



# Exploring Biofluid Protein Expression with CATalog, an Interactive Proteomics Dashboard

Alex W. Joyce<sup>1</sup>, Katelyn B. Brusach<sup>2</sup>, Ariana Shannon<sup>1,3</sup>, Jessica M. Quimby<sup>2</sup>, and Brian C. Searle<sup>1,3</sup>

<sup>1</sup>-Department of Biomedical Informatics, <sup>2</sup>-Veterinary Clinical Sciences, <sup>3</sup>– Pelatonia Institute of Immuno-Oncology

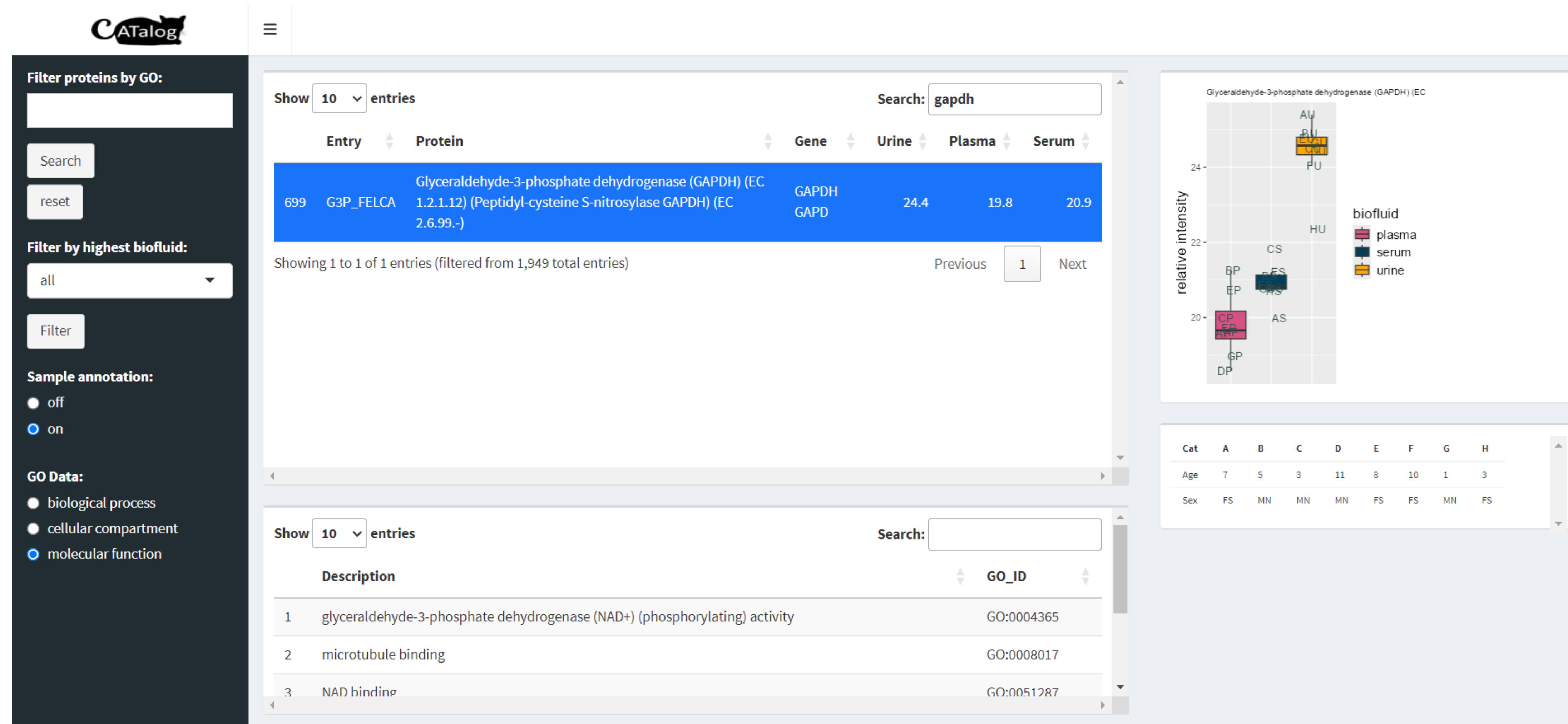


Searle

## Introduction

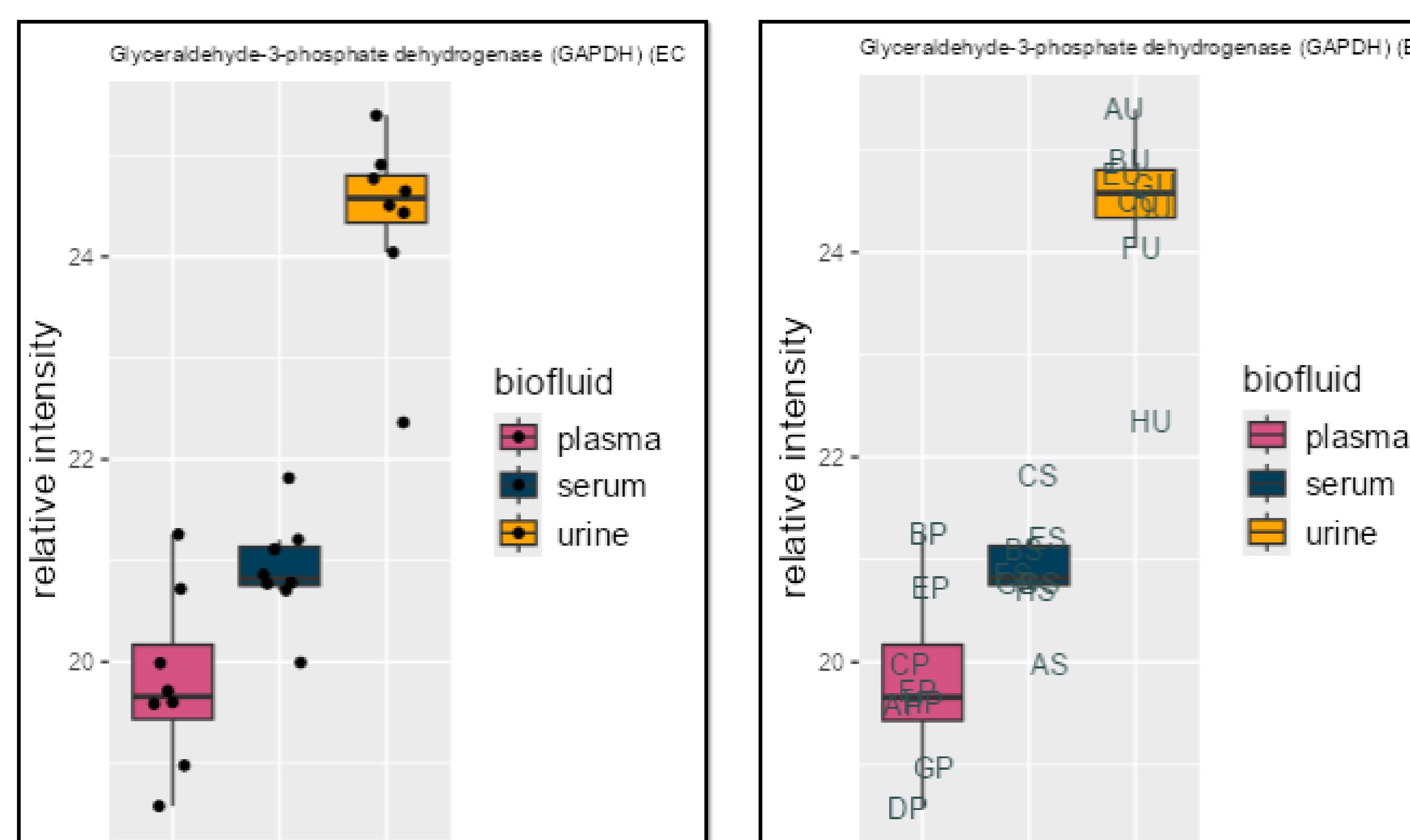
Biomarkers are a vital tool for identifying aberrant states in a biological system, either for early detection of a disease or for assessing symptoms of an existing condition. One of the abundant sources of biomarkers are biofluids which can be easily sampled from an organism and stored for later analysis. However, due to the diversity of potential biomarkers, they oftentimes appear in different concentrations among various types of biofluids, making it difficult to identify the optimal sample to analyze. CATalog can assist in both biofluid and biomarker selection by displaying the relative abundances of selected biomarkers from healthy cats across three paired samples (urine, serum, and plasma) [1] collected using mass spectrometry. Additionally, relevant gene ontology (GO) [2] information is provided for each biomarker, showing involved biological processes, subcellular localization, and molecular function, annotating each biomarker and assisting with selection.

## CATalog Presents Data in an Interactive Format



## Boxplots Provide Demographic Context

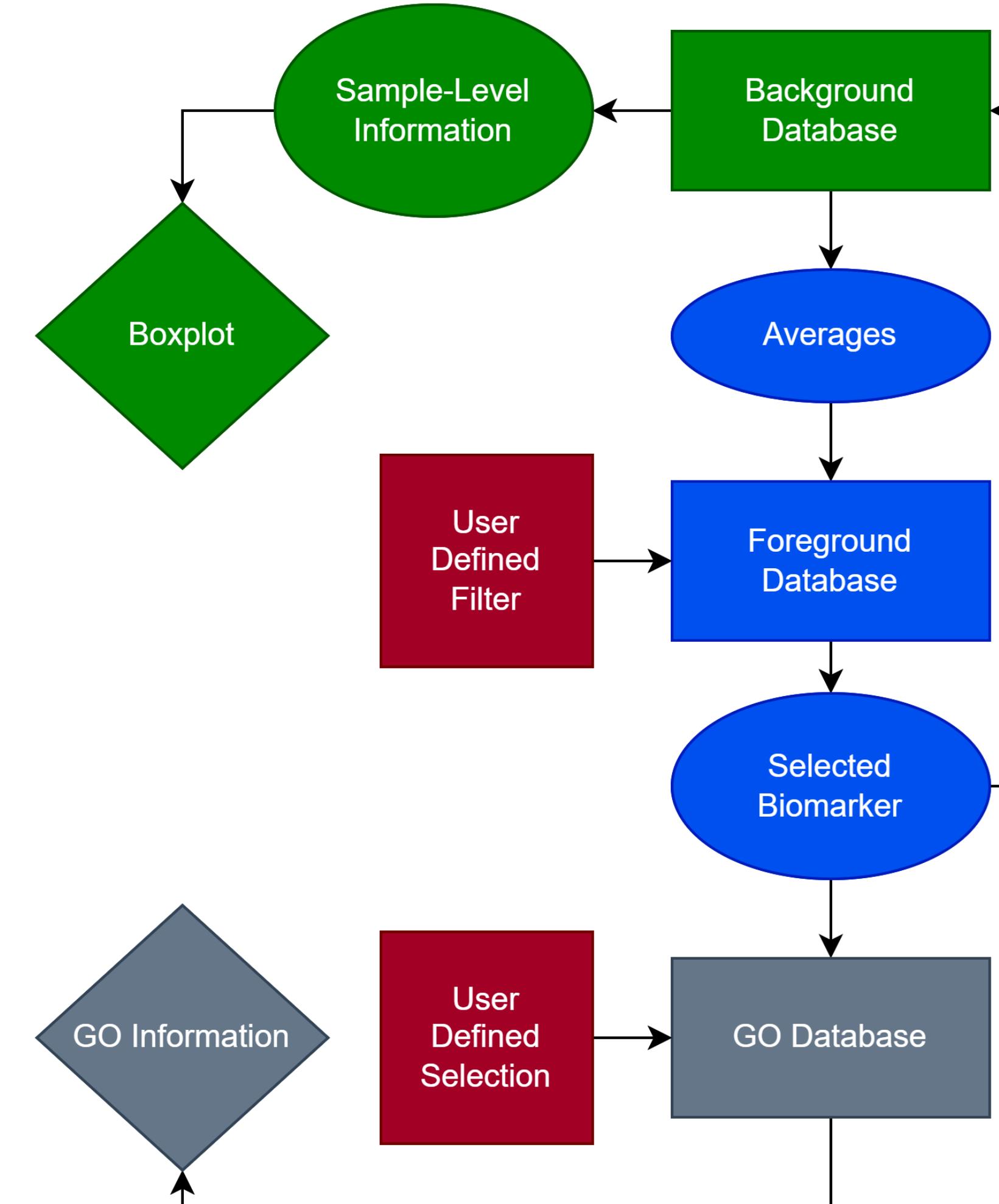
Figure 3: Each biomarker in the database has an associated boxplot which displays sample-level information of relative abundances. Annotations provide information about the corresponding cat's age and sex, connecting demographics to potential outliers in the biomarker's relative abundance.



Cat	A	B	C	D	E	F	G	H
Age	7	5	3	11	8	10	1	3
Sex	FS	MN	MN	MN	FS	FS	MN	FS

## Data Structure

- CATalog was written in R using the Shiny framework which provides a modular structure.
- Only the foreground dataset is shown to the user, greatly reducing the amount of information at the forefront.
- Complete sample-level information is held in the background which is displayed to the user in the form of a boxplot.
- The gene ontology (GO) database was obtained from UniProt for the organism *felis catus* (taxon id: ). Which portion of the information is displayed can be selected by the user.



## GO Information Facilitates Biomarker Selection

Figure 2: Table of GO information for the glyceraldehyde-3-phosphate dehydrogenase, concatenated from the three individual tables in CATalog.

GO Term	GO ID
<b>Biological Process</b>	
glucose metabolic process	GO:0006006
glycolytic process	GO:0006096
innate immune response	GO:0045087
...	...
<b>Cellular Compartment</b>	
cytoplasm	GO:0005737
cytosol	GO:0005829
GAIT complex	GO:0097452
...	...
<b>Molecular Function</b>	
glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity	GO:004365
microtubule binding	GO:0008017
NAD binding	GO:0051287
...	...

## Future Directions

- Adding a feature to download selected peptides from a “shopping cart”
- Comparison of user-uploaded data to enable direct comparison with CATalog’s control data.
- Expansion of the central CATalog design to peptide-level quantitative analysis and/or with other species. This is currently in development as ‘PeptideBrowser’.

