



# FlowCyto

## Cell-type predictor

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# OUR TEAM



**Itxaso Alonso**

Database curation &  
Schema design



**Nahia Urra**

Backend, Frontend &  
Full Stack



**Diego Vicente**

Backend & Project design



**Pau Villén**

SQL & Backend



# GENERAL AIM

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

## → HOW DOES IT WORK?

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**.

- ★ 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)

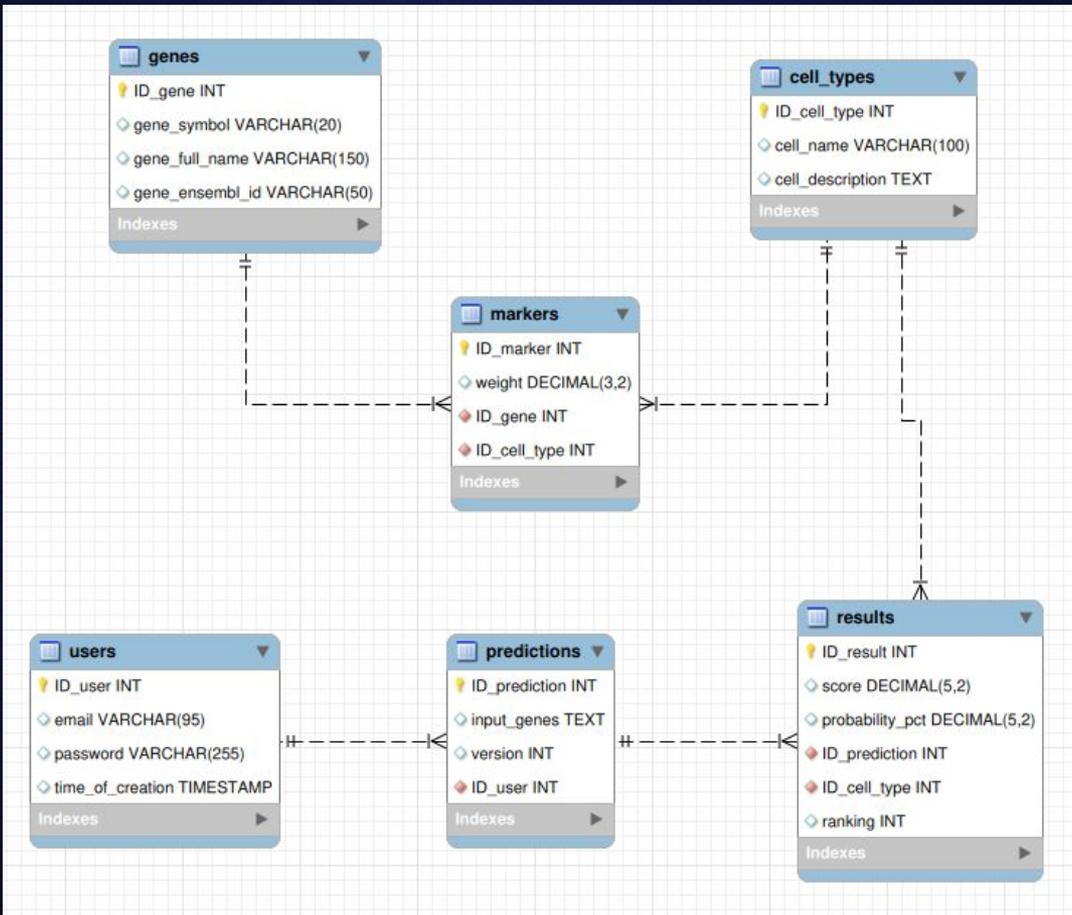
- Table 1: **cell types** (id + name)
- Table 2: **genes** (id + symbol)
- Table 3: **markers** (connections + weights)



## 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. A central white box contains the title "Blood Cell-type predictor" and the instruction "Enter gene symbols separated by commas (HGNC)". Below this is a text input field labeled "QUERY GENES" with the example text "Ex: MS4A1, CCR7, IL7R". At the bottom of the box are two buttons: a red "Predict" button and a grey "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

The screenshot shows a web application interface for a 'Blood Cell-type predictor'. At the top, there are navigation links for 'Home', 'Search', 'Profile', and 'Logout'. Below the navigation is a search bar with the text 'QUERY GENES' and an example 'Ex: MS4A1, CCR7, IL7R'. A red 'Predict' button and a 'Clear' button are positioned below the search bar. The main content area is titled 'Top Results' and contains a table with the following data:

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



# User interface



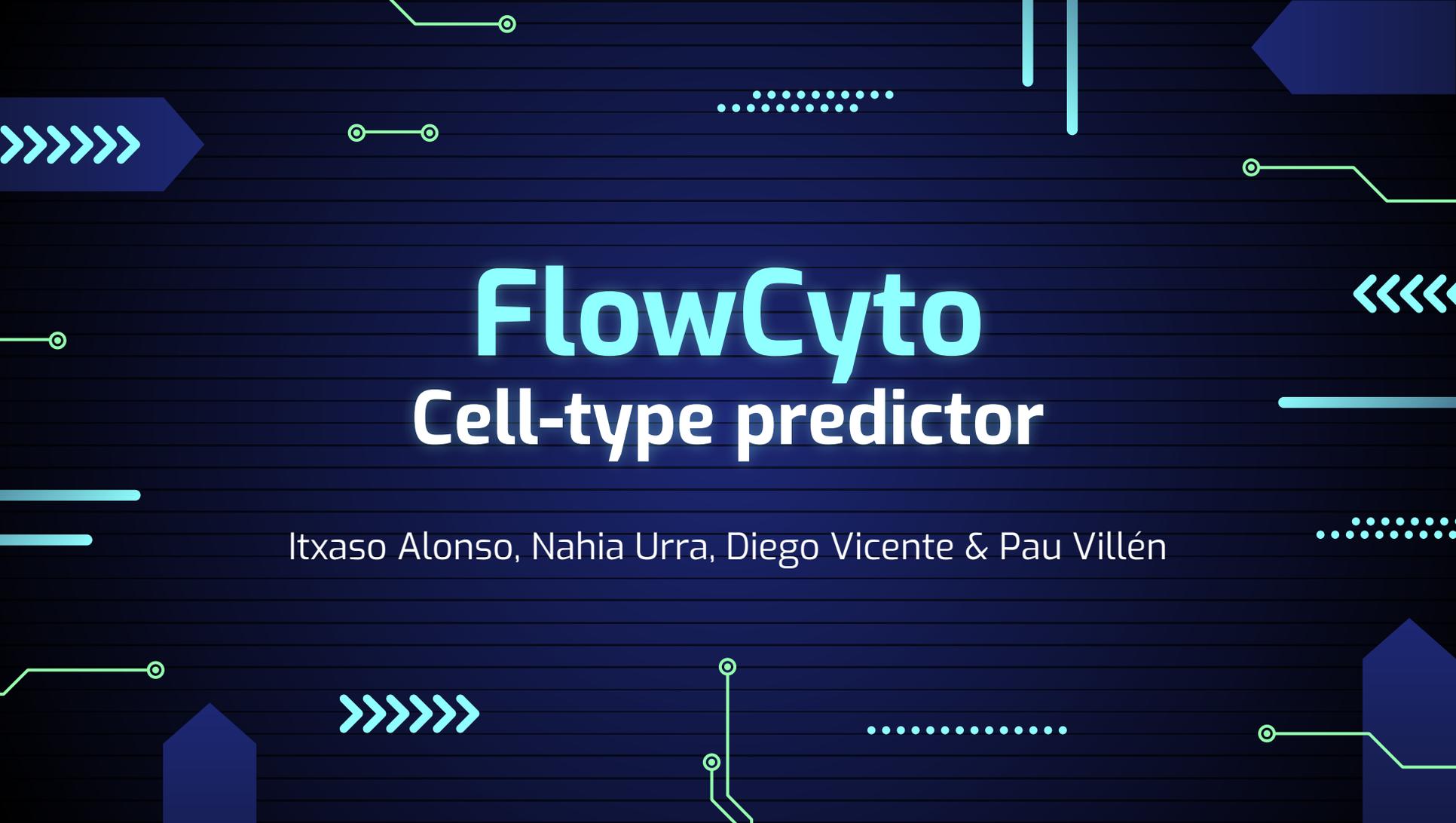
The screenshot shows a user interface with a dark theme. At the top, there are navigation links: Home, Search, Profile (highlighted in red), and Logout. Below this is the 'My Profile' section, indicating the user is logged in as '@estudiant.upf.edu'. The main content is the 'Prediction History' section, which contains a table of prediction results for a specific date and time (2026-03-07 19:28). The table has columns for Cell Type, Description, Source, Score, and Prob %. The results show four cell types, each with a score of 1.00 and a probability of 25.00%. A red label 'IL7R' is visible in the top right of the table area. Below the table, there is another entry for the same date and time, with a red label 'MS4A1, CCR7, IL7R'.

CELL TYPE	DESCRIPTION	SOURCE	SCORE	PROB %
CD4+ T cell	Circulating helper T lymphocyte coordinating adaptive immune responses.	CellMarker2.0	1.00	25.00%
M1 macrophage	Pro-inflammatory macrophage derived from blood monocytes in inflammatory contexts.	CellMarker2.0	1.00	25.00%
Natural killer cell	Circulating innate lymphocyte with cytotoxic activity against infected or transformed cells.	CellMarker2.0	1.00	25.00%
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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