Bioinformatics Consortium of Taiwan

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A pipeline to facilitate interpretation of genome-wide association study data

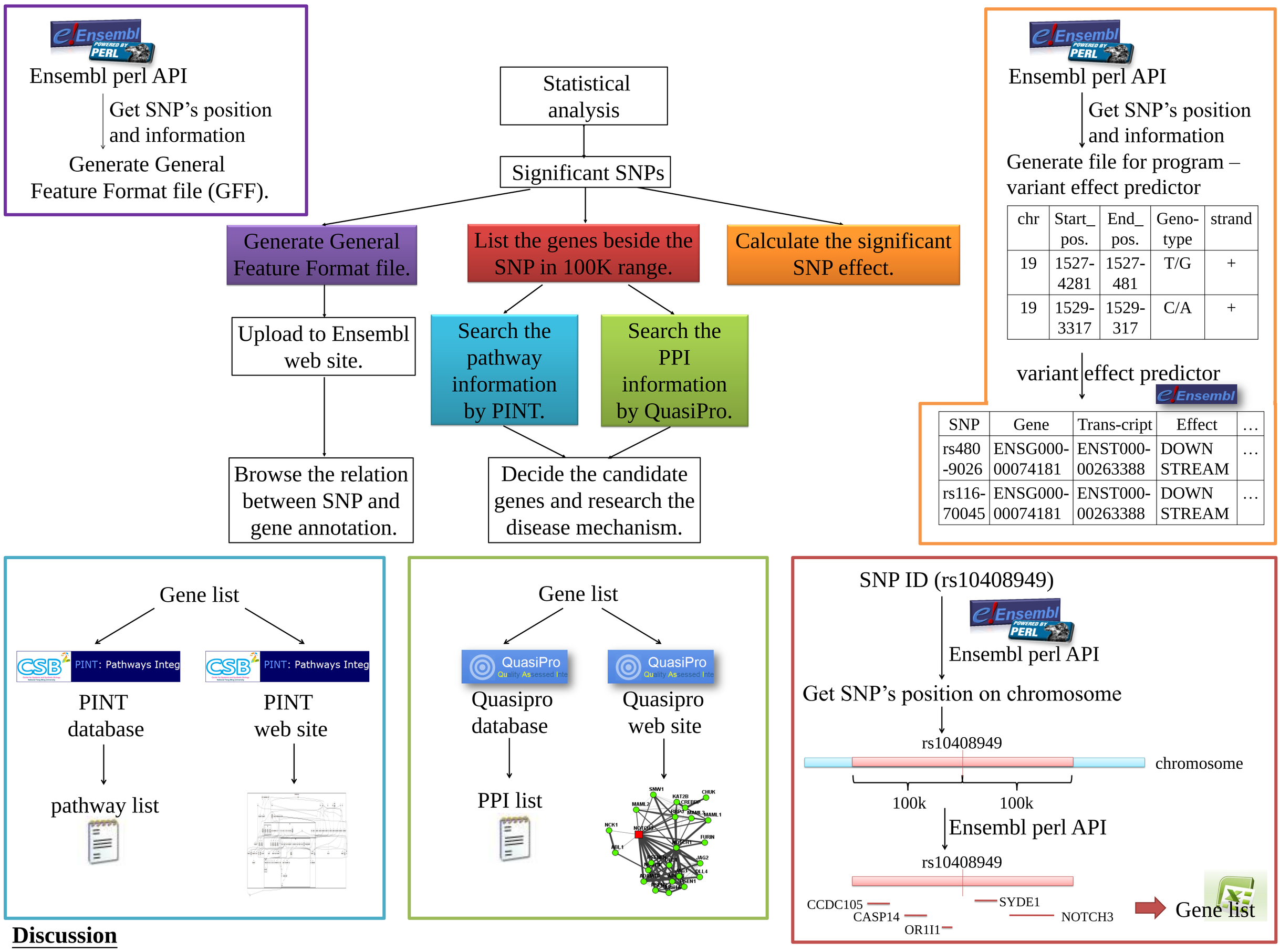
National Core Facility Program for Biotechnology- Bioinformatics Consortium of Taiwan

Introduction

In this era of knowledge explosion, how to use the information efficiently is important. After PLINK analysis, we may find many significant SNPs. In order to exploring the disease genes, we still need to collecting more information from public resource or other databases. But these information are sundry and luxuriant, the time which people spend on analysis will grow exponentially along with the raising amount of significant SNPs. So, if the analysis process could be establish as an automatic pipeline, then it's not only accelerating the speed of analysis but also decreasing the human resources. Otherwise we can also add more objects in the pipeline. For these reasons, we has combined some public domain resources and two databases - Pathways Integration Tool (PINT) and Quality Assessed Interacting Protein database (QuasiPro) to established an automatic SNP annotation pipeline in this study.

Methods and Results

The Ensembl website has provided many application programming interface (API) for users getting the information they wanted.



Discussion

This automatic pipeline include generating GFF file, which could be upload to Ensembl website showing the SNP position on gene, SNP effect calculating, picking out the genes located beside the SNP and importing these genes into PINT and QuasiPro to search the pathway and PPI information. This pipeline has been applied on a genome-wide scanning approach, and 4 genes have been found, which may related with migraine.

Reference

1. Wang, Y.T., Huang, Y.H., Chen, Y.C., Hsu, C.L., and Yang, U.C. (2010). PINT：Pathways INtegration Tool. Nucleic Acids Res *38*, W124-131.

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