## Mahdi\_Anvari.compG\_HW2

May 3, 2025

## 1 Computational Genomics - HW2

To identify five SNPs with significant allele frequency (AF) differences between two ethnic groups—while minimizing the risk of linkage disequilibrium (LD)—I plan to extract one SNP from each of five distinct genes. To achieve this, I first explored various genomic resources to select genes known for high population-specific variation. These genes will then be examined using the Iranome database to identify suitable SNPs.

**HLA-B:** Highly polymorphic immune gene with strong ethnic differentiation.

CYP2D6: Key gene in drug metabolism, known for copy number and allele variability across populations.

LCT: Associated with lactase persistence; exhibits clear ancestral selection signals.

**ABO:** Determines blood type; shows distinct allele frequency patterns among populations.

**G6PD:** Enzyme gene with variants common in certain regions due to malaria-driven selection.

```
[60]: import pandas as pd
pd.DataFrame({
    "Gene_Name": ["HLA-B", "CYP2D6", "LCT", "ABO", "G6PD"],
    "SNP_Count": [449, 255, 568, 484, 145]
})
```

```
[60]:
         Gene_Name
                      SNP_Count
       0
             HLA-B
                             449
            CYP2D6
       1
                             255
       2
                LCT
                             568
       3
                ABO
                             484
       4
               G6PD
                             145
```

Manually checking each SNP within the selected genes is not feasible. Therefore, I used an automated approach with Selenium to extract all available SNPs for each gene from the Iranome

database. After gathering the data, I will apply several criteria to identify the most suitable SNP for each gene.

```
[61]: gene_variants = {"HLA-B": [],
                   "CYP2D6": [],
                   "LCT": [],
                   "ABO": [],
                   "G6PD": []}
[62]: gene_variants
[62]: {'HLA-B': [], 'CYP2D6': [], 'LCT': [], 'ABO': [], 'G6PD': []}
 [7]: from selenium import webdriver
      from selenium.webdriver.edge.service import Service
      from selenium.webdriver.common.by import By
      from selenium.webdriver.common.keys import Keys
      from selenium.webdriver.support.ui import WebDriverWait
      from selenium.webdriver.support import expected_conditions as EC
      import time
      import re
      import pandas as pd
      import warnings
      warnings.filterwarnings("ignore")
[64]: options = webdriver.EdgeOptions()
      options.add_argument("start-maximized")
      service = Service()
      driver = webdriver.Edge(service=service, options=options)
      for gene_name in GENE_LIST:
          print(f"{gene_name} variants:")
          try:
              url = GENE_LIST[gene_name]
              driver.get(url)
              WebDriverWait(driver, 15).until(
                  EC.presence of element located((By.CSS SELECTOR, "table tbody tr"))
              )
              rows = driver.find_elements(By.CSS_SELECTOR, "table tbody tr")
              for i in range(len(rows)):
                  rows = driver.find_elements(By.CSS_SELECTOR, "table tbody tr")
                  link = rows[i].find_element(By.CSS_SELECTOR, "td:nth-child(1) a")
                  href = link.get attribute("href")
                  link_text = link.text
                  driver.get(href)
                  print(f"Visited: {href}")
```

```
html = driver.page_source
            tables = pd.read_html(html)
            if tables:
                df = tables[0]
                if link_text not in gene_variants[gene_name]:
                    gene_variants[gene_name].append(link_text)
                    df.to_csv("db/"+ gene_name +"/"+ re.sub(r'[<>:"/\\|?*]',__

    '_', link_text) +".csv", index=False)
            else:
                print("No table found on the page.")
            time.sleep(3)
            driver.back()
            WebDriverWait(driver, 15).until(
                EC.presence_of_element_located((By.CSS_SELECTOR, "table tbody"

¬tr"))
            )
    finally:
        print(f"Done with gene {gene_name}.")
driver.quit()
```

```
G6PD variants:
```

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Done with gene CYP2D6.
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Visited: https://www.iranome.com/variant/6-31324320-G-T
Visited: https://www.iranome.com/variant/6-31324325-T-C
Visited: https://www.iranome.com/variant/6-31324335-G-T
Visited: https://www.iranome.com/variant/6-31324336-C-G
Visited: https://www.iranome.com/variant/6-31324346-G-T
Visited: https://www.iranome.com/variant/6-31324348-C-T
Visited: https://www.iranome.com/variant/6-31324369-A-_
Visited: https://www.iranome.com/variant/6-31324372-GA-
Visited: https://www.iranome.com/variant/6-31324373-A-
Visited: https://www.iranome.com/variant/6-31324373-A-G
Visited: https://www.iranome.com/variant/6-31324375-G-T
Visited: https://www.iranome.com/variant/6-31324376-C-T
Visited: https://www.iranome.com/variant/6-31324389-C-T
Visited: https://www.iranome.com/variant/6-31324390-G-A
Visited: https://www.iranome.com/variant/6-31324399-G-A
Visited: https://www.iranome.com/variant/6-31324402-C-A
Visited: https://www.iranome.com/variant/6-31324415-A-C
Visited: https://www.iranome.com/variant/6-31324419-G-C
Visited: https://www.iranome.com/variant/6-31324424-A-T
Visited: https://www.iranome.com/variant/6-31324431-_-GGG
Visited: https://www.iranome.com/variant/6-31324448-G-A
```

```
Visited: https://www.iranome.com/variant/6-31324467-G-T
Visited: https://www.iranome.com/variant/6-31324489-_-GG
Visited: https://www.iranome.com/variant/6-31324489-_-GGAG
Visited: https://www.iranome.com/variant/6-31324489-C-A
Visited: https://www.iranome.com/variant/6-31324489-C-G
Visited: https://www.iranome.com/variant/6-31324491-C-A
Visited: https://www.iranome.com/variant/6-31324493-C-
Visited: https://www.iranome.com/variant/6-31324494-A-
Visited: https://www.iranome.com/variant/6-31324495-GGT-
Visited: https://www.iranome.com/variant/6-31324497-T-_
Visited: https://www.iranome.com/variant/6-31324497-T-G
Visited: https://www.iranome.com/variant/6-31324499-C-G
Visited: https://www.iranome.com/variant/6-31324506-C-T
Visited: https://www.iranome.com/variant/6-31324507-T-C
Visited: https://www.iranome.com/variant/6-31324509-T-A
Visited: https://www.iranome.com/variant/6-31324516-C-A
Visited: https://www.iranome.com/variant/6-31324523-T-C
Visited: https://www.iranome.com/variant/6-31324525-CC-_
Visited: https://www.iranome.com/variant/6-31324526-CT-_
Visited: https://www.iranome.com/variant/6-31324528-G-T
Visited: https://www.iranome.com/variant/6-31324529- -GA
Visited: https://www.iranome.com/variant/6-31324529- -TT
Visited: https://www.iranome.com/variant/6-31324530-G-C
Visited: https://www.iranome.com/variant/6-31324531-C-G
Visited: https://www.iranome.com/variant/6-31324531-C-T
Visited: https://www.iranome.com/variant/6-31324534-_-TCA
Visited: https://www.iranome.com/variant/6-31324536-T-A
Visited: https://www.iranome.com/variant/6-31324536-T-C
Visited: https://www.iranome.com/variant/6-31324536-T-G
Visited: https://www.iranome.com/variant/6-31324537-AGA-_
Visited: https://www.iranome.com/variant/6-31324538-G-C
Visited: https://www.iranome.com/variant/6-31324539-A-T
Visited: https://www.iranome.com/variant/6-31324542-T-C
Visited: https://www.iranome.com/variant/6-31324547-G-C
Visited: https://www.iranome.com/variant/6-31324549-T-C
Visited: https://www.iranome.com/variant/6-31324552-G-C
Visited: https://www.iranome.com/variant/6-31324561-A-G
Visited: https://www.iranome.com/variant/6-31324562-C-T
Visited: https://www.iranome.com/variant/6-31324574-C-T
Visited: https://www.iranome.com/variant/6-31324580-T-C
Visited: https://www.iranome.com/variant/6-31324582-T-C
Visited: https://www.iranome.com/variant/6-31324586-C-T
Visited: https://www.iranome.com/variant/6-31324595-C-G
Visited: https://www.iranome.com/variant/6-31324599-T-G
Visited: https://www.iranome.com/variant/6-31324600-C-
Visited: https://www.iranome.com/variant/6-31324602-_-A
Visited: https://www.iranome.com/variant/6-31324602-_-G
Visited: https://www.iranome.com/variant/6-31324602-T-C
```

```
Visited: https://www.iranome.com/variant/6-31324603-C-G
Visited: https://www.iranome.com/variant/6-31324603-C-T
Visited: https://www.iranome.com/variant/6-31324604-T-
Visited: https://www.iranome.com/variant/6-31324604-T-C
Visited: https://www.iranome.com/variant/6-31324605- -C
Visited: https://www.iranome.com/variant/6-31324615-C-T
Visited: https://www.iranome.com/variant/6-31324633-T-G
Visited: https://www.iranome.com/variant/6-31324641-T-A
Visited: https://www.iranome.com/variant/6-31324643-G-C
Visited: https://www.iranome.com/variant/6-31324647-T-C
Visited: https://www.iranome.com/variant/6-31324664-T-G
Visited: https://www.iranome.com/variant/6-31324666-A-C
Visited: https://www.iranome.com/variant/6-31324666-A-T
Visited: https://www.iranome.com/variant/6-31324667-G-A
Visited: https://www.iranome.com/variant/6-31324691-G-A
Visited: https://www.iranome.com/variant/6-31324702-C-T
Visited: https://www.iranome.com/variant/6-31324705-A-C
Visited: https://www.iranome.com/variant/6-31324706-G-T
Visited: https://www.iranome.com/variant/6-31324710-T-A
Visited: https://www.iranome.com/variant/6-31324711-A-C
Visited: https://www.iranome.com/variant/6-31324711-A-G
Visited: https://www.iranome.com/variant/6-31324719-C-T
Visited: https://www.iranome.com/variant/6-31324730-G-A
Visited: https://www.iranome.com/variant/6-31324738-G-A
Visited: https://www.iranome.com/variant/6-31324740-GGT-_
Visited: https://www.iranome.com/variant/6-31324741-G-A
Visited: https://www.iranome.com/variant/6-31324742-T-C
Visited: https://www.iranome.com/variant/6-31324743-G-C
Visited: https://www.iranome.com/variant/6-31324744- -CA
Visited: https://www.iranome.com/variant/6-31324749-G-T
Visited: https://www.iranome.com/variant/6-31324750-G-A
Visited: https://www.iranome.com/variant/6-31324752-C-T
Visited: https://www.iranome.com/variant/6-31324756-G-A
Visited: https://www.iranome.com/variant/6-31324764-C-A
Visited: https://www.iranome.com/variant/6-31324774-C-A
Visited: https://www.iranome.com/variant/6-31324776-C-A
Visited: https://www.iranome.com/variant/6-31324777-G-T
Visited: https://www.iranome.com/variant/6-31324786-C-T
Visited: https://www.iranome.com/variant/6-31324788-T-C
Visited: https://www.iranome.com/variant/6-31324790-A-G
Visited: https://www.iranome.com/variant/6-31324791-G-A
Visited: https://www.iranome.com/variant/6-31324798-C-A
Visited: https://www.iranome.com/variant/6-31324808-_-G
Visited: https://www.iranome.com/variant/6-31324808-T-G
Visited: https://www.iranome.com/variant/6-31324819-C-T
Visited: https://www.iranome.com/variant/6-31324820-G-T
Visited: https://www.iranome.com/variant/6-31324829-G-C
Visited: https://www.iranome.com/variant/6-31324829-G-T
```

```
Visited: https://www.iranome.com/variant/6-31324830-G-A
Visited: https://www.iranome.com/variant/6-31324836-G-A
Visited: https://www.iranome.com/variant/6-31324847-C-G
Visited: https://www.iranome.com/variant/6-31324852-_-C
Visited: https://www.iranome.com/variant/6-31324852- -T
Visited: https://www.iranome.com/variant/6-31324864-G-A
Visited: https://www.iranome.com/variant/6-31324887-G-C
Visited: https://www.iranome.com/variant/6-31324888-G-T
Visited: https://www.iranome.com/variant/6-31324889-G-A
Visited: https://www.iranome.com/variant/6-31324891-C-T
Visited: https://www.iranome.com/variant/6-31324892-G-C
Visited: https://www.iranome.com/variant/6-31324895-G-C
Visited: https://www.iranome.com/variant/6-31324911-C-G
Visited: https://www.iranome.com/variant/6-31324921-C-T
Visited: https://www.iranome.com/variant/6-31324925-A-G
Visited: https://www.iranome.com/variant/6-31324931-A-C
Visited: https://www.iranome.com/variant/6-31324938-C-T
Visited: https://www.iranome.com/variant/6-31324941-C-T
Visited: https://www.iranome.com/variant/6-31324953-C-T
Visited: https://www.iranome.com/variant/6-31324955-C-T
Done with gene HLA-B.
```

Now that all SNP variants for each selected gene have been successfully extracted from Iranome using automated Selenium scripts, the next step is to conduct a meta-analysis to identify the most informative SNPs for distinguishing between two specific ethnic groups.

# 2 1)

#### 2.0.1 SNP Selection Strategy: Focus on Arab and Zartoshti Populations

In this analysis, the focus is on the Arab and Zartoshti populations, which have distinct historical and genetic backgrounds. These differences make them suitable candidates for identifying population-specific allele frequency divergence. The objective is to select one representative SNP per gene that shows the greatest allele frequency difference between these two groups. To ensure meaningful and reliable results, the following criteria are applied during SNP selection:

- 1. Considerable Allele Frequency (AF) Difference Purpose: Select SNPs with the largest absolute difference in allele frequency between the Arab and Zartoshti groups. This is the primary selection criterion.
- 2. Minor Allele Frequency (MAF) > 0.1 Rationale: Ensures that the SNP is not ultra-rare and has enough variability to be informative.

**Application:** Discard SNPs where the alternative allele frequency is less than 10% in both Arab and Zartoshti groups.

3. Sufficient Sample Support Criteria: - Allele count > 10 in both groups - At least 50 genotyped individuals per group

Rationale: Ensures statistical robustness and avoids unreliable frequency estimates due to sparse data.

**4. Presence of Heterozygotes Rationale:** The existence of both homozygous and heterozygous genotypes increases flexibility for downstream modeling, especially when simulating heterozygous individuals.

**Application:** Prefer SNPs with non-zero heterozygote counts in both groups.

**5.** Biallelic SNPs Only Rationale: Simplifies probabilistic modeling and interpretation. Triallelic variants and indels may introduce unnecessary complexity.

**Application:** Exclude SNPs with more than two alleles or complex indel patterns.

**6.** Coverage Across All 12 Iranome Ethnic Groups Rationale: To enable comprehensive allele frequency analysis across all populations included in the study.

**Application:** Discard SNPs that lack allele frequency data for any of the 12 Iranome ethnic groups.

```
[72]:
           Gene_Name
                                                      Variant_Name
               HLA-B
                                     6:31321657 G / A (rs3177747)
      0
      1
               HLA-B
                                     6:31321681 C / T (rs1058067)
                                     6:31321685 A / C (rs1058026)
      2
               HLA-B
      3
                                     6:31321686 A / C (rs1049268)
               HLA-B
      4
               HLA-B
                                   6:31321694 A / G (rs878941341)
                                    X:153775343 A / C (rs3021074)
      1896
                G6PD
      1897
                G6PD
                      X:153775360 A / C (rs1390716946,rs3021072)
                                                 X:153775365 C / A
      1898
                G6PD
                                  X:153775421 G / T (rs185623633)
      1899
                G6PD
      1900
                G6PD
                                  X:153775785 T / C (rs111827785)
```

[1901 rows x 2 columns]

```
[111]: SNPs_df.to_excel("SNPs_table.xlsx", index=False)
```

I begin the filtering process by applying the primary selection criterion: identifying SNPs that show the **maximum allele frequency (AF) difference** between Arab and Zartoshti populations.

This step narrows down the candidate SNPs per gene by selecting those with the most pronounced divergence between these two ethnic groups.

Other criteria (e.g., sample support, heterozygosity, biallelic status, full population coverage) will be manually evaluated in subsequent steps after narrowing the list using this primary filter.

```
[103]:
      SNPs_df = pd.read_excel("SNPs_table.xlsx")
[104]: pop1 = "Arab"
       pop2 = "Zartoshti"
       def extract_AF_difference(gene_name, variant_name):
           df = pd.read_csv("db/"+ gene_name +"/"+ re.sub(r'[<>:"/\\|?*]', '_', |
        ⇔variant_name) +".csv")
           AF difference = float(df[df["Population"] == pop1]["Allele,
        →Frequency"])-float(df[df["Population"]==pop2]["Allele Frequency"])
           return abs(AF difference)
       def extract_AF_divergance(gene_name, variant_name):
           df = pd.read_csv("db/"+ gene_name +"/"+ re.sub(r'[<>:"/\\|?*]', '_', |
        ⇔variant_name) +".csv")
           AF1_divergance = float(df[df["Population"] == pop1]["Allele Frequency"])-0.5
           AF2_divergance = float(df[df["Population"] == pop2]["Allele Frequency"])-0.5
           result1 = abs(AF1_divergance - AF2_divergance)
           result2 = abs(AF1 divergance + AF2 divergance)
           return min([result1, result2])
[105]: SNPs_df["AF_difference"] = SNPs_df.apply(lambda row:
        extract_AF_difference(row['Gene_Name'], row['Variant_Name']), axis=1)
```

Because we aim to estimate the fractional ancestry of a heterozygous individual, an additional criterion is needed to ensure that the selected SNPs are informative for such inference. For example, although a SNP with a large allele frequency difference between two populations (e.g., 0.8 in population 1 and 0.2 in population 2) may appear ideal at first glance, it is actually not informative for a heterozygous individual. This is because both populations strongly favor opposite homozygous genotypes, making the presence of a heterozygote equally unlikely in either group. To address this, I introduce a criterion called allele frequency divergence, which captures how far the allele frequencies in both populations deviate from 0.5. This balance ensures that the SNP can meaningfully contribute to distinguishing ancestry while still being consistent with the heterozygous genotype observed.

```
[108]:
            Gene_Name
                                           Variant_Name AF_difference AF_divergance
                         2:136578703 A / G (rs4954451)
       1070
                  LCT
                                                                0.30250
                                                                               0.30250
       1607
                  ABO
                         9:136140462 C / T (rs1633513)
                                                                0.28710
                                                                               0.28710
       804
                  LCT
                         2:136554797 T / C (rs6430588)
                                                                0.28370
                                                                               0.28370
                          9:136146920 T / G (rs663054)
       1706
                  ABO
                                                                0.27657
                                                                               0.27657
       742
                  LCT
                         2:136550806 G / C (rs2083190)
                                                                0.27390
                                                                               0.27390
       1784
                 G6PD
                       X:153762330 G / A (rs781917123)
                                                                0.00000
                                                                               0.00000
                       X:153762467 G / A (rs917134021)
                                                                0.00000
                                                                               0.00000
       1785
                 G6PD
       1786
                 G6PD
                       X:153762472 C / T (rs782036244)
                                                                0.00000
                                                                               0.00000
       1787
                                      X:153762517 C / T
                                                                               0.00000
                 G6PD
                                                                0.00000
       559
               CYP2D6
                                      22:42524478 C / G
                                                                0.00000
                                                                               0.00000
       [1901 rows x 4 columns]
[109]: selected_variants = {}
       for i in SNPs_sorted_df.index:
           if SNPs_sorted_df.loc[i]["Gene_Name"] not in selected_variants:
               selected_variants[SNPs_sorted_df.loc[i]["Gene_Name"]] = SNPs_sorted_df.
        ⇔loc[i]["Variant_Name"]
[110]: selected variants
[110]: {'LCT': '2:136578703 A / G (rs4954451)',
        'ABO': '9:136140462 C / T (rs1633513)',
        'HLA-B': '6:31324201 C / G (rs1071652)',
        'CYP2D6': '22:42526049 C / G (rs1931826324,rs28371701)',
        'G6PD': 'X:153775343 A / C (rs3021074)'}
      These are my selected variants. Let's save their tables into another folder and check the other
      criteria manually.
[111]: selected_variants_DFs = []
       for gene in selected_variants:
           df = pd.read_csv("db/"+ gene +"/"+ re.sub(r'[<>:"/\\|?*]', '_',_\|
        ⇔selected_variants[gene]) +".csv")
           selected variants DFs.append(df)
           df.to_csv("db/SELECTED_SNPS/" + re.sub(r'[<>:"/\\|?*]', '_',_
        ⇔selected variants[gene]) +".csv")
[112]: print(selected_variants["LCT"], "table:")
       selected_variants_DFs[0]
      2:136578703 A / G (rs4954451) table:
[112]:
                      Population Allele Count Allele Number Number of Homozygotes \
       0
                          Mazani
                                             90
                                                            200
                                                                                     45
```

```
200
                                                                                           42
       1
                         Zartoshti
                                                 86
       2
                            Baloch
                                                 66
                                                                202
                                                                                           33
       3
                                                                                           29
            Persian Gulf Islander
                                                 58
                                                                200
       4
                           Sistani
                                                47
                                                                200
                                                                                           23
       5
                            Gilaki
                                                 38
                                                                198
                                                                                           19
       6
                             Azeri
                                                 34
                                                                200
                                                                                           17
       7
                                                28
                              Kurd
                                                                200
                                                                                           14
       8
                              Arab
                                                26
                                                                204
                                                                                           13
       9
                           Persian
                                                                200
                                                                                           7
                                                 14
       10
                           Turkmen
                                                 14
                                                                200
                                                                                            7
       11
                                Lur
                                                 12
                                                                200
                                                                                            6
       12
                             Total
                                               513
                                                               2404
                                                                                         255
            Number of Heterozygotes
                                       Homozygous Genotype Freq.
       0
                                    0
                                                          0.450000
                                    2
       1
                                                          0.420000
       2
                                    0
                                                          0.326700
                                    0
       3
                                                          0.290000
       4
                                    1
                                                          0.230000
       5
                                    0
                                                          0.191900
       6
                                    0
                                                          0.170000
       7
                                    0
                                                          0.140000
       8
                                    0
                                                          0.127500
       9
                                    0
                                                          0.070000
                                    0
       10
                                                          0.070000
                                    0
       11
                                                          0.060000
       12
                                    3
                                                          0.212146
            Heterozygous Genotype Freq.
                                            Allele Frequency
       0
                                 0.00000
                                                       0.4500
       1
                                 0.020000
                                                       0.4300
       2
                                 0.000000
                                                       0.3267
       3
                                 0.000000
                                                       0.2900
       4
                                 0.010000
                                                       0.2350
       5
                                 0.000000
                                                       0.1919
       6
                                 0.000000
                                                       0.1700
       7
                                 0.000000
                                                       0.1400
       8
                                 0.000000
                                                       0.1275
       9
                                 0.000000
                                                       0.0700
       10
                                 0.000000
                                                       0.0700
       11
                                 0.000000
                                                       0.0600
       12
                                 0.002496
                                                       0.2134
[113]: print(selected_variants["ABO"], "table:")
       selected_variants_DFs[1]
```

9:136140462 C / T (rs1633513) table:

```
[113]:
                        Population Allele Count
                                                    Allele Number
                                                                    Number of Homozygotes
       0
                         Zartoshti
                                                               200
                                                78
                                                                                          38
       1
            Persian Gulf Islander
                                                60
                                                               200
                                                                                          28
       2
                            Mazani
                                                56
                                                               200
                                                                                          27
       3
                            Baloch
                                                               202
                                                41
                                                                                          19
       4
                           Sistani
                                                26
                                                               200
                                                                                          12
       5
                              Arab
                                                21
                                                               204
                                                                                          10
       6
                            Gilaki
                                                20
                                                               198
                                                                                          10
       7
                                                               200
                                                                                           8
                             Azeri
                                                16
                                                                                           8
       8
                           Turkmen
                                                16
                                                               200
                                                                                           7
       9
                                                15
                                                               200
                               Lur
       10
                                                 8
                                                               200
                                                                                           4
                              Kurd
                                                                                           3
                                                 6
                                                               200
       11
                           Persian
       12
                             Total
                                               363
                                                              2404
                                                                                         174
            Number of Heterozygotes
                                       Homozygous Genotype Freq.
       0
                                    2
                                                          0.380000
                                    4
       1
                                                          0.280000
                                    2
       2
                                                          0.270000
       3
                                    3
                                                          0.188100
                                    2
       4
                                                          0.120000
       5
                                    1
                                                          0.098000
                                    0
       6
                                                          0.101000
       7
                                    0
                                                          0.080000
       8
                                    0
                                                          0.080000
       9
                                    1
                                                          0.070000
                                    0
       10
                                                          0.040000
                                    0
       11
                                                          0.030000
       12
                                   15
                                                          0.144759
           Heterozygous Genotype Freq.
                                            Allele Frequency
                                 0.020000
       0
                                                       0.3900
       1
                                 0.040000
                                                       0.3000
                                                       0.2800
       2
                                 0.020000
       3
                                 0.029700
                                                       0.2030
       4
                                 0.020000
                                                       0.1300
       5
                                 0.009800
                                                       0.1029
       6
                                 0.00000
                                                       0.1010
       7
                                 0.000000
                                                       0.0800
       8
                                 0.000000
                                                       0.0800
       9
                                 0.010000
                                                       0.0750
       10
                                 0.000000
                                                       0.0400
       11
                                 0.000000
                                                       0.0300
       12
                                 0.012479
                                                       0.1510
[114]: print(selected_variants["CYP2D6"], "table:")
       selected_variants_DFs[2]
```

## 22:42526049 C / G (rs1931826324,rs28371701) table:

[114]:	Population	Allele Count	Allele Number	Number of Homozygotes	\
0	Persian	84		27	
1	Gilaki	83	198	28	
2	Kurd	82	200	22	
3	Zartoshti	81	200	22	
4	Mazani	80	200	25	
5	Lur	74	200	22	
6	Persian Gulf Islander	73	200	20	
7	Turkmen	72	200	26	
8	Azeri	61	200	12	
9	Baloch	58	202	9	
10	Sistani	57	200	11	
11	Arab	42	204	8	
12	Total	847	2404	232	
	Number of Heterozygotes	s Homozygous	Genotype Freq.	\	
0	30	)	0.270000		
1	27	7	0.282800		
2	38	3	0.220000		
3	37		0.220000		
4	30		0.250000		
5	30		0.220000		
6	33		0.200000		
7	20		0.260000		
8	37		0.120000		
9	40		0.089100		
10	35		0.110000		
11	26		0.078400		
12	383	3	0.193012		
Heterozygous Genotype Freq. Allele Frequency					
0	0.30	00000	0.4200		
1	0.27	72700	0.4192		
2	0.38	80000	0.4100		
3	0.3	70000	0.4050		
4	0.30	00000	0.4000		
5	0.30	00000	0.3700		
6	0.33	30000	0.3650		
7	0.20	00000	0.3600		
8	0.3	70000	0.3050		
9	0.39	96000	0.2871		
10	0.38	50000	0.2850		
11	0.25	54900	0.2059		
12	0.3	18636	0.3523		

#### selected\_variants\_DFs[3] 6:31324201 C / G (rs1071652) table: Number of Homozygotes [115]: Population Allele Count Allele Number 0 Baloch 73 1 Zartoshti 69 200 24 68 2 Mazani 200 24 3 Persian Gulf Islander 66 200 26 4 Sistani 64 200 22 5 Kurd 44 200 18 6 Arab 32 204 15 7 31 200 Azeri 14 8 Gilaki 30 198 14 9 Lur 16 200 6 10 Turkmen 200 3 8 11 Persian 7 200 3 12 Total 508 2404 198 Number of Heterozygotes Homozygous Genotype Freq. 0 15 0.287100 1 21 0.240000 2 20 0.240000 3 14 0.260000 4 20 0.220000 5 8 0.180000 6 2 0.147100 7 3 0.140000 2 8 0.141400 9 4 0.060000 10 2 0.030000 11 1 0.030000 12 112 0.164725 Heterozygous Genotype Freq. Allele Frequency 0.148500 0 0.3614 1 0.210000 0.3450 2 0.200000 0.3400 3 0.140000 0.3300 4 0.200000 0.3200 5 0.080000 0.2200

[115]: print(selected\_variants["HLA-B"], "table:")

6

7

8

9

10

0.1569

0.1550

0.1515

0.0800

0.0400

0.019600

0.030000

0.020200

0.040000

0.020000

```
[116]: print(selected_variants["G6PD"], "table:")
       selected_variants_DFs[4]
      X:153775343 A / C (rs3021074) table:
[116]:
                                                    Allele Number
                                                                    Number of Homozygotes
                        Population Allele Count
       0
                         Zartoshti
                                                               200
                                                                                          73
                                               146
                                                               200
       1
                            Mazani
                                               142
                                                                                          71
       2
                            Baloch
                                                               202
                                               124
                                                                                          62
            Persian Gulf Islander
                                               118
                                                               200
       3
                                                                                          59
                           Persian
       4
                                                94
                                                               200
                                                                                          47
       5
                           Sistani
                                                94
                                                               200
                                                                                          47
       6
                                                90
                                                               200
                             Azeri
                                                                                          45
       7
                                                88
                                                               200
                                                                                          44
                               Lur
       8
                              Kurd
                                                86
                                                               200
                                                                                          43
       9
                                                82
                                                               204
                                                                                          41
                              Arab
       10
                           Turkmen
                                                61
                                                               200
                                                                                          30
                            Gilaki
       11
                                                54
                                                               198
                                                                                          27
       12
                             Total
                                              1179
                                                              2404
                                                                                         589
            Number of Heterozygotes
                                       Homozygous Genotype Freq.
       0
                                    0
                                                          0.730000
       1
                                    0
                                                          0.710000
                                    0
       2
                                                          0.613900
       3
                                    0
                                                          0.590000
                                    0
       4
                                                          0.470000
       5
                                    0
                                                          0.470000
       6
                                    0
                                                          0.450000
       7
                                    0
                                                          0.440000
       8
                                    0
                                                          0.430000
                                    0
       9
                                                          0.402000
       10
                                    1
                                                          0.300000
                                    0
       11
                                                          0.272700
       12
                                    1
                                                          0.490017
            Heterozygous Genotype Freq.
                                           Allele Frequency
       0
                                 0.000000
                                                       0.7300
       1
                                 0.000000
                                                      0.7100
       2
                                 0.000000
                                                       0.6139
       3
                                 0.000000
                                                       0.5900
       4
                                 0.000000
                                                      0.4700
       5
                                 0.000000
                                                      0.4700
       6
                                 0.000000
                                                      0.4500
       7
                                 0.000000
                                                      0.4400
```

0.010000

0.093178

 0.0350

0.2113

```
      8
      0.000000
      0.4300

      9
      0.000000
      0.4020

      10
      0.010000
      0.3050

      11
      0.000000
      0.2727

      12
      0.000832
      0.4904
```

## 3 2)

We now proceed to estimate the fractional ancestry of a newly observed individual who is heterozygous at all selected SNP loci

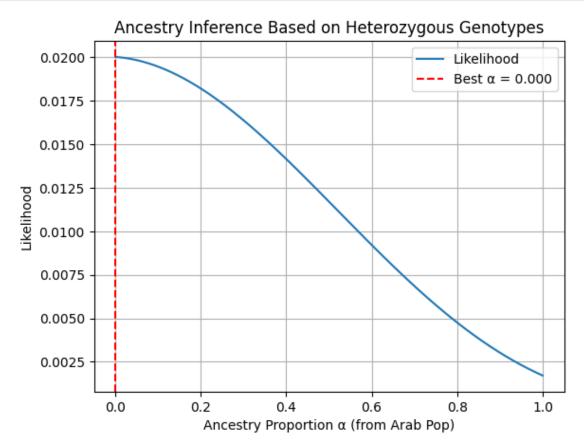
```
[141]: import numpy as np
      Arab Probs = np.array([])
      Zartoshti_Probs = np.array([])
      for df in selected variants DFs:
          Arab_Probs = np.append(Arab_Probs, float(df[df["Population"] == pop1]["Allele_

→Frequency"]))
          Zartoshti_Probs = np.append(Zartoshti_Probs,__

¬float(df[df["Population"]==pop2]["Allele Frequency"]))

[142]: Arab_Probs
[142]: array([0.1275, 0.1029, 0.2059, 0.1569, 0.402])
[143]: Zartoshti Probs
[143]: array([0.43, 0.39, 0.405, 0.345, 0.73])
[144]: import matplotlib.pyplot as plt
[145]: alphas = np.linspace(0, 1, 1000)
      likelihoods = []
      for alpha in alphas:
          probs = 2 * ((alpha * Arab_Probs + (1 - alpha) * Zartoshti_Probs) *
                       (1 - (alpha * Arab_Probs + (1 - alpha) * Zartoshti_Probs)))
          likelihood = np.prod(probs)
          likelihoods.append(likelihood)
      likelihoods = np.array(likelihoods)
      best_alpha = alphas[np.argmax(likelihoods)]
      plt.plot(alphas, likelihoods, label="Likelihood")
      plt.axvline(best_alpha, color='red', linestyle='--', label=f'Best =_ |
        plt.xlabel('Ancestry Proportion (from Arab Pop)')
```

```
plt.ylabel('Likelihood')
plt.title('Ancestry Inference Based on Heterozygous Genotypes')
plt.legend()
plt.grid(True)
plt.show()
```



Based on the genotype likelihood modeling, the analysis indicates that this individual has 0% ancestry from population 1 (Arab), suggesting that the selected SNPs effectively differentiate between the Arab and Zartoshti populations.