FlowCyto

Cell-type predictor

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OUR TEAM

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GENERAL AIM

★ Develop a specialized web application (inspired by *PanglaoDB*) designed to automate cell-type identification within Blood tissue:

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By calculating a similarity score, the app provides a **statistical prediction of the sample's identity.**

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★ This approach offers researchers a **fast**, **accessible**, and **focused** tool for interpreting biological results.

SPECIFICATIONS

DATA:

A **local database** was created extracting information from public and curated databases, focusing on **blood cells**.

From the markers found on the databases, the ones with >0.00 sensitivity and minimum 1 support/score (mentioned in one reference at least) were selected.

→ Original tables and the data processing pipelines are available in Github.

SPECIFICATIONS

DATABASE

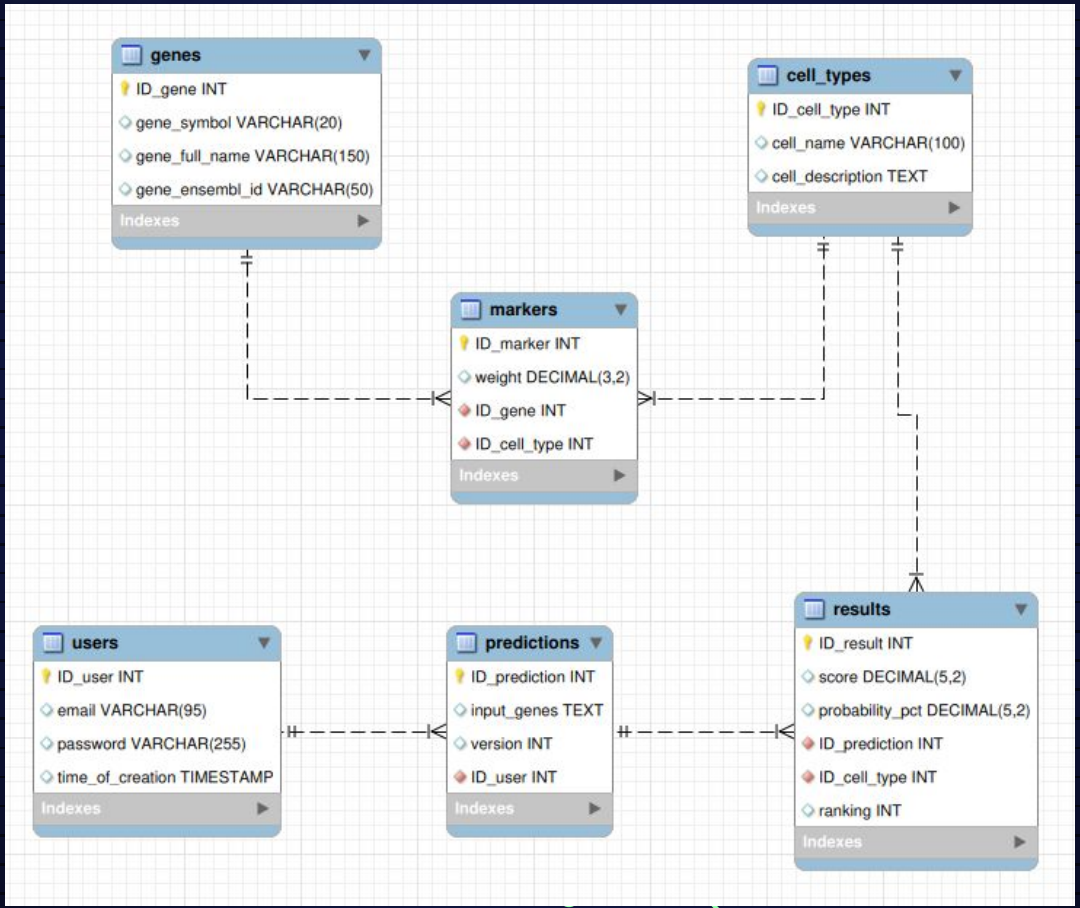
MySQL (many-to-many relation)

- Table 1: **cell types** (id + name)
- Table 2: **genes** (id + symbol)
- Table 3: **markers** (connections + weights)

LOGIC

- User's **input**: list of genes
- **Algorithm**: look for genes in Table 3 → assign points to cells → obtain the cell type with the highest score
- **Output**: predicted cell type (with a probability)

Initial data model

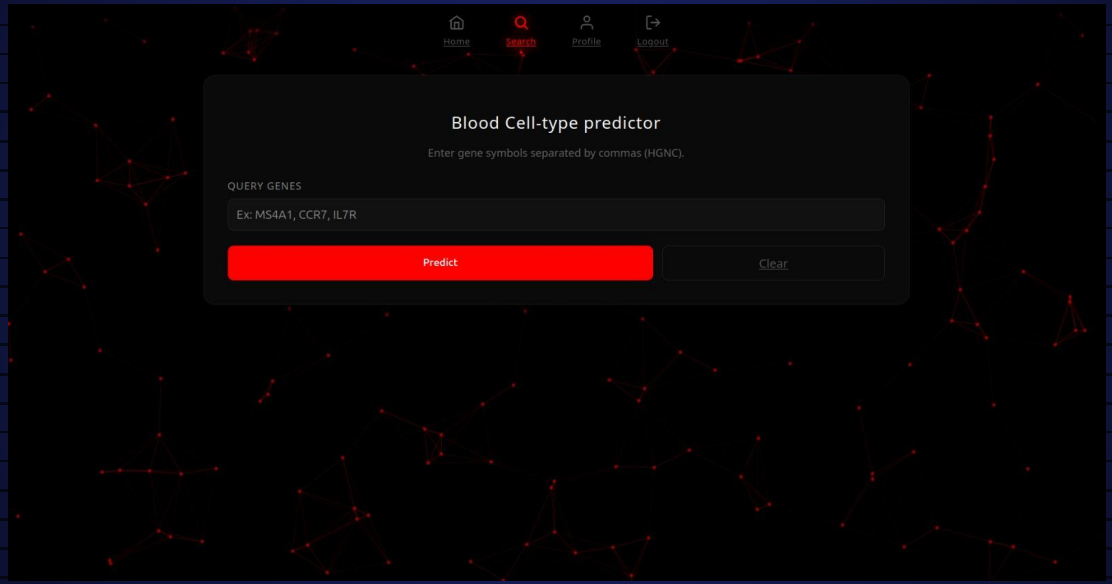


How does the app work?

Users must be registered to use the predictor

If user has not log in, a login request will automatically pop up. Sign up for new users will also appear from home and login pages.

Search



Input must be provided in GENE SYMBOL format

Results

Score

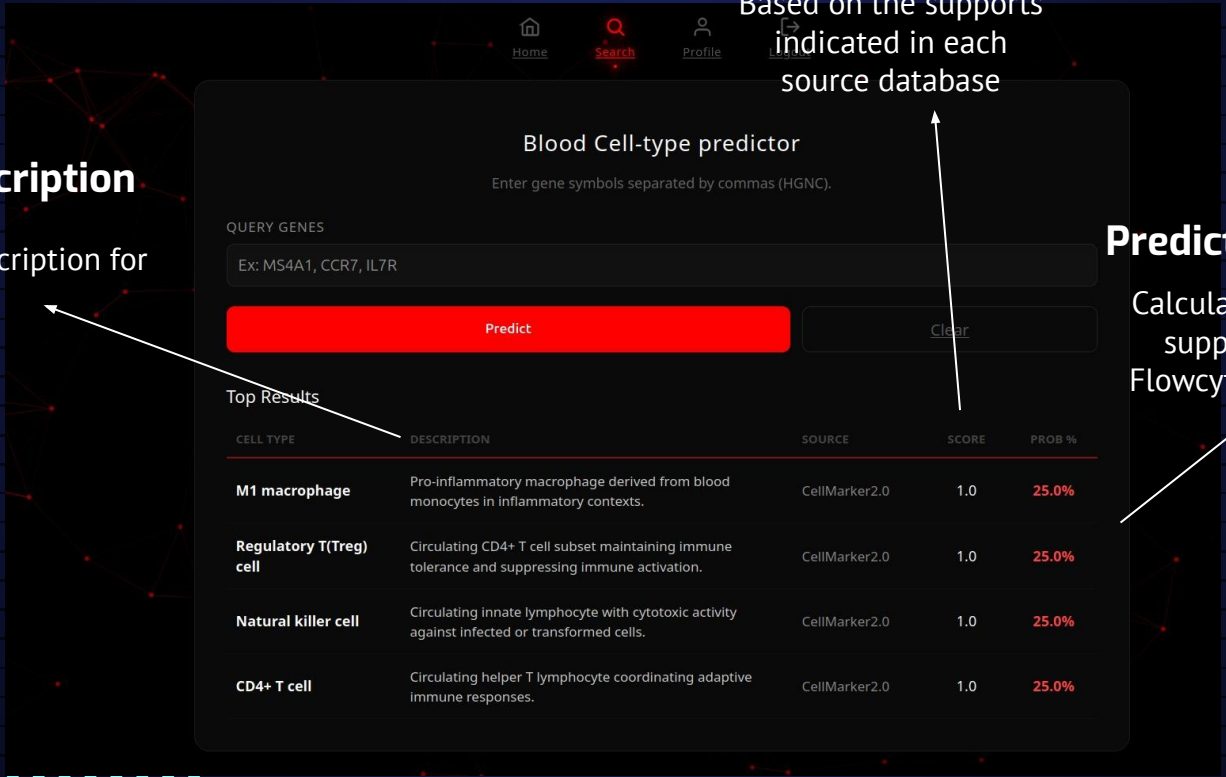
Based on the supports indicated in each source database

Cell-type description

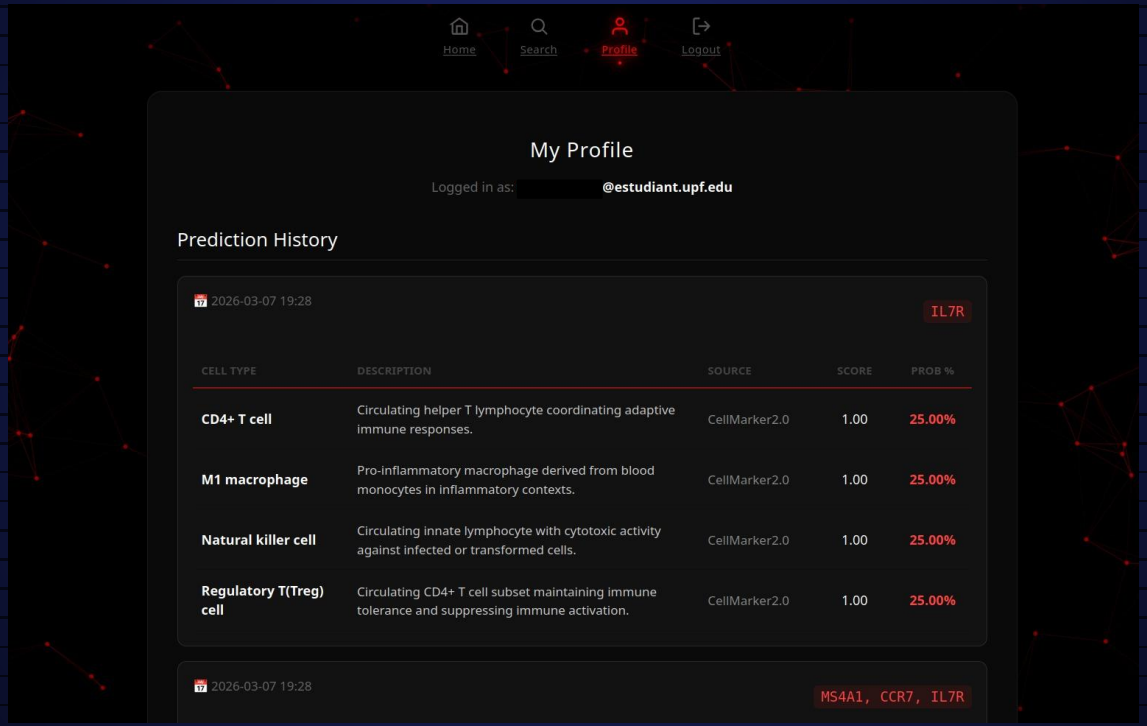
Short cell-type description for users

Prediction probability

Calculated using the total support scores of the Flowcyto precito database



User interface



History

User can access their prediction history, to recover old searches.

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