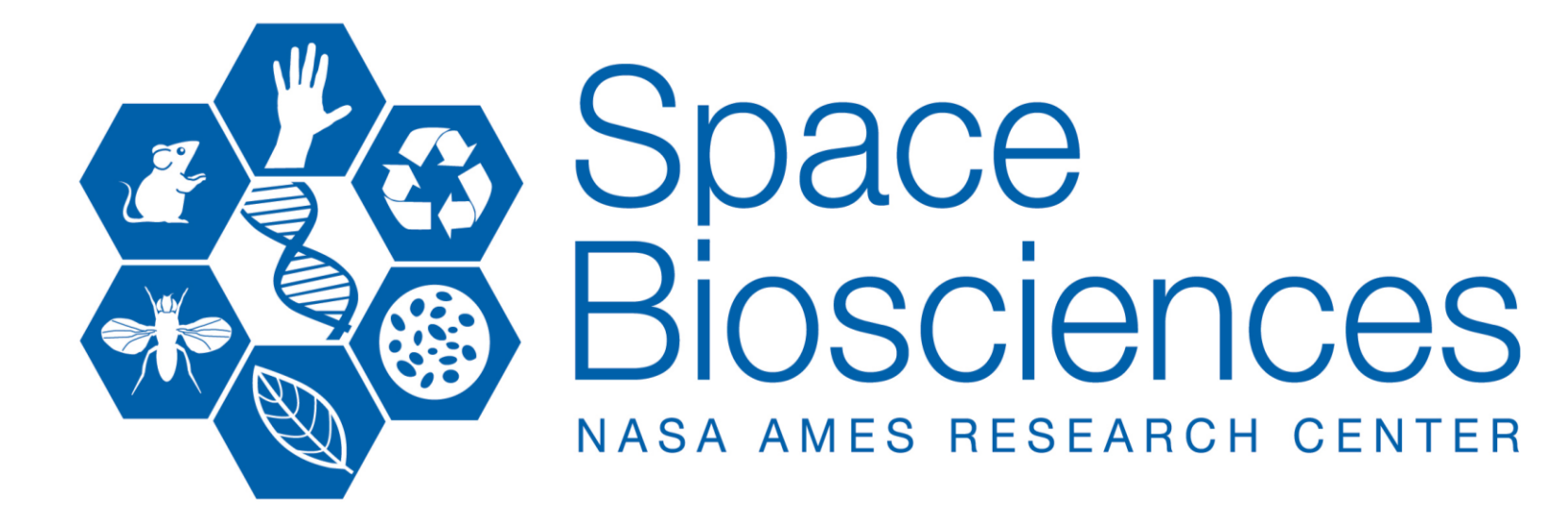# Reanalysis of Rodent Data from Spacelab Life Sciences-1

Crystal Rain Fowler[1], Eva Soler Cruz[1], Jonathan Galazka Ph.D.[2]

[1]Space Life Science Training Program, Moffett Field, CA, [2]NASA Ames Research Center, Moffett Field, CA

Abstract

In the space biosciences, reusing and reanalyzing NASA legacy experimental data and metadata is one way that scientists can draw new conclusions feasibly without multiple spaceflight experiments. The *Rattus norvegicus* has been a model organism for both research experiments conduced on Earth and in space. This study utilizes a biological model of *Rattus norvegicus* based on the legacy 1991 SpaceLab Life Sciences 1 (SLS-1) NASA Mission, the first designated spacelab flown. This project's motivation was to analyze all the data and metadata taken from SLS-1 to create a comprehensive biological model that can be supplemented with current data to allow new discoveries in space flown organisms to the space environment. To build the model, all the data and metadata, including graphs and tables, for SLS-1 were resourced from NASA archives, specifically the Life Science Data Archives (LSDA), and published research utilizing the samples from the mission. Then, each piece of data was organized and analyzed by different biological systems in the model and added to a data frame. The outcome of this project will allow NASA GeneLab scientists and others to couple the biological model with current data analysis methods, like RNA sequencing, to research gaps to further our knowledge.

Background and Introduction

The pace of discovery in space life science is limited by the cost and complexity of spaceflight experimentation. Therefore, reusing and reanalyzing legacy life science experiments will help identify patterns and nuances in processed data sets. The aim is to study and analyze all the data and metadata taken from the Spacelab Life Science-1 (SLS-1) to create a comprehensive biological model that is supplemented with current data to allow new discoveries.

SLS-1 Background Purpose:
1) Study the acute and chronic results of rats in spaceflight [1].
2) Compare both the Animal Enclosure Module (AEM) and Rodent Animal Holding Facility (RAHF) [1]

Why SLS-1?
We want to reuse and repurpose this "rare" space data and maximize utilization of biospecimens. There are multiple challenges when reusing this space data, such as:
1) Compiling multiple datasets from different sources
2) Creating parameters, operationalized variables, and a standardized way of seeing data sets
3) Programming all the unstandardized documents
4) Filtering relevant data

Methods

Scavenge for all existing sources
- Compile all data and metadata available, and extract information from non-programmable documents

Filter, organize, and re-analyze acquired rat data
- Organize and categorize data using data analysis and modeling techniques

Create a reliable data frame with the help of NASA SME's
- Build a data framework that combines processed data with other data sets

SLS-1 Dataset Distribution

Tools: seaborn, NumPy, Jupyter, matplotlib, pandas

WebPlotDigitizer
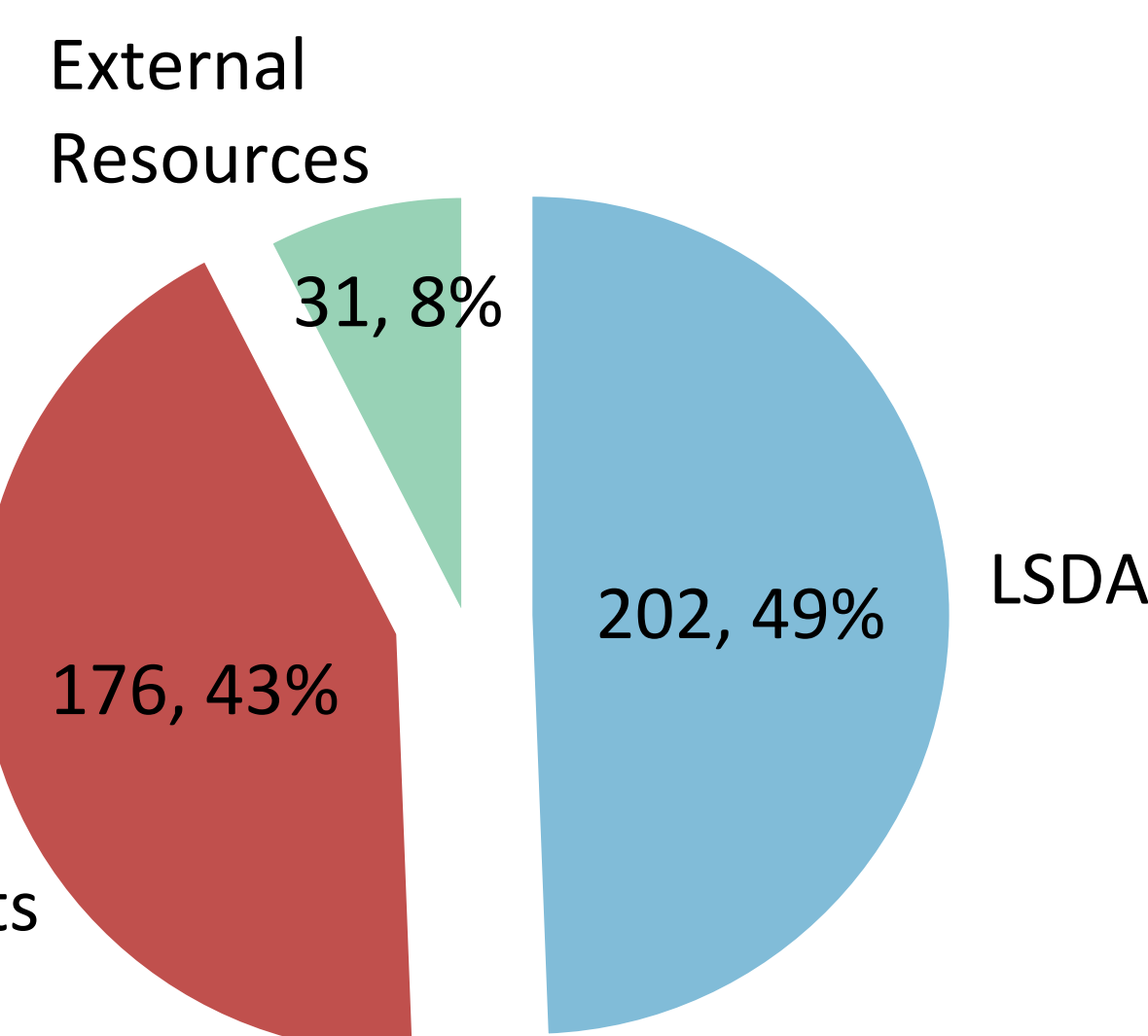Web based tool to extract data from plots, images, and maps

Figure 1. The dataset distribution of acquired data from the SLS-1 mission. Most of the data was from LSDA [2], then NASA contacts, and then external resources.
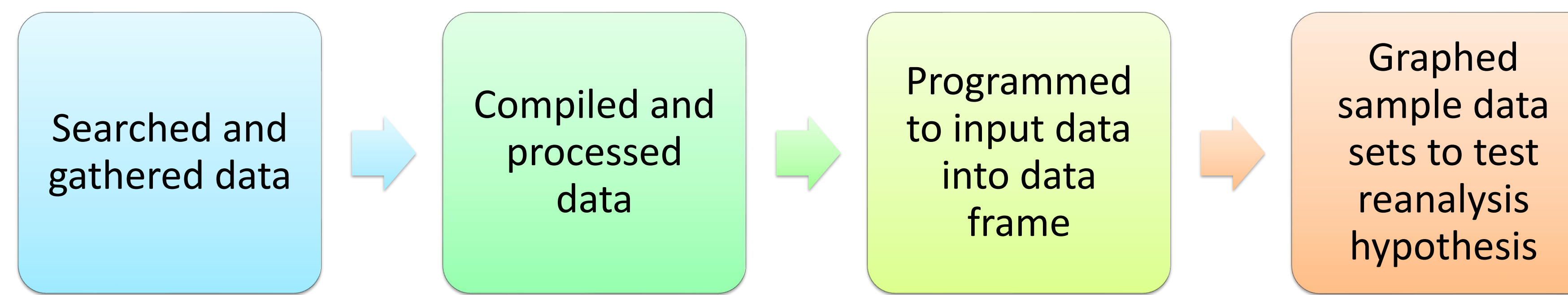
Process

Figure 2. The data process that was followed from gathering all the data, compiling and processing, and finally inputting into a data frame with some examples of using the data frame for future use.
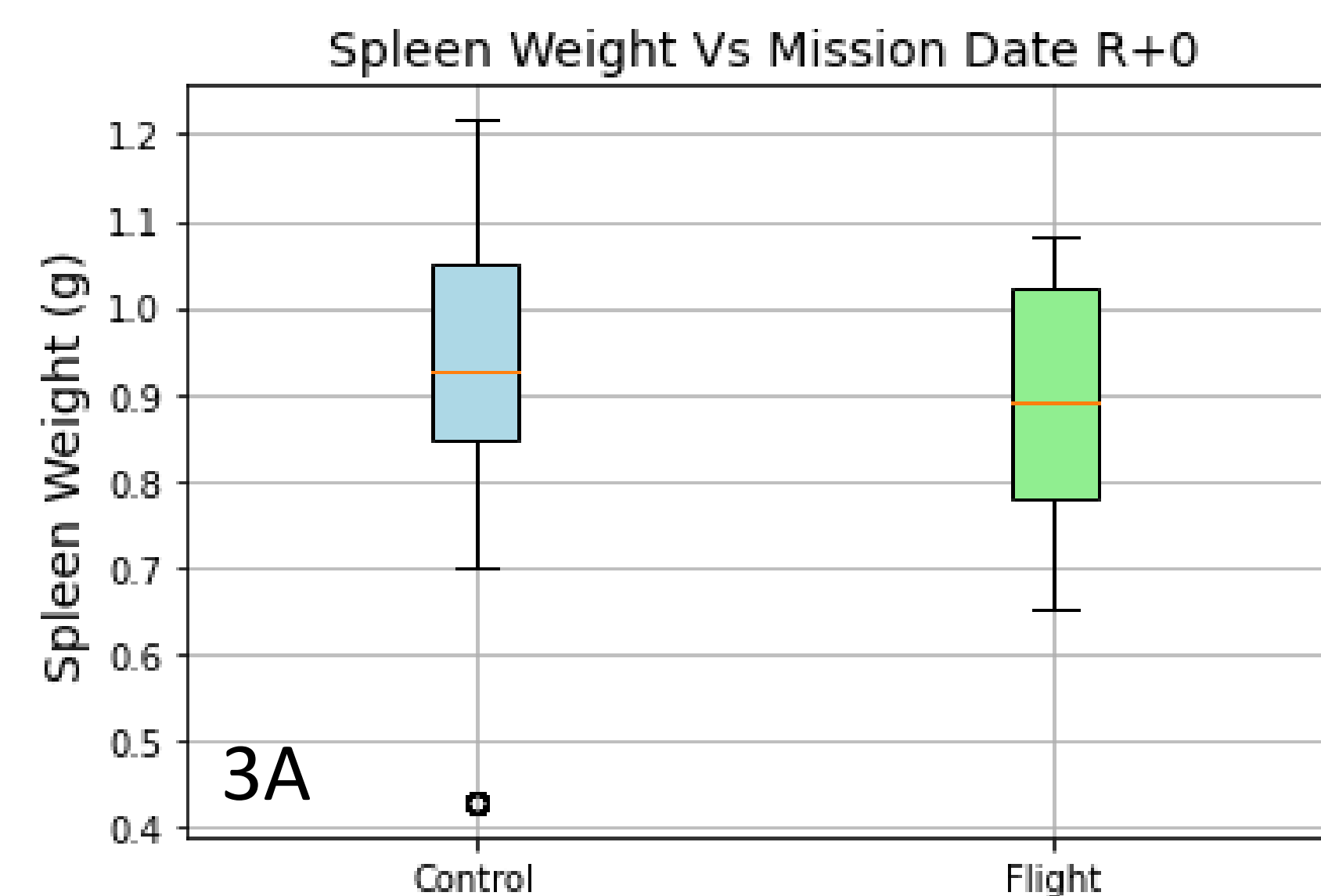

Figure 3A. The spleen weight was recorded R+0 mission date for control and flight rats. There is not a noticeable difference between the control and flight rats.
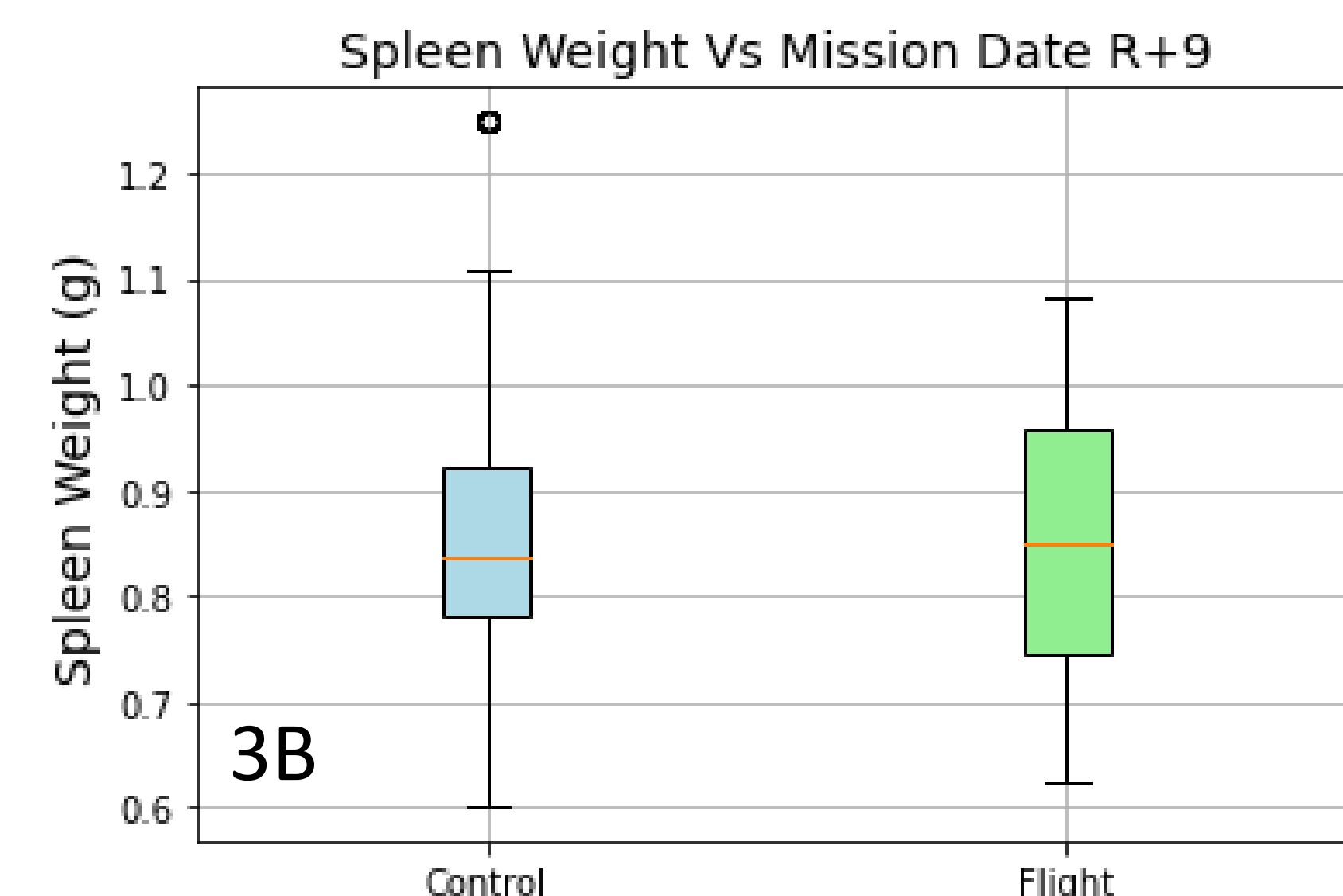

Figure 3B. The spleen weight for both control and flight rats were recorded on mission date R+9. There is not a noticeable difference between the control and flight rats.
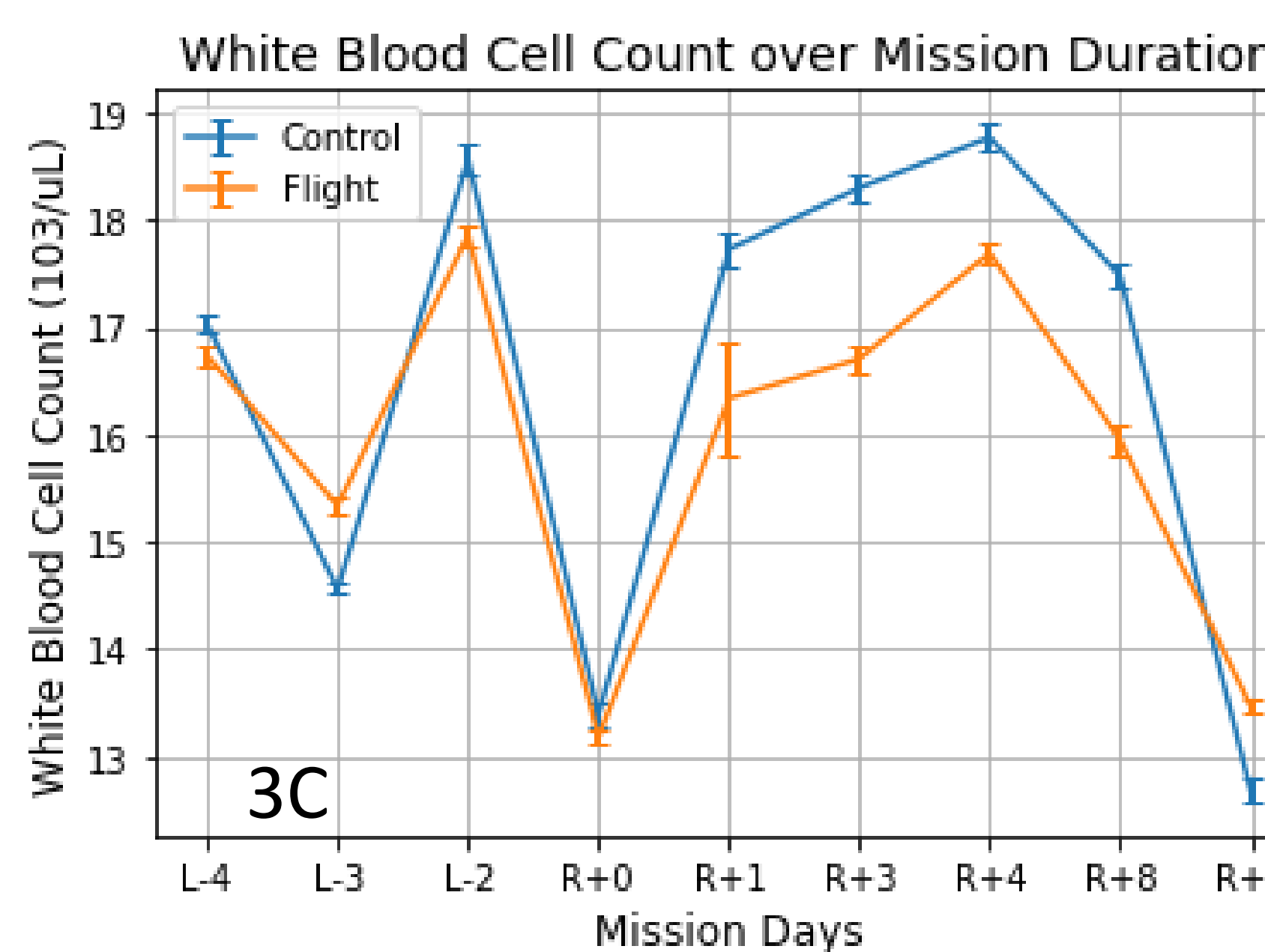

Figure 3C. The white blood cell (WBC) count was recorded for pre-launch (L-) and recovery (R+). In the recovery stage, there is a considerable difference between the control and flight. The error bars were calculated with a standard error of measurement.

POC: (Crystal, Ph.D. student, crf78@cornell.edu)
NASA Space Biosciences SLSTP: https://www.nasa.gov/ames/research/space-life-sciences-training-program
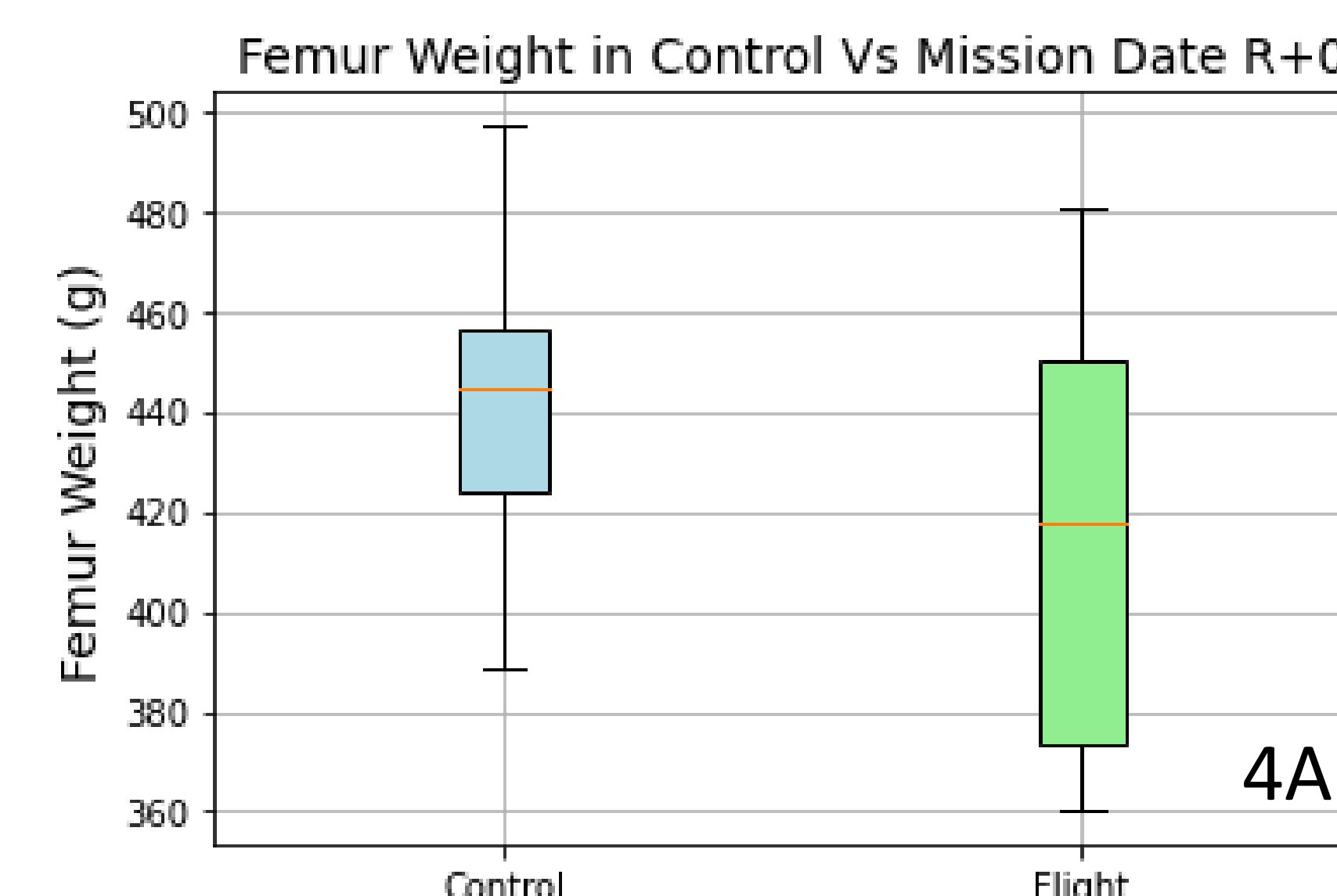NASA Space Biology Program: https://science.nasa.gov/biological-physical/programs/space-biology

Figure 4A. The femur weight of control and flight rats for mission date R+0. The flight median is lower than the control median. This could be due to the muscular atrophy reaction from space.
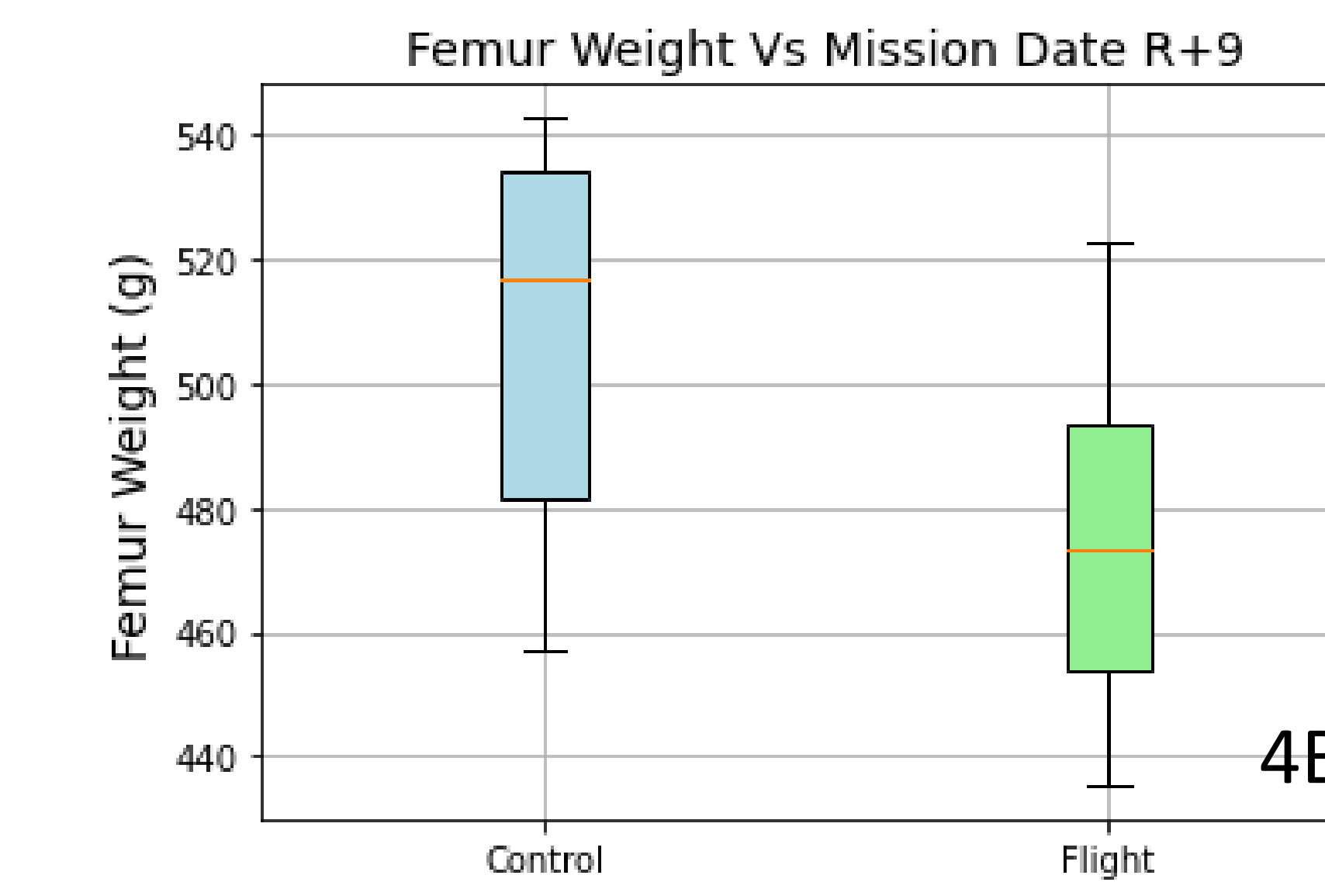

Figure 4B. The femur weight of the control and flight rats for mission date R+9. The flight median is still less than the control median. There is a noticeable larger difference in the R+9 mission date than the R+0 mission date.
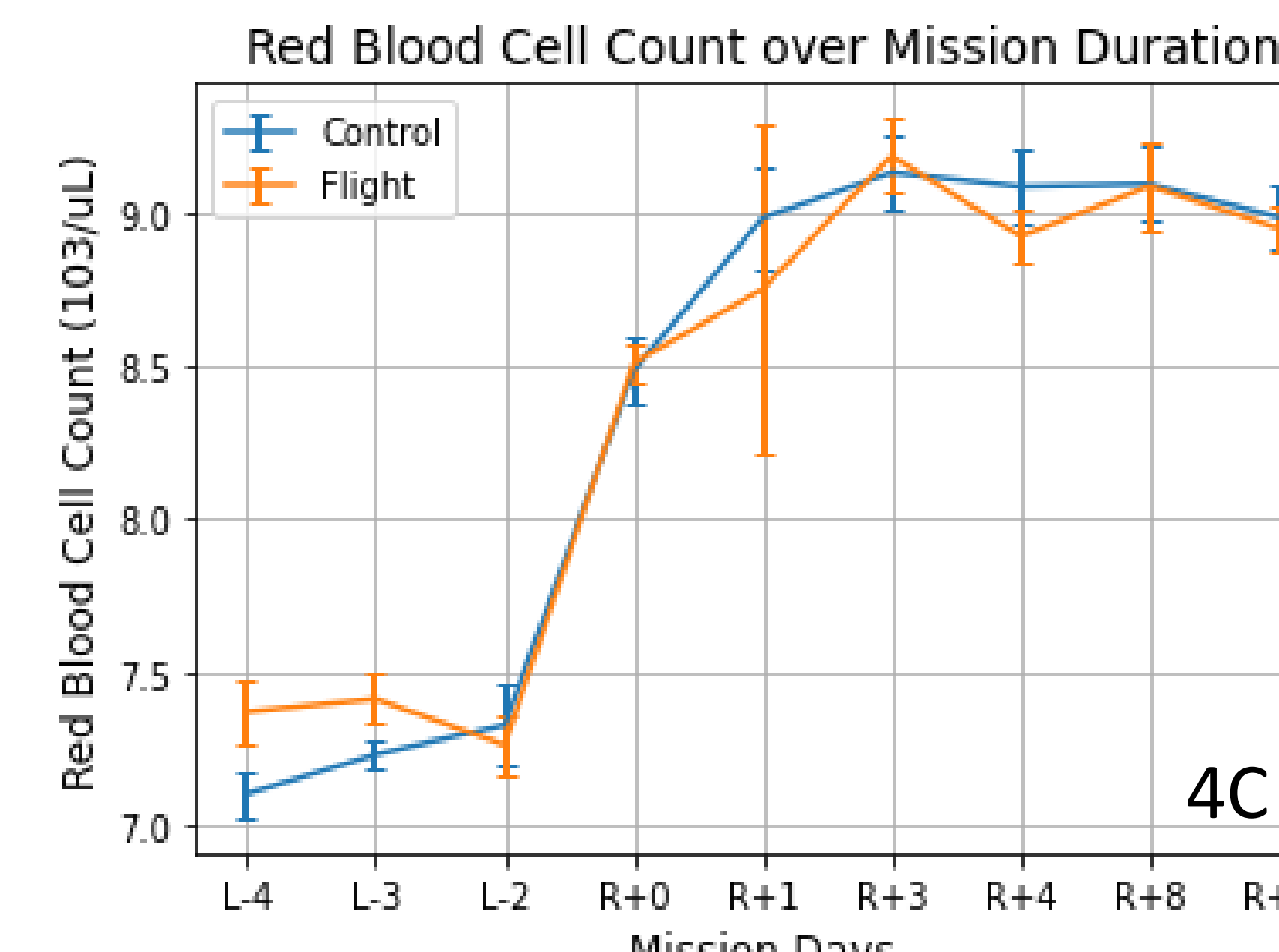

Figure 4C. The red blood cell (RBC) for flight and control rats. There were some discrepancies between the control and flight rats before the mission. Also, there were some unstable RBC after touchdown. Data for the rats were only collected before (L-) and after (R+) the 9-day mission duration. The error bars were calculated with a standard error of measurement.
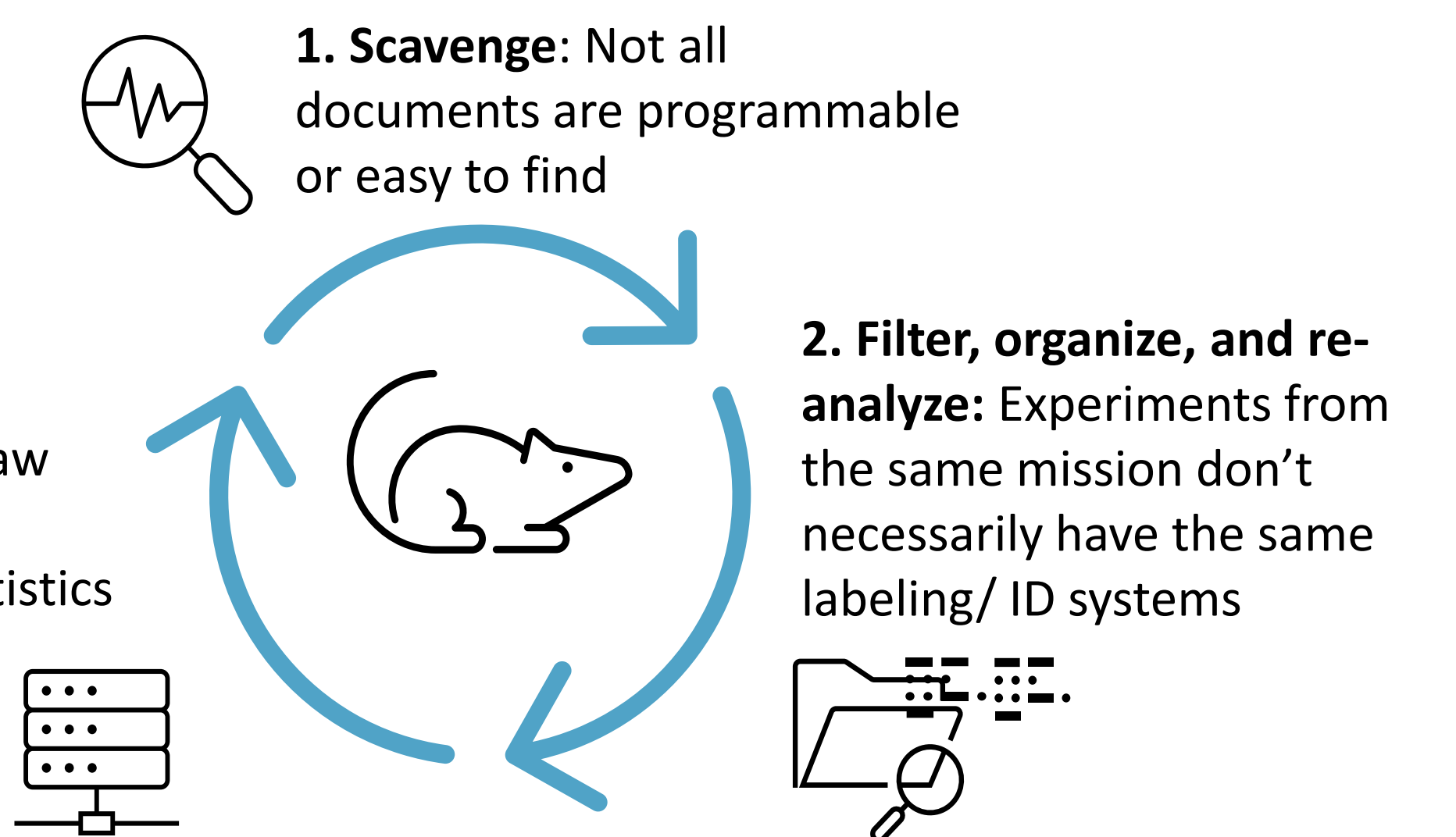
Data Organization

Data and meta data organized in a 13-column data frame:

Column Name	Function
Sample #	Order in the data frame
RID	Rat ID specified data was taken from
Measurement	Actual measurement recorded
Unit	Unit of measurement
Error	If specified
Factor Value	Control, Flight, Delayed Flight Profile Test (DFPT)
House	Animal Enclosure Module (AME), Rodent Animal Holding Facility (RAHF)
Date	Represented in mission date (Launch, Recovery)
Experiment	Experiment title
PI	PI of experiment
Tissue	Tissue measurement was taken from (if specified)
Assay	Assay used to obtain measurement
File Name	Original filename obtained

Table 1. Each column of the data frame with its respective function. The table was made for the user to specify what group of data they would like to compare, that is why specifications like "Factor Value", "House", and "Tissue" were included.

Lessons Learned

1. Scavenge: Not all documents are programmable or easy to find

2. Filter, organize, and re-analyze: Experiments from the same mission don't necessarily have the same labeling/ ID systems

3. Rat Model: Prioritize the raw data, then implement statistics and metadata

Results

Finally, we created a standard data pipeline with our tools and processes. We have created the standard pipeline of processing the data and provided all the documents available for SLS-1. In all, one of our goals was to allow our work to be open to any research to utilize for their own research. Therefore, we uploaded our program and code to Mendeley data, a cloud-based repository website. The DOI can be scanned with this QR code (right).

Future Direction

With 8 datasets (4,800 data points) processed to the SLS-1 data frame, there are still 400 more datasets to add to the data frame. It takes ~7 minutes to add to a dataset to the data frame because of some of the user-inputted aspects of the code. Therefore, it will take about 46 hours and 20 minutes to compute the rest of the datasets for SLS-1.

Acknowledgements

References

[1] Dalton, B. (1991). Spacelab Life Sciences 1 Final Report. NASA Technical Reports Server.

[2] NASA Life Science Data Archive. (2022). LSDA Search Engine. NASA LSDA. Source found in https://lsda.jsc.nasa.gov