A logo with blue and orange letters

AI-generated content may be incorrect.**CompIgS – Comparative Analysis of Clonotypes Across Antibody Subclasses**

**CompIgS** is an open-source computational tool for the comparative analysis of related clonotypes across antibody subclasses from the same sample.

**📅 Introduction**

Antibodies, or immunoglobulins (Ig), are produced by B cells and form a diverse repertoire critical for adaptive immunity. Each antibody is defined by unique V(D)J gene recombination forming clonotypes, which may exist in various subclasses. These subclasses, such as IgM, IgE, IgG, etc., have different effector functions.

Affinity maturation and somatic hypermutation refine antibody specificity. However, tools for comparing clonotypes across isotypes remain limited.

**CompIgS** fills this gap by identifying shared and divergent clonotypes using annotated output from IMGT/HighV-QUEST and IMGT/StatClonotype. It facilitates clonal expansion, mutation profile comparison, and divergence analysis between isotypes such as IgE and IgG1, as demonstrated in a murine food allergy model.

**📦 Key Features**

* 🔍 Compare antibody isotypes (e.g., IgE (Ig1) vs. IgG1 (Ig2)) in one sample
* 🧠 Filter clonotypes based on various metrics: divergent CDR3AA, clonal size, shared vs. unique, mutated vs. unmutated
* 🖥️ GUI for local, interactive analysis
* ☁️ Google Colab notebook for quick, cloud-based access
* 🫿 Windows executable – no coding required

**🔹 Table of Contents**

* Quick Start
* Overview
* Data/Samples

**🚀 Quick Start**

**Get the Software**

**Option 1: Run the Windows .exe version**

Download the standalone executable from:

* 🔗 GitHub Releases
* 📓 Zenodo DOI

**Option 2: Use via Google Colab**

Open and run CompIgS.ipynb in Google Colab and follow the instructions to upload your data and begin analysis.

**Option 3: Run GUI locally (Python required)**

**🛠️ Requirements**

* Python ≥ 3.1
* Libraries: pandas, numpy, PyQt5, seaborn, matplotlib, peptides

**📁 Project Structure**

CompIgS/

├── CompIgS.ipynb # Google Colab notebook

├── CompIgS\_GUI.py # GUI version for local use

├── README.md # This file

└── releases/ # Downloadable EXE binaries

**📂 CompIgS Notebook: Local GUI and Colab Versions**

We offer one notebook version and one .py file, tailored for cloud-based (Colab) execution or local (GUI).

**Google Colab Version**

* CompIgS.ipynb (without GUI)
* Usage: Upload your IMGT/HighV-QUEST and IMGT/StatClonotype output data and follow the instructions
* Open notebook in [Google Colab](https://colab.research.google.com/drive/1y45LgoJmTWHnUwAIn3RmcEkNPEeqHv07#scrollTo=f11ba5c1-0e84-40e8-9984-b2b5d8d70559)
* Dependencies: pandas, numpy, biopython, seaborn, matplotlib, google.colab, collections
* Example data: [Google Colab](https://colab.research.google.com/drive/1y45LgoJmTWHnUwAIn3RmcEkNPEeqHv07#scrollTo=f11ba5c1-0e84-40e8-9984-b2b5d8d70559) or [Zenodo](https://doi.org/10.5281/zenodo.15774119)

**Input Data Requirements**

Place the following IMGT/StatClonotype and IMGT/HighV-QUEST .txt files in the directory or use example\_data/. Use Ig1 for the query isotype, in the example IgE is Ig1:

* stats\_IgE.txt- IgE\_IMGT StatClonotype
* stats\_IgG1.txt- IgG1\_IMGT StatClonotype
* stats\_IgE\_mut.txt- IgE\_8\_V-REGION-nt-mutation-statistics
* stats\_IgG1\_mut.txt-IgG1\_8\_V-REGION-nt-mutation-statistics
* stats\_IgE\_Aminotab.txt-IgE\_5\_AA-sequences
* stats\_IgG1\_Aminotab.txt-IgG1\_5\_AA-sequences
* stats\_IgE\_Aminotab\_change.txt-IgE\_7\_V-REGION-mutation-and-AA-change-table
* stats\_IgG1\_Aminotab\_change.txt-IgG1\_7\_V-REGION-mutation-and-AA-change-table
* sequences.fasta

**Local GUI Version (PyQt5)**

* CompIgS\_GUI.py – includes GUI elements

**Input Data Requirements**

Run the .py file and upload files via the GUI or use [Zenodo](https://doi.org/10.5281/zenodo.15774119): Use Ig1 for the query isotype:

**Reference VH Amino acid sequence**

* [Human VH reference](https://doi.org/10.5281/zenodo.15774119)
* [Mouse VH reference](https://doi.org/10.5281/zenodo.15774119)

**🧪 Input Format**

* Accepted formats: .txt files from IMGT/HighV-QUEST and IMGT/StatClonotype
* Required fields: V\_gene, D\_gene, J\_gene, Sequence.ID, V-DOMAIN Functionality, V-REGION Nb of nucleotides, CDR3-IMGT Nb of nonsilent mutations, etc.

**📄 Output**

* Summary plots in a folder named BCR\_Analysis\_Plots in your Downloads directory
* 18 CSV files: one for summary statistics (captured.csv) and 17 for different Ig1 and Ig2 subpopulations VH amino acids.

**📚 Citation**

If you use **CompIgS**, please cite:

Udoye, C. C., Mehrabani Khasraghi, S., Witt, P., Biswas, S., Manz, R., & Fähnrich, A. (2025). *CompIgS: A Computational Workflow for Comparative Analysis of Related Clonotypes within Distinct Antibody Subclasses*. BMC Bioinformatics.

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**🙋‍♀️ Contact**

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