frequencies are averaged

# Allele Frequencies

- ❖ Used PLINK to filter VCF and make .bed .bim .fam files
- ❖ PLINK again to calculate minor Allele frequency
- ❖ Calculated the Reference and Alternate Allele frequencies from that.

# Genotype Frequency

- ❖ Used PLINK to filter and make .bed .bim .fam files
- ❖ Split the .bed files in 27 smaller files one for each populations
- ❖ PLINK again on each population .bed file to calculate the genotype frequencies
- ❖ Label each file with their population and super pop population
- ❖ Join back together

# Limitations



INCOMPLETE SNP GENE  
NAMING



LIMITED SNP SEARCH  
FUNCTIONALITY



HARD-CODED SAMPLE  
SIZES IN FST  
CALCULATION



INEFFICIENT SOFTWARE  
ARCHITECTURE AND  
QUERY



DATA SCHEMA  
REDUNDANCY

# Future Developments

- ❖ Integration of statistical analyses like Tajima's D
- ❖ Improvement in design responsivity
- ❖ Database and software optimisation
- ❖ Enhanced SNP analysis features
- ❖ Data compression and efficient storage



# Acknowledgements

We would like to thank our supervisors Dr Matteo Fumagalli and Professor Conrad Bessant for their guidance and support through the project.

Thank you for listening ☺

Any questions?