

# LIBRA

## Your Personal Variant Query System

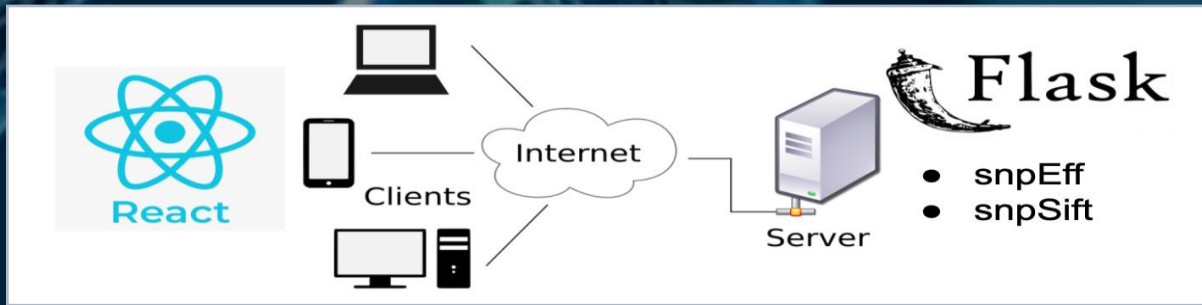


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### ❖ OVERVIEW

LIBRA is a genetic annotation and filtering tool that allows you to organize and analyze the genetic information of patients. It assists you in finding out the genetic diseases of patients. It is also a platform that matches and connects patients that suffer from similar diseases. **Save your time and maybe... Your life.**

### ❖ INFRASTRUCTURE



### ❖ VISUALIZATIONS

The screenshot shows the 'LIBRA - Welcome naisila' interface. It features a 'Summary' section with two pie charts: 'dbSNP Variant Distribution' (showing 21.4% dbSNP and 78.6% Novel) and 'HG Variant Distribution (not found in the annotation)' (showing 100% Novel). Below the charts is a 'VCF Table' with columns for chrom, pos, id, ref, alt, qual, annotation, impact, gene\_name, and gene\_id. A table with 5 rows of variant data is visible.

Upload, annotate and filter VCF files

The screenshot shows the 'LIBRA - Welcome melih' interface. It features a 'CREATE NEW PROJECT' button and a 'Your Projects' section. The projects are displayed as cards with titles like 'Default', 'Dwarfism', 'Anemia-BilkentResearch', 'MFS-2020', 'HD-Research2020', and 'Galactose in the Blood'. Each card includes a brief description of the project.

You can manage your projects

The screenshot shows the 'MatchMaker For Patient: Alice' interface. It displays search results for 'Abnormality of the nervous system' and 'Cough'. The results are organized into sections: 'Manual HPO MatchMaker Results', 'HPO MatchMaker Results', and 'GO MatchMaker Results'. Each section contains a table with columns for Patient Contact, Patient ID, Diagnosis, and Phenotypes.

Match patients based on phenotype and affected genes

The screenshot shows the 'LIBRA Similarity Report' interface. It displays a notification: 'You have a new patient match! Patient ID: 1 Matched Patient ID: 3'. Below the notification is a 'Contact Doctor' button.

Get notifications when there is a match