



FlowCyto

Cell-type predictor

Itxaso Alonso, Nahia Urra, Diego Vicente & Pau Villén

OUR TEAM



Itxaso Alonso

Frontend Developer



Nahia Urra

Fullstack



Diego Vicente

Data Curator
Bioinformatician



Pau Villén

Backend Developer



GENERAL AIM

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

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The user **inputs** a list of highly **expressed genes** from their experiments, and the application then queries a curated internal database to compare these markers against known **biological profiles**.

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.



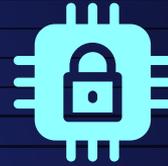
SPECIFICATIONS



DATABASE

MySQL (many-to-many relation)

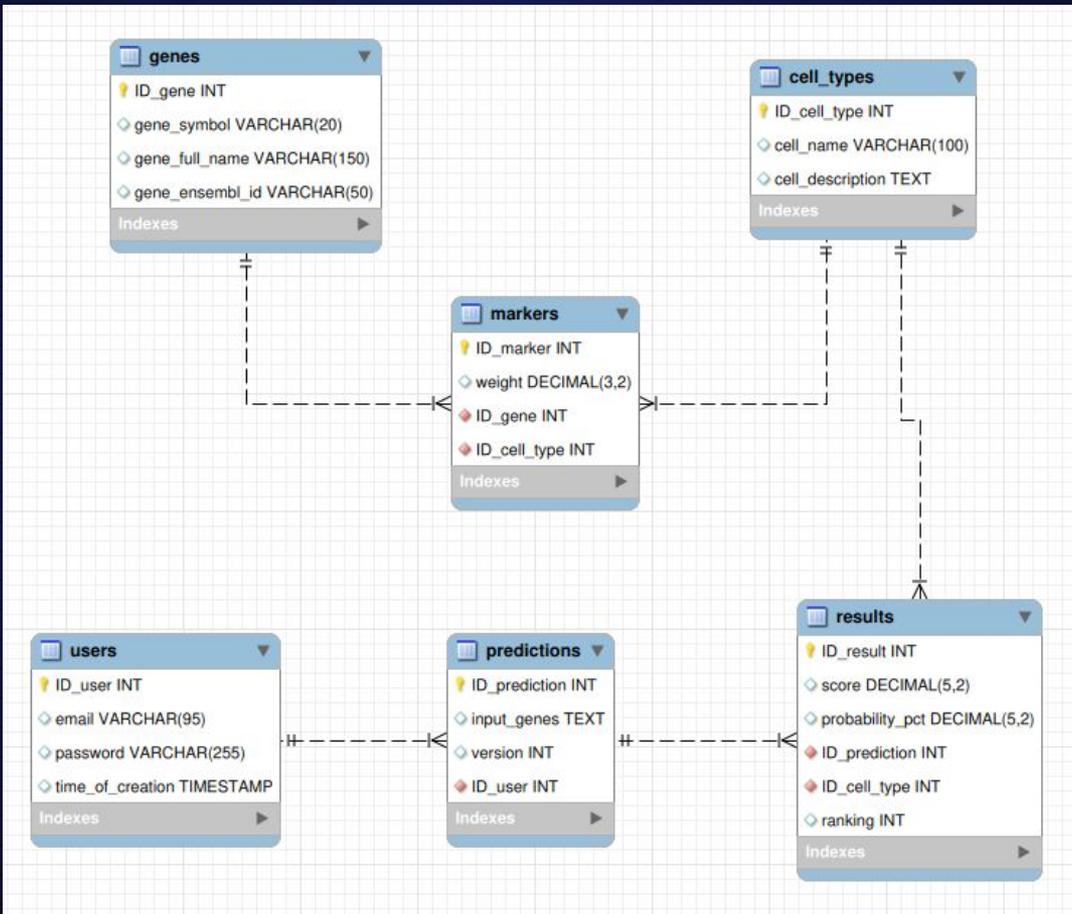
- Table 1: **cell types** (id + name)
- Table 2: **genes** (id + symbol)
- Table 3: **markers** (connections + weights)



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



The screenshot shows a web interface for a "Blood Cell-type predictor". At the top, there is a navigation bar with icons for Home, Search, Profile, and Logout. The main content area has a dark background with a network graph pattern. The predictor interface includes a title "Blood Cell-type predictor", a subtitle "Enter gene symbols separated by commas (HGNC).", a label "QUERY GENES", a text input field containing "Ex: MS4A1, CCR7, IL7R", a red "Predict" button, and a "Clear" button.

Input must be provided in GENE SYMBOL format



Results



Cell-type description

Short cell-type description for users



Score

Based on the supports indicated in each source database

Prediction probability

Calculated using the total support scores of the Flowcyto precito database

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CELL TYPE	DESCRIPTION	SOURCE	SCORE	PROB %
M1 macrophage	Pro-inflammatory macrophage derived from blood monocytes in inflammatory contexts.	CellMarker2.0	1.0	25.0%
Regulatory T(Treg) cell	Circulating CD4+ T cell subset maintaining immune tolerance and suppressing immune activation.	CellMarker2.0	1.0	25.0%
Natural killer cell	Circulating innate lymphocyte with cytotoxic activity against infected or transformed cells.	CellMarker2.0	1.0	25.0%
CD4+ T cell	Circulating helper T lymphocyte coordinating adaptive immune responses.	CellMarker2.0	1.0	25.0%



User interface



The screenshot displays a user interface for a profile page. At the top, there are navigation links: Home, Search, Profile (highlighted in red), and Logout. Below this, the page title is "My Profile" and the user is logged in as "@estudiant.upf.edu". The main section is titled "Prediction History" and contains a table of search results. The table has columns for CELL TYPE, DESCRIPTION, SOURCE, SCORE, and PROB %. The first entry is dated 2026-03-07 19:28 and is associated with the marker IL7R. The table lists four cell types: CD4+ T cell, M1 macrophage, Natural killer cell, and Regulatory T(Treg) cell, all with a score of 1.00 and a probability of 25.00%. A second entry is partially visible at the bottom, dated 2026-03-07 19:28, with markers MS4A1, CCR7, and IL7R.

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CD4+ T cell	Circulating helper T lymphocyte coordinating adaptive immune responses.	CellMarker2.0	1.00	25.00%
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Regulatory T(Treg) cell	Circulating CD4+ T cell subset maintaining immune tolerance and suppressing immune activation.	CellMarker2.0	1.00	25.00%

History

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





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