**README about the Admixture and PCA input:**

- For ADMIXTURE program, we used the ordinary PLINK (.ped) formatted files; a corresponding PLINK style .map file should be in the same directory as specified in ADMIXTURE manual. In the table below are the different file used, containing the different set of markers and a same set of 706 individuals.

|  |  |  |
| --- | --- | --- |
| **.ped file** | **.map file** | **content** |
| 706individuals\_600SNP\_dist.ped | 706individuals \_600SNP\_dist.map | 706 individuals, 602 SNP selected using Kennard-Stone algorithm on physical distances between markers. |
| 706individuals\_600SNP\_LD.ped | 706individuals\_600SNP\_LD.map | 706 individuals, 602 SNP minimizing the LD between SNPs by applying the Kennard and Stone algorithm |
| 706individuals \_600SNP\_random.ped | 706individuals \_600SNP\_random.map | 706 individuals, 602 SNP selected randomly. |
| 706individuals \_2000SNP\_LD.ped | 706individuals \_2000SNP\_LD.map | 706 individuals, 1995 SNP minimizing the LD between SNPs by applying the Kennard and Stone algorithm |
| 706individuals\_allSNP.ped | 706individuals\_allSNP.map | 706 individuals, 7896 SNP. |

- For PCA, we use adegenet R package and the Structure format (.str); the file contain data for 706 individuals and 602 SNP markers:

706individuals\_12populations\_602SNP\_LD\_PCA.str