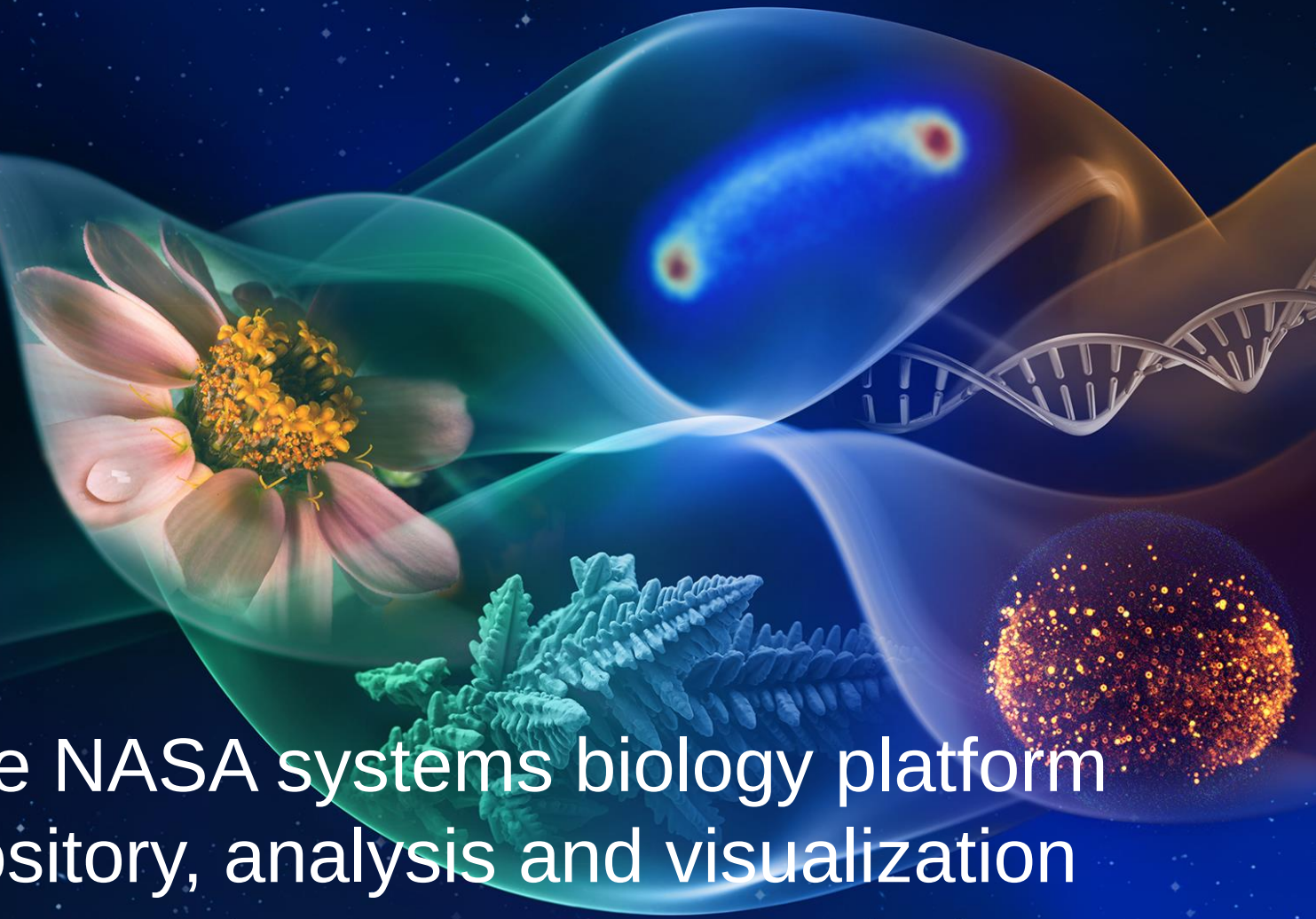
National Aeronautics and Space Administration

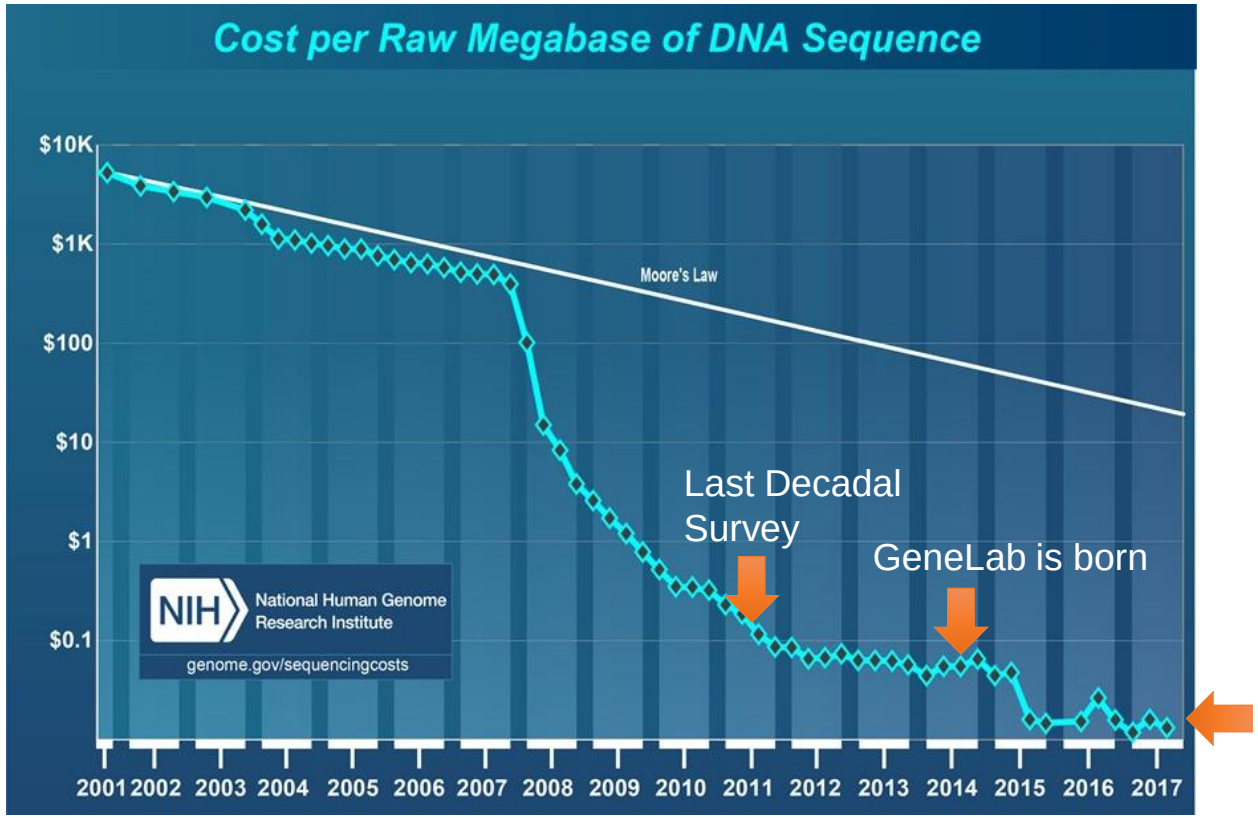
BPS
BIOLOGICAL AND PHYSICAL SCIENCES

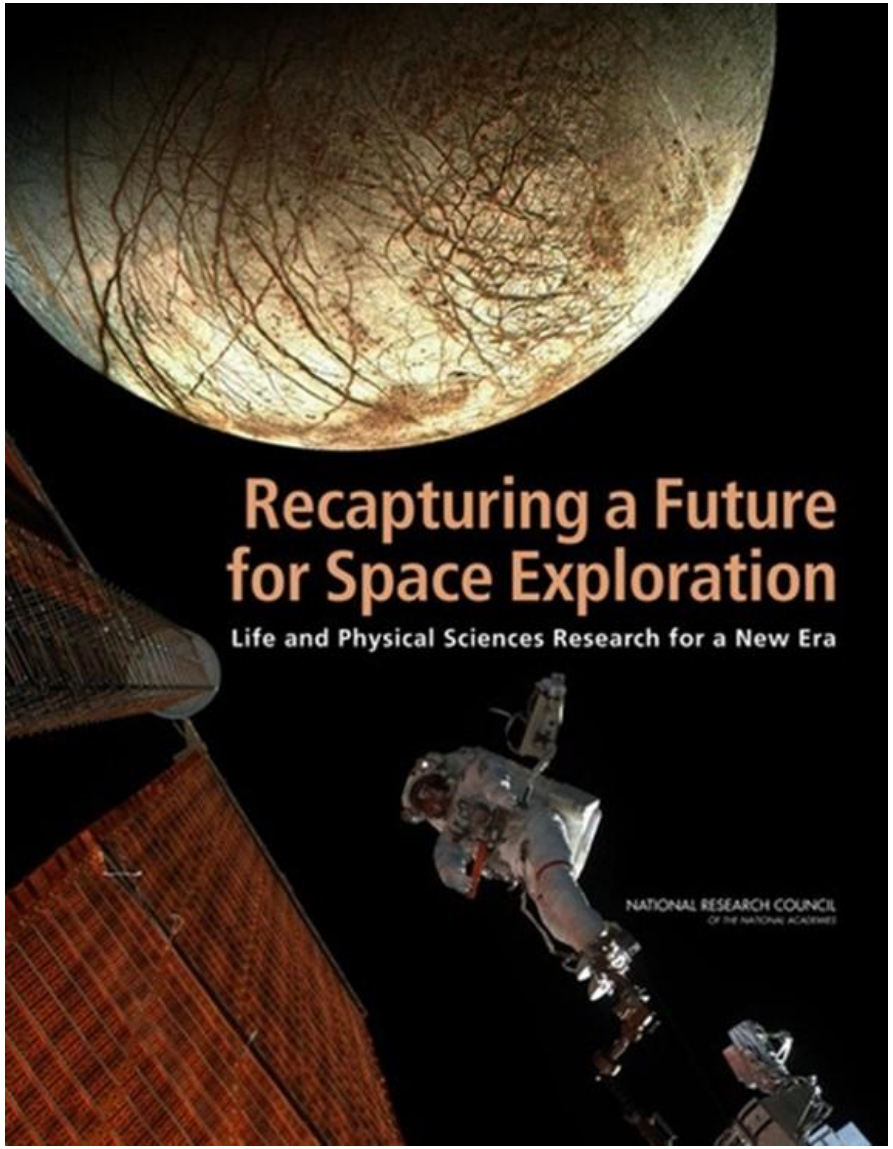


NASA GeneLab: The NASA systems biology platform for spaceomics repository, analysis and visualization

Sylvain Costes and Samrawit Gebre

2011 NRC Decadal Survey and the Sequencing Paradigm Shift

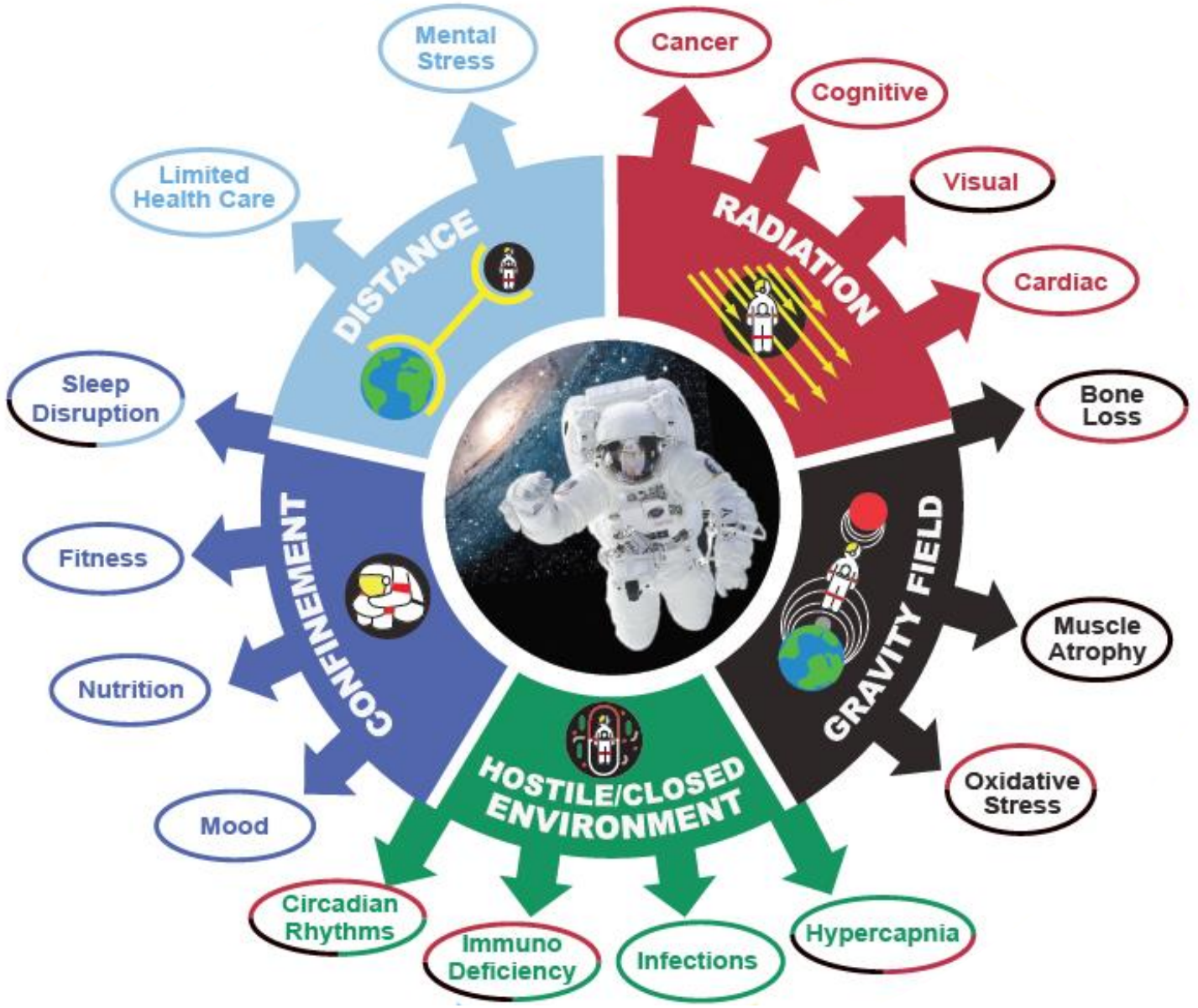




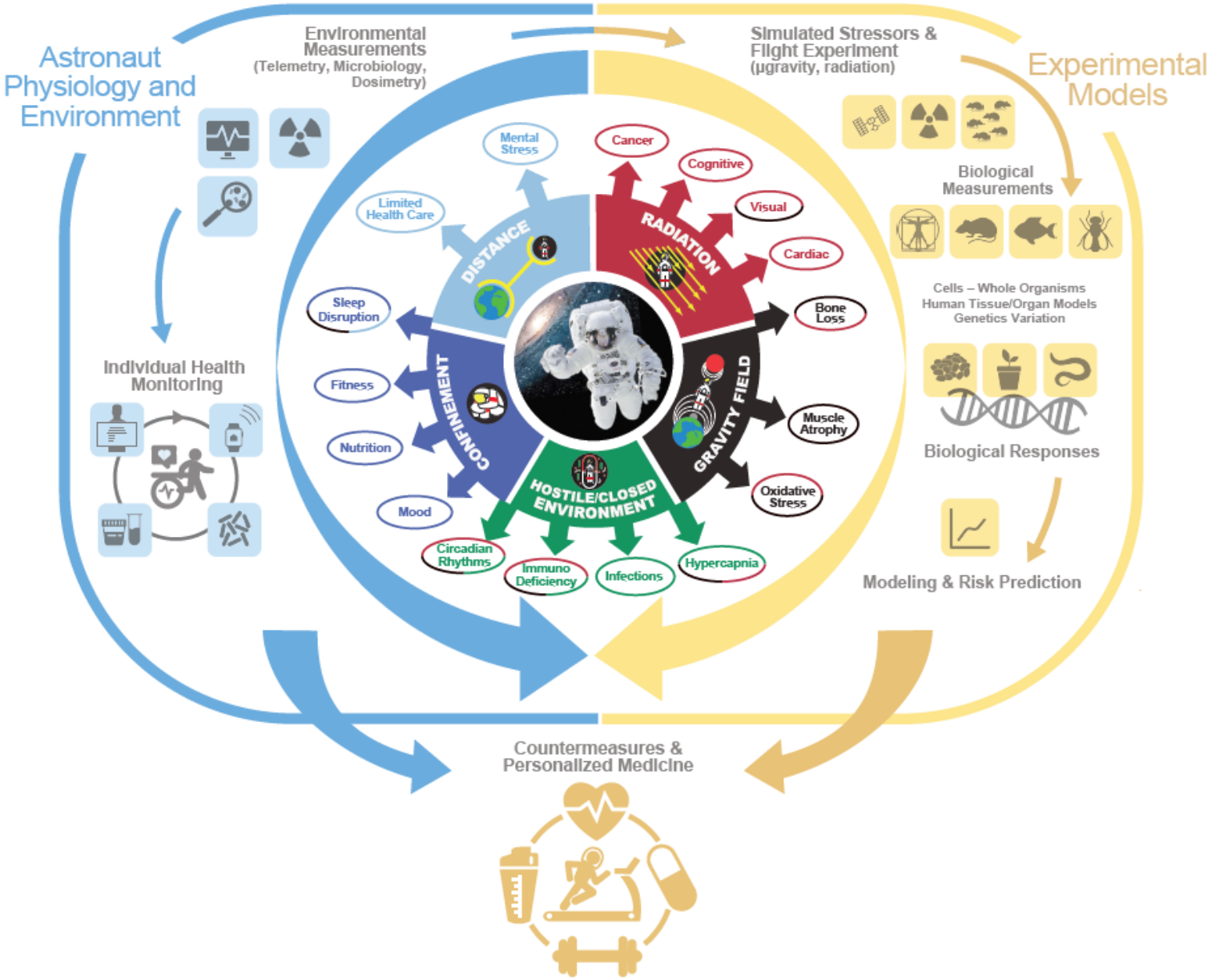
*"…**genomics, transcriptomics, proteomics, and metabolomics** offer an immense opportunity to understand the effects of spaceflight on biological systems…"*

*"…Such techniques generate considerable amounts of **data that can be mined and analyzed** for information by multiple researchers…"*

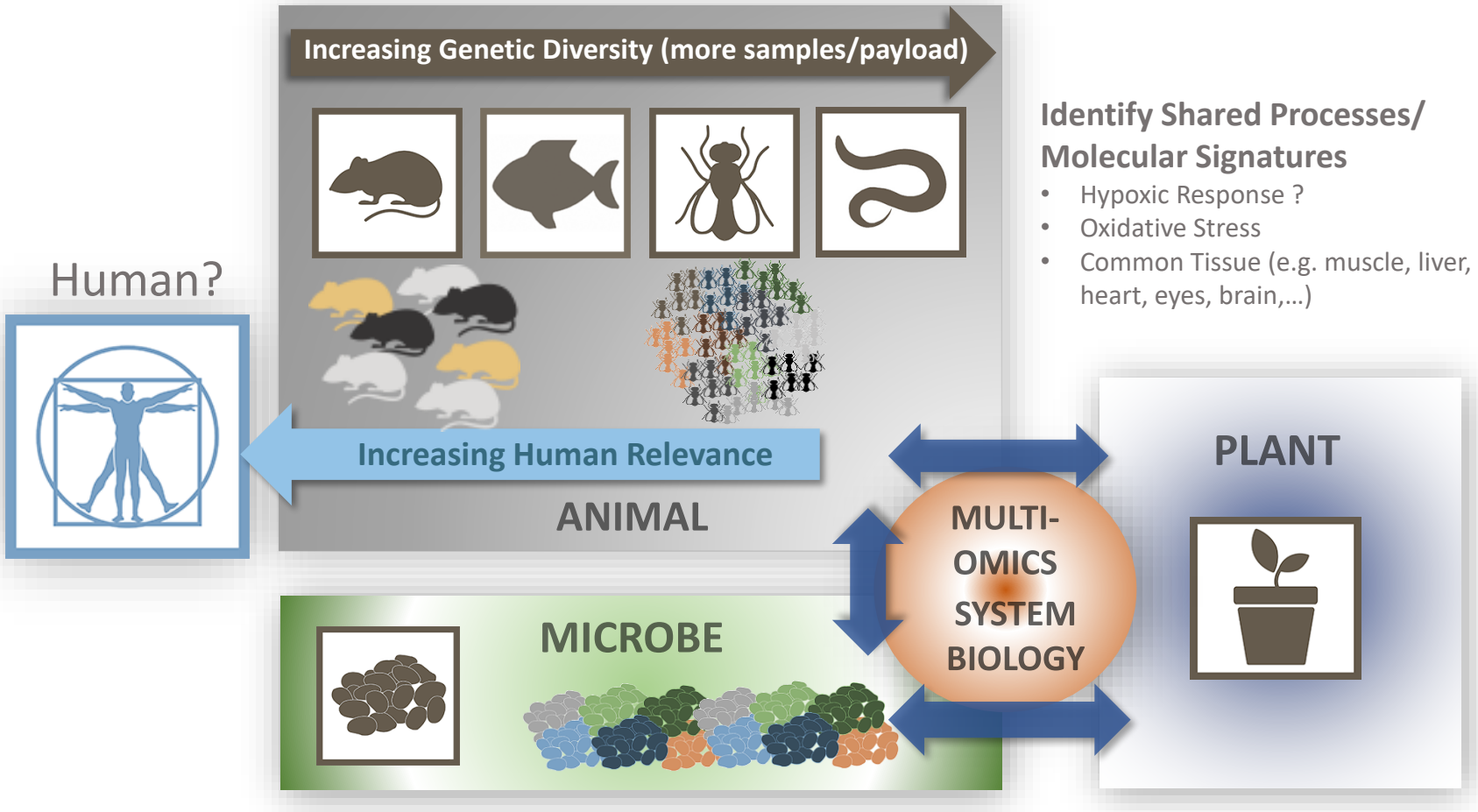
Stresses on Space Travelers



Towards Personalized Space Medicine

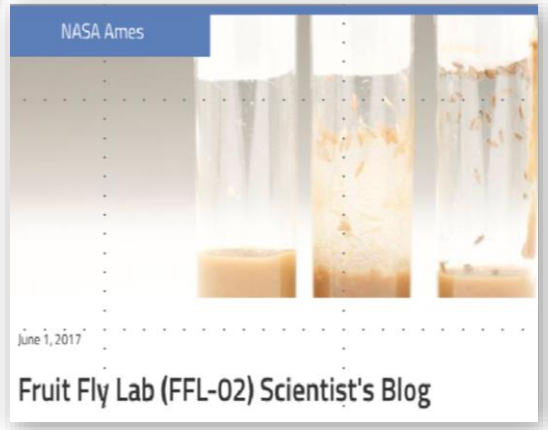


GeneLab ecosystem: maximizing knowledge by bringing experiments together as a system



Identify Shared Processes/ Molecular Signatures

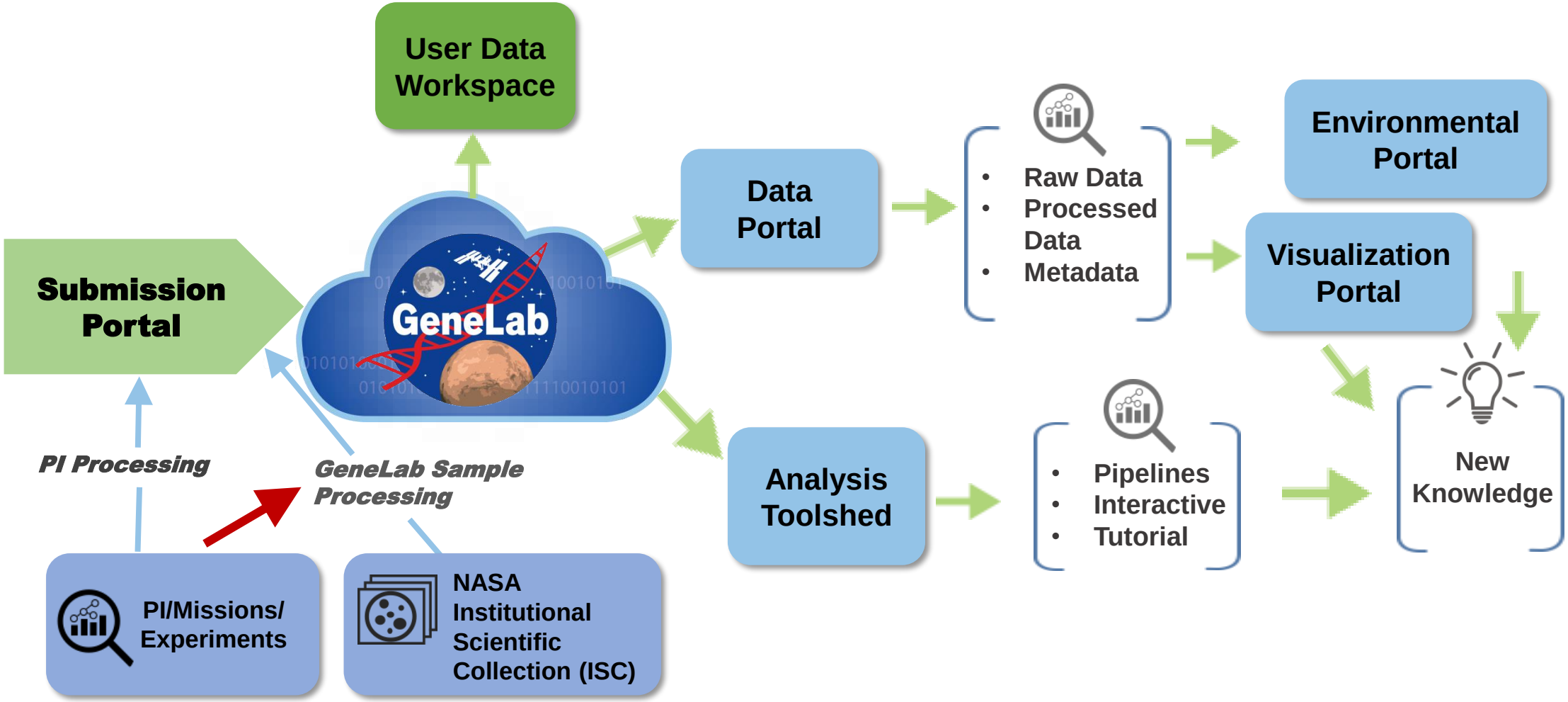
- Hypoxic Response ?
- Oxidative Stress
- Common Tissue (e.g. muscle, liver, heart, eyes, brain,…)



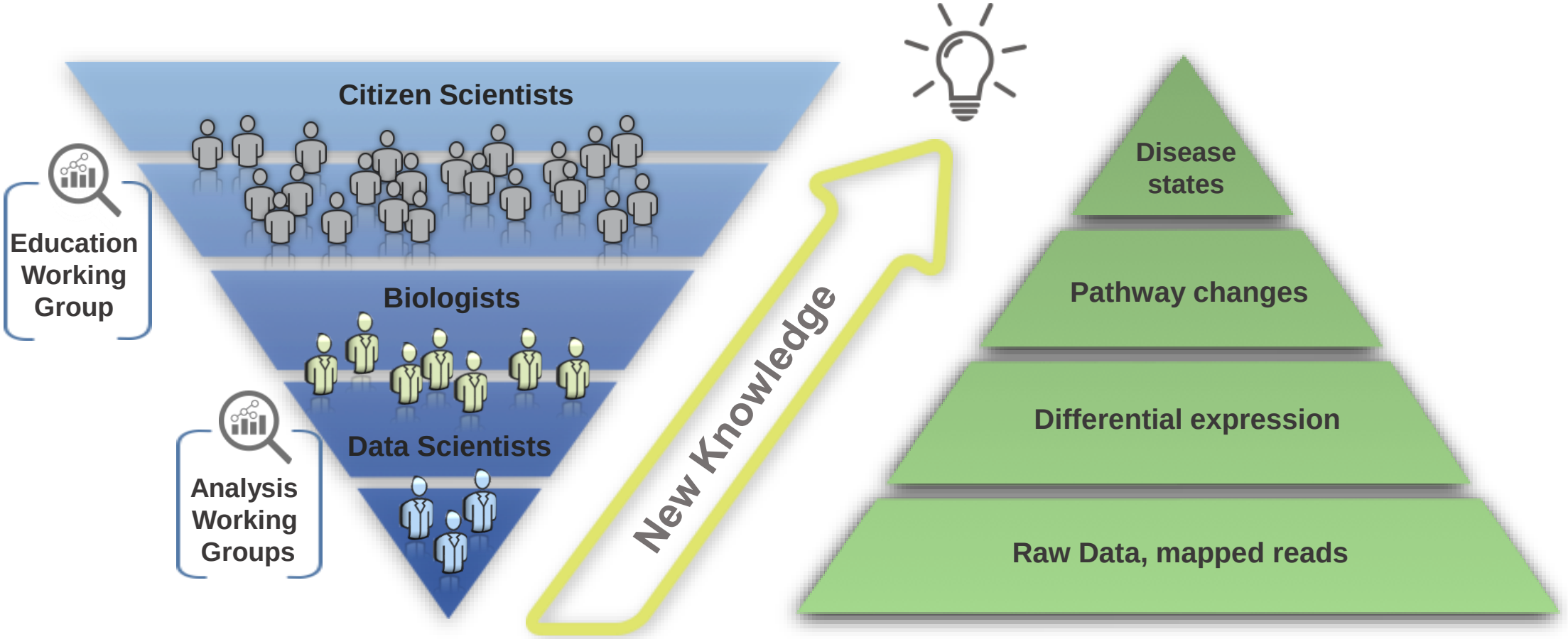
For Spaceflight

- High “n” number – statistically significant data
- Genetically identical animals
- Low resource requirements
- Short life cycle - multiple generations
- Measure response of a whole multicellular animal
- **Flies used as a model for humans for innate immunity, circadian rhythm, oxidative stress, neurobehavior, development, genetics, GWAS, “omics” studies etc**

GeneLab Data System



GeneLab Data Democratization



GeneLab Power Users

- ***GeneLab Analysis Working Groups (AWGs)*** *consist of 120+ scientists from multiple space agencies, international institutions, and industry. Scientists meet monthly with each group to analyze data in the GeneLab repository. Majority of members are non-NASA PI's – many have applied for NASA funding following AWG interactions.*
- ***https://genelab.nasa.gov/awg/join***

Total AWG Members: ~120

Members are now group leads

AWG Members Per Group:

Animal	30
Multi-Omics/System Biology	45
Plants	15
Microbes	17

**Some members are in multiple groups*

- ***Educational Working Work (EWG)*** *consists of educators and scientists spanning across high school and college, focusing on developing content to learn about spaceflight OMICS, promoting the use of GeneLab's database via the repository, and the visualization and analytical portals.*
- ***Contact us for more information.***



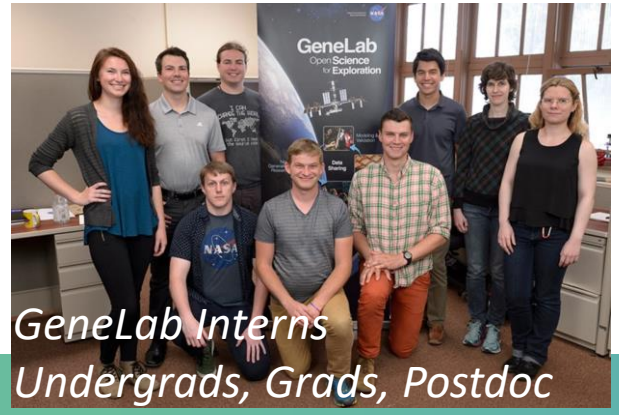
GeneLab for High School (Tutorial + Tools)

SJSU SAN JOSÉ STATE UNIVERSITY

GeneLab included in Bioinformatics curriculum of degree granting university



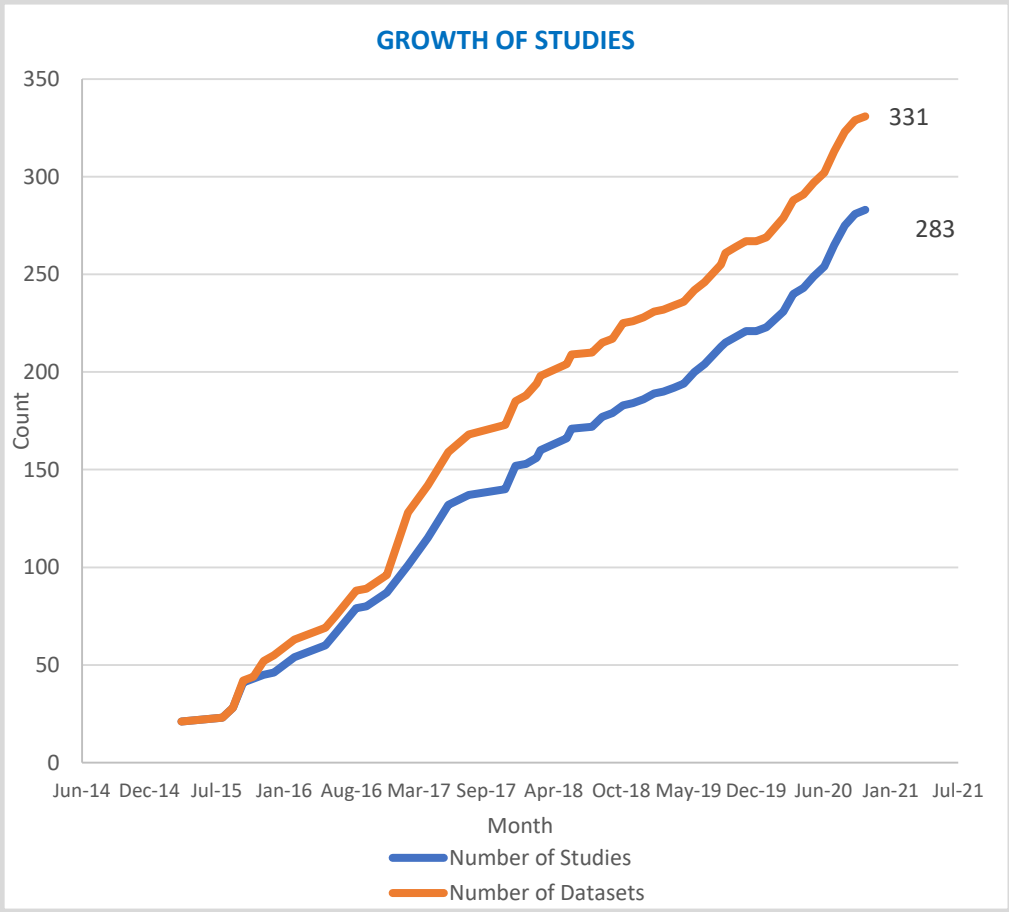
Annual AWG Workshop



GeneLab Interns
Undergrads, Grads, Postdoc

AWG Members represent:

- 48 US Universities
- 4 NASA Centers
- 4 Other Government-funded Organizations
- 3 Institutes or Private Industry
- 3 International Universities



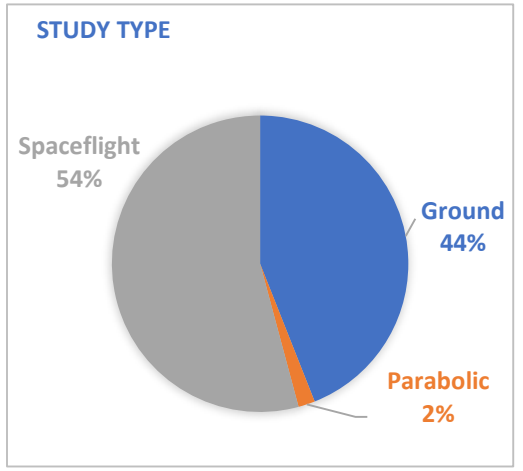
283
Studies

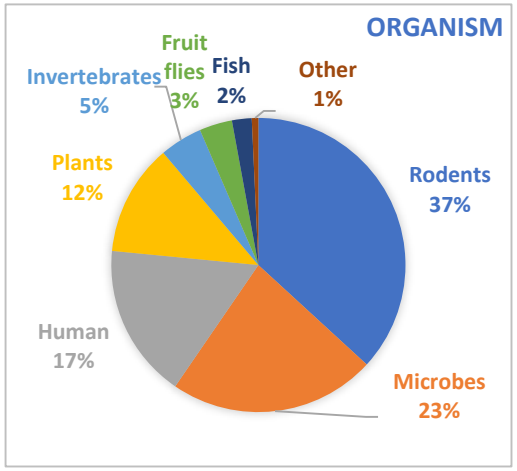
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Datasets

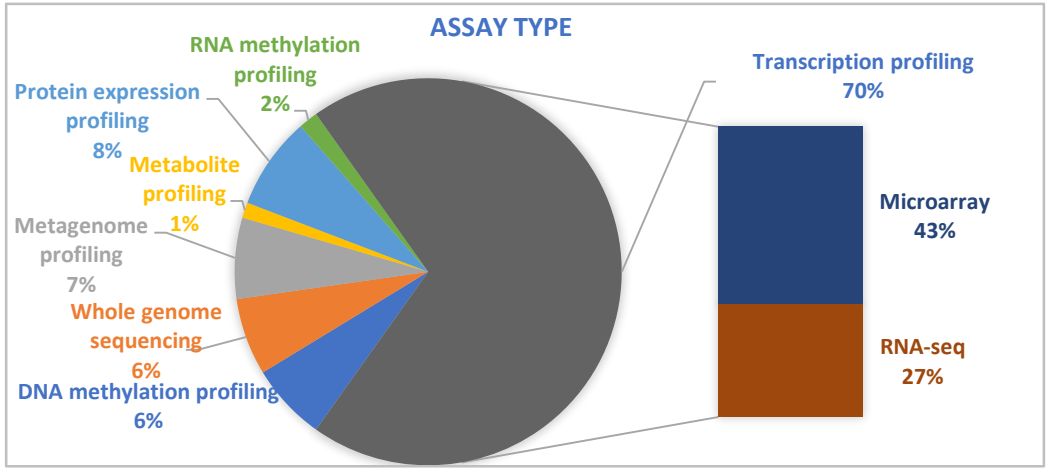
45
Species

>10
Assays

>130TB
Data







Return On Investment – Publication Metrics

47
Original Publication linked to GeneLab

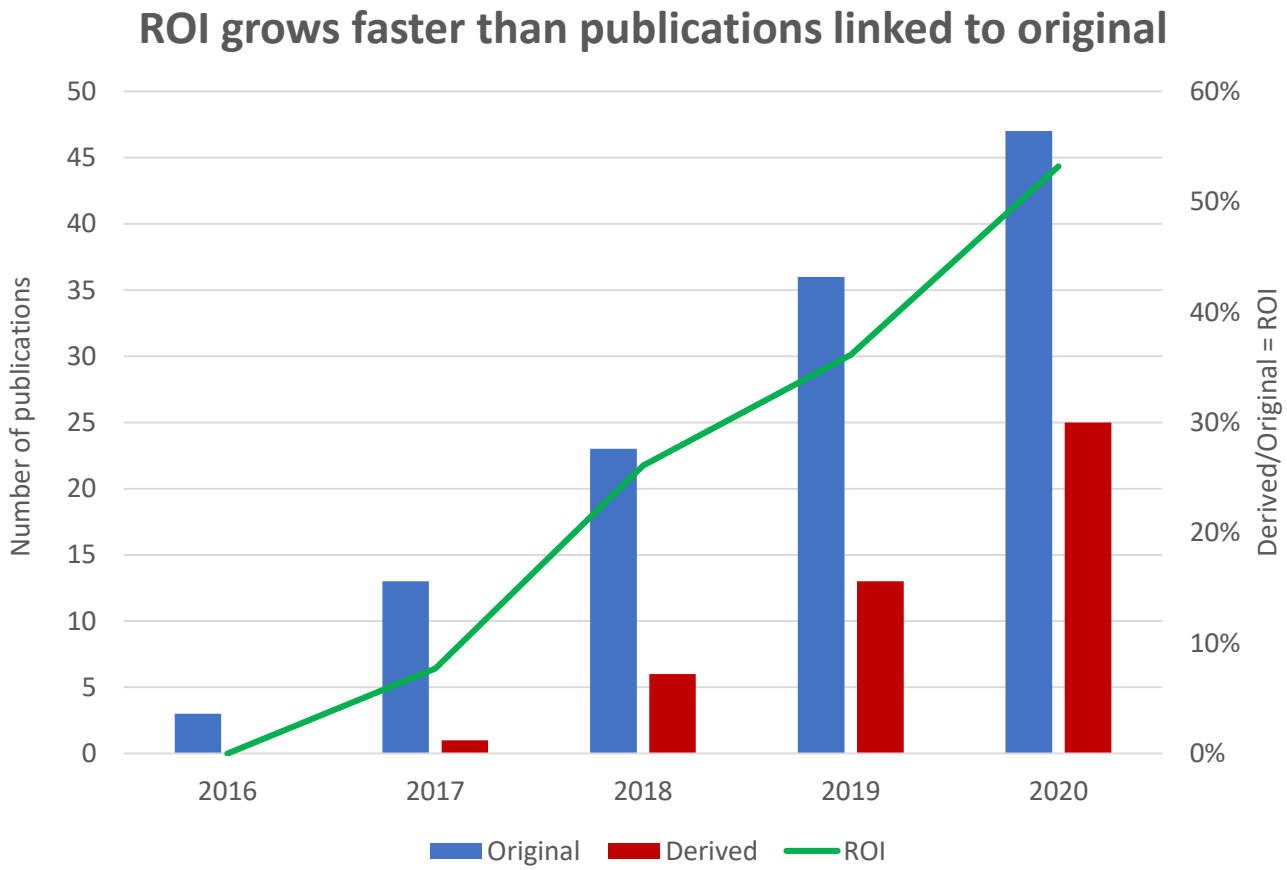
25
Derived Publication linked to GeneLab

60+
Presentations linked to GeneLab

78
Datasets used in derived publications

Original – Publications with original dataset submitted to GeneLab

Derived – Publications using data submitted to GeneLab repository



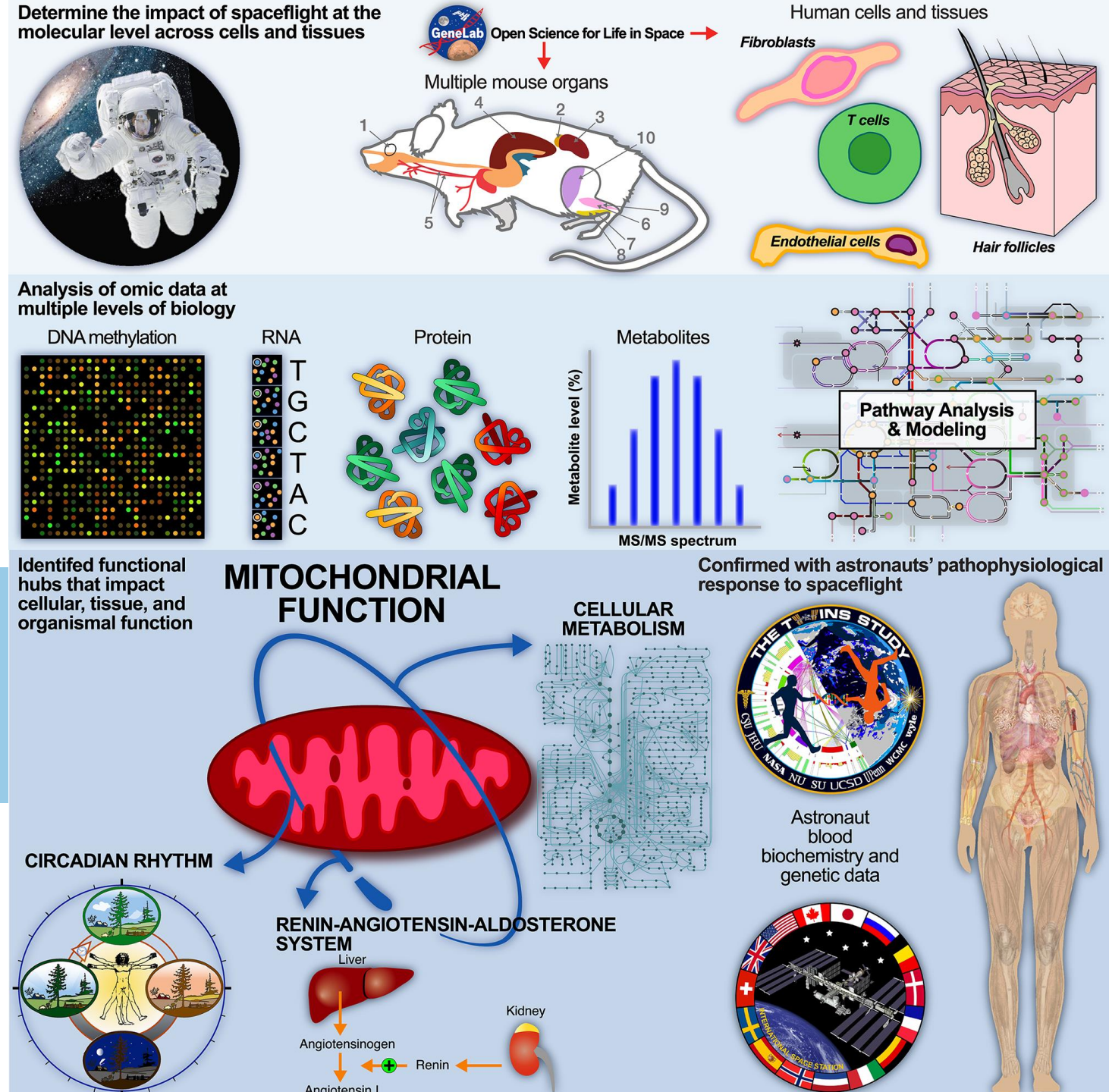
Multi-Omics Analysis using GeneLab database recognizes Mitochondrial Dysfunction as a mediator of spaceflight health risks

da Silviera, W., et al. (2020). "*Comprehensive Multi-Omics Analysis Reveals Mitochondrial Stress as a Central Hub for Spaceflight Biological Impact.*" Cell **In presss**

Regulates:

- **Immune dysregulation**
- **Circadian Rhythm disruption**
- **Lipid accumulation and dysregulation**
- **Olfactory issues**

Largest amount of astronaut data in one paper!



Analysis Working Group (AWG) Members and Others Involved


Gary Hardiman

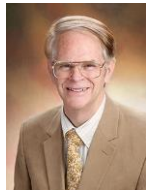

Willian da Silveira

Queen's University Belfast


Deanne Taylor


Hossein Fazelinia


Komal Rathi


Douglas Wallace


Larry Singh


Benjamin Stear


"Jimmy" Mansuck Kim

Children's Hospital of Philadelphia

Perelman School of Medicine University of Pennsylvania

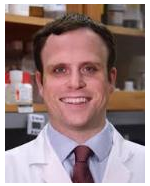

Kathleen Fisch


Brin Rosenthal

University of California, San Diego School of Medicine


Jonathan Schisler

UNC School of Medicine Pharmacology


Chris Mason


Cem Meydan


Jonathan Foox

Cornell University


Evagelia Laiakis

Georgetown University Medical Center


J. Tyson McDonald


Jeffrey Willey

Wake Forest University


Yared Kidane

Scottish Rite Hospital for Children


Susana Zanello

imec

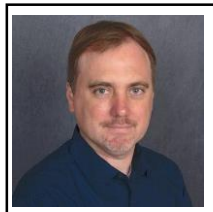

Scott Smith


Brian Crucian


Sara Zwart

NASA

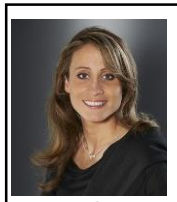
Space Center Houston
Manned Space Flight Education Foundation

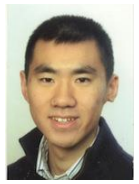

Todd Treangen


Leo Elworth


Nick Sapoval

RICE


Sonja Schrepfer


Dong Wang

UCSF
University of California San Francisco


Stacy Horner


Nandan Gokhale

Duke University School of Medicine


Robert Meller

Morehouse School of Medicine


Helio Costa


Kathryn Grabek

Stanford University


Afshin Beheshti

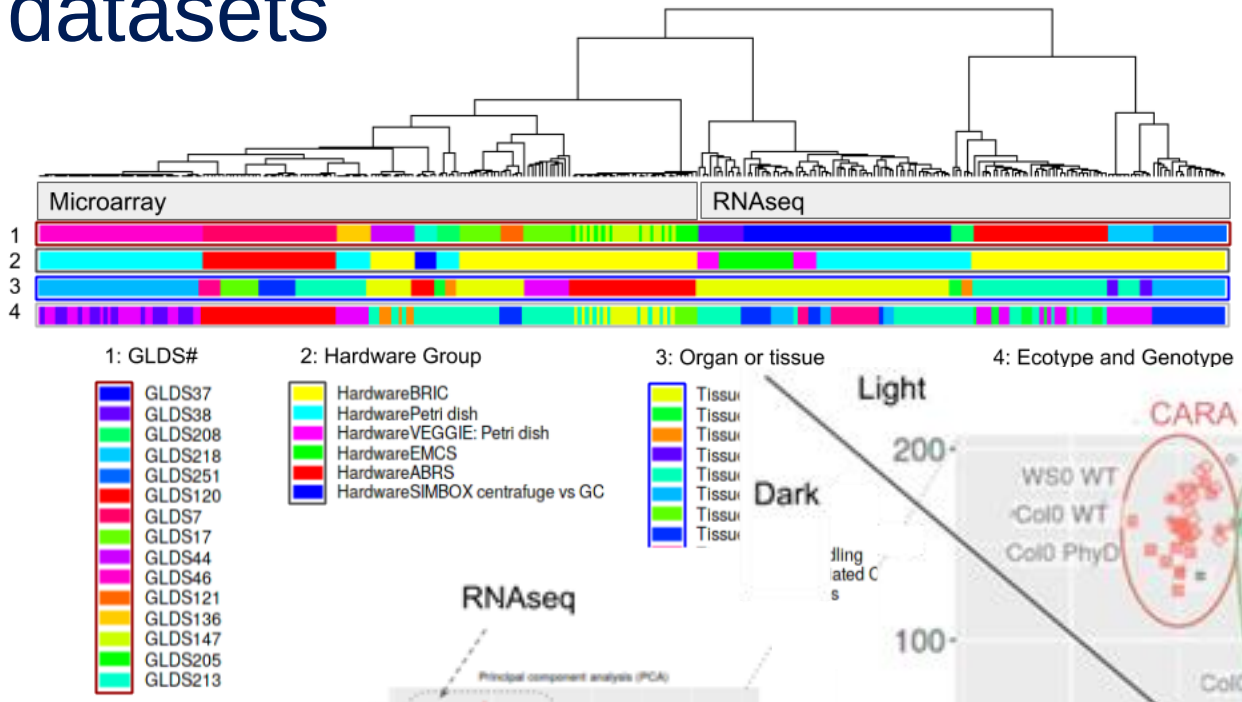

Sylvain Costes

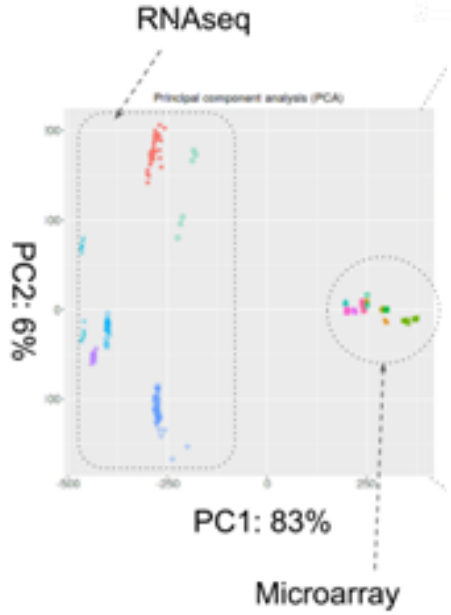
NASA

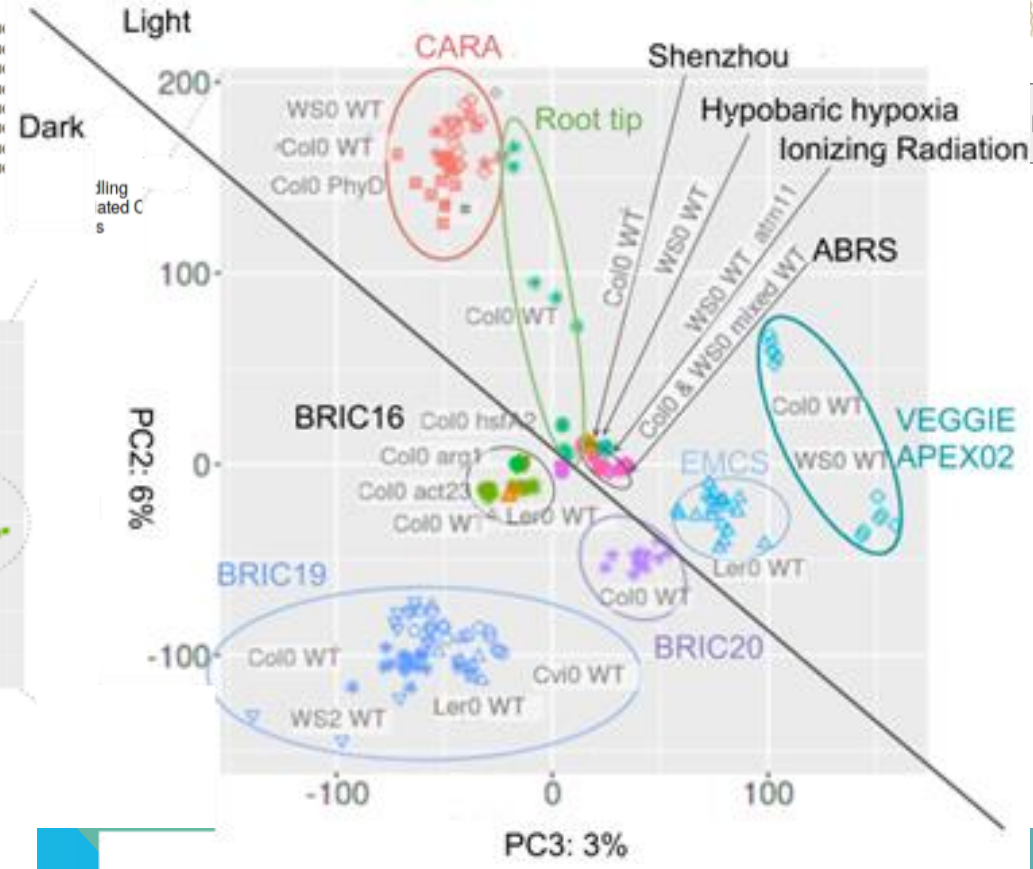
Ames Research Center

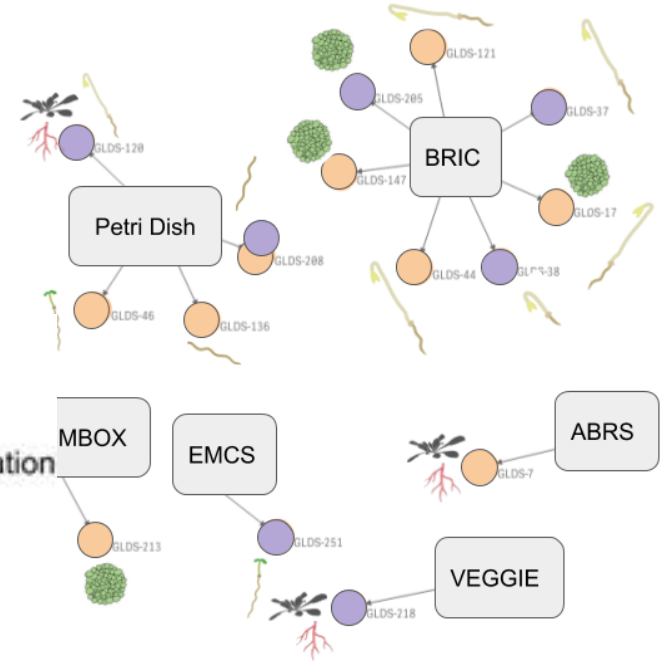
Meta-analysis of space flown *Arabidopsis thaliana* datasets

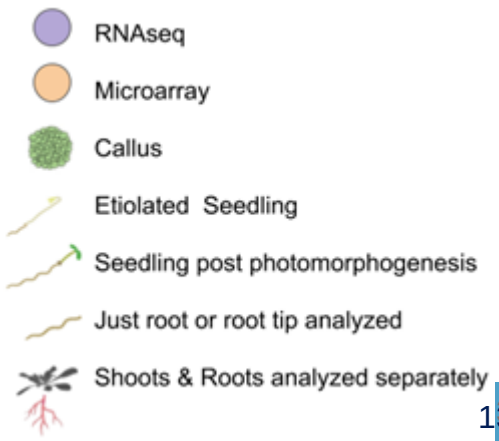
Plant AWG
Manuscript in preparation









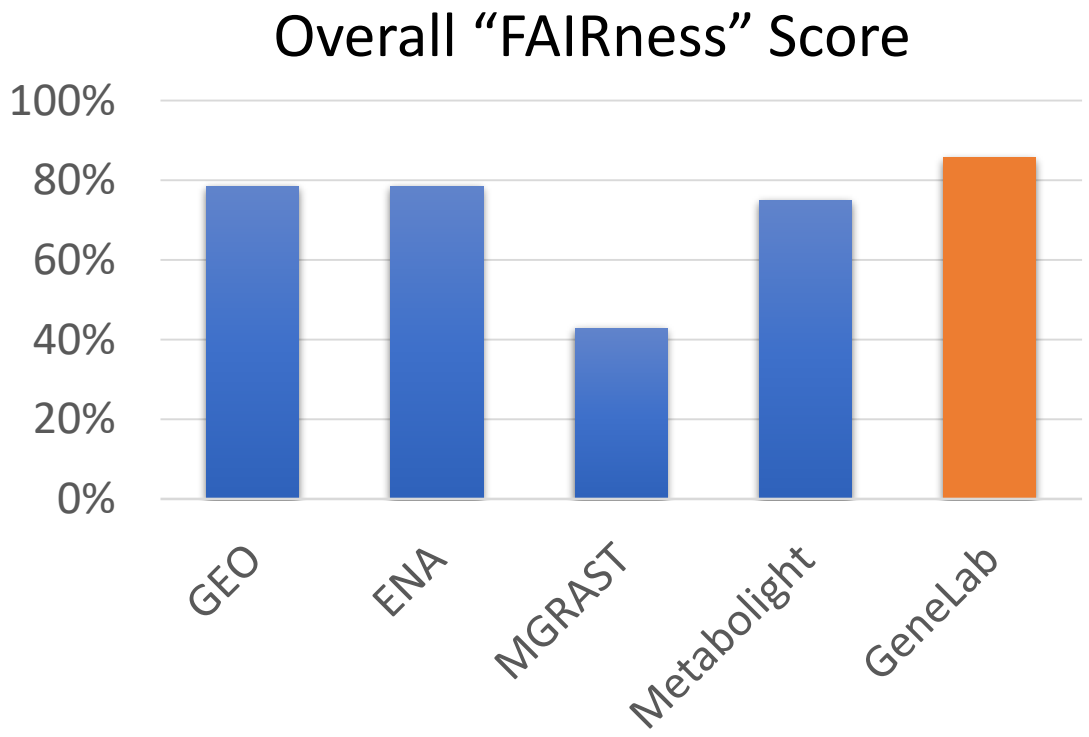


STANDARDS



GeneLab: The most FAIR Life Science Data Repository Systems





- **Findable**
  - Persistent IDs (**GLDS, DOIs**), provide rich metadata – **ISA-TAB**, **NASA's Open data policy, APIs**
- **Accessible**
  - Retrievable by their ID using a standard protocol (**NASA Open data policy, APIs**), metadata remain accessible even when data are no longer available (**DOIs**)
- **Interoperable**
  - Use formal, broadly applicable languages, **JSON-LD**, use standard vocabularies (**ontologies**), qualified references
- **Reusable**
  - Rich, accurate metadata (**ISA-TAB, controlled vocabulary**), clear licenses, provenance, use of community standard (**ontologies**), **DOI-enabled citation in research papers**

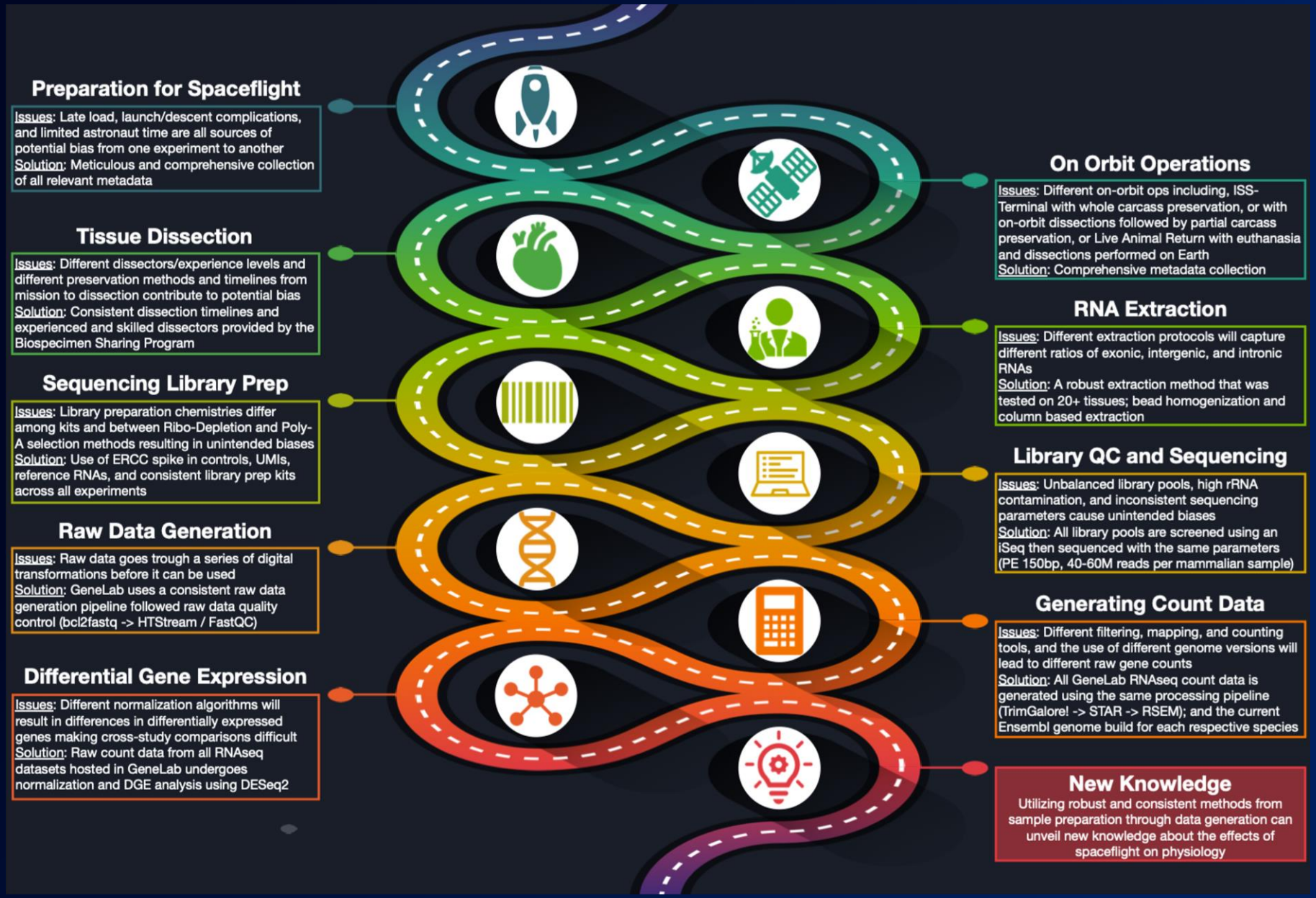
Berrios DC, Beheshti A, Costes SV. FAIRness and Usability for Open-access Omics Data Systems. *AMIA Annu Symp Proc*. 2018;2018:232-241. Published 2018 Dec 5.

Wilkinson, M. D. *et al.* The FAIR Guiding Principles for scientific data management and stewardship. *Sci. Data* 3:160018 doi: 10.1038/sdata.2016.18 (2016).

Adoption of Standards for Space Omics

Methods to control for the confounding variables of biological experiments in space

- Standards for sample processing and sequencing
- Standard pipelines to process the data



International Standards for Space Omics Processing (ISSOP)

The ISSOP is a global consortium comprised of scientists from around to develop, share, and encourage sample processing standardization and metadata normalization of spaceflight omics experiments.

The ISSOP activities focus on:

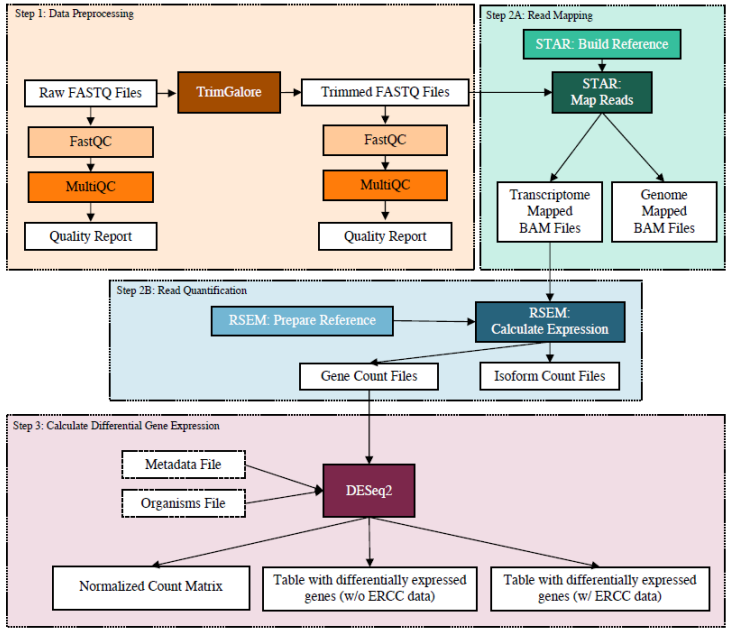
- Publishing standard operating procedures (SOP) for spaceflight omics experiments
- Enhancing information exchange between space biologists at the global level
- Incentivize engagement toward space omics and metadata standardization in the space biology research community

Interested? Visit http://issop.space/

Publication: *A New Era for Space Life Science: International Standards for Space Omics Processing (ISSOP)*

AWG Consensus Pipelines for Data Processing

Standard data processing pipelines for all omics data types reviewed and baselined with our Analysis Working Groups. **Currently, processed data available for microarray, RNA-Seq, and amplicon sequencing data in GeneLab.**



Example workflow for the RNA-Seq Short read consensus pipeline

Publication: *NASA GeneLab RNA-Seq Consensus Pipeline: Standardized Processing of Short-Read RNA-Seq Data*

GeneLab Sequencing Group

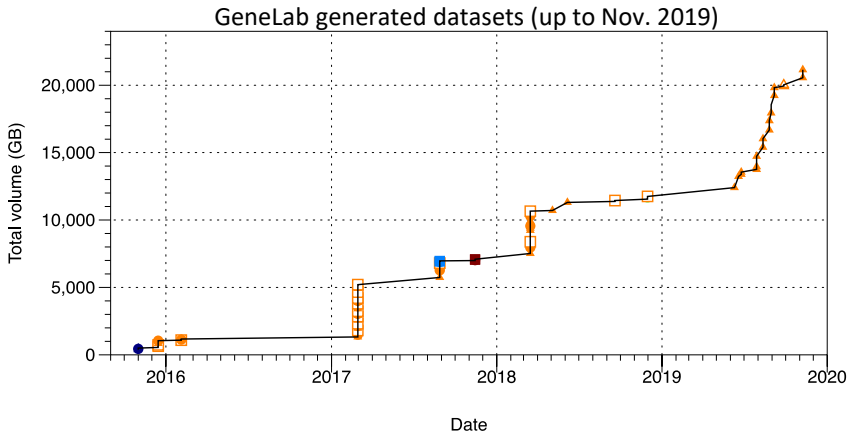


- **State-of-the-art facility with automated equipment and processes**
- **Standard Operating Procedures (SOPs) optimized for spaceflight samples**
- **QC Standards**
  - ERCC spike-ins
  - Universal Reference RNAs
  - QC analysis at each step
- **Set of sequencing standards to maintain consistency across experiments**
- **Provides sequencing and data analysis service for NASA-funded Principal Investigators**

GeneLab Collaborations: ISS National Lab Rodent Research Reference Missions

Background

GeneLab has generated >20 TB of open science data from unused spaceflight tissues.



Shapes: Assay type
Triangle: Transcriptional profiling
Open square: DNA methylation profiling
Closed square: Metabolite profiling
Circle: Protein expression profiling
Diamond: RNA methylation profiling

Color: Species
Dark blue: *Arabidopsis thaliana*
Light blue: *Bacillus subtilis*
Green: *Drosophila melanogaster*
Orange: *Mus musculus*
Red: *Staphylococcus aureus*

Data has been used to generate new knowledge (*e.g.*):

- *Overbey EG, Paul AM, da Silveira WA, et al. Mice Exposed to Combined Chronic Low-Dose Irradiation and Modeled Microgravity Develop Long-Term Neurological Sequelae. Int J Mol Sci. 2019.*
- *Morrison MD, Fajardo-Cavazos P, Nicholson. Comparison of Bacillus subtilis transcriptome profiles from two separate missions to the International Space Station. NPJ Microgravity. 2019.*
- *Beheshti A, Chakravarty K, Fogle H, et al. Multi-omics analysis of multiple missions to space reveal a theme of lipid dysregulation in mouse liver [published correction appears in Sci Rep. 2020.*

Rodent Research Reference Mission-1 (RRRM-1):

Tissue	Groups	Assays
Adrenal glands	FLT, GC, basal, VIV from LAR & ISS-T young and old	Bulk RNA-seq
Brain	Same as above	Spatial and Single-cell RNA-seq, Single-cell ATAC-seq (profiles chromatin accessibility), etc.
Kidney	Same as above	Bulk RNA-seq
Liver	Same as above	Bulk RNA-seq
Dorsal skin	Same as above	Bulk RNA-seq
Spleen	Same as above	Bulk RNA-seq
Head skin with whiskers	Same as above	Bulk RNA-seq

Rodent Research Reference Mission-2 (RRRM-2) scRNA-seq:

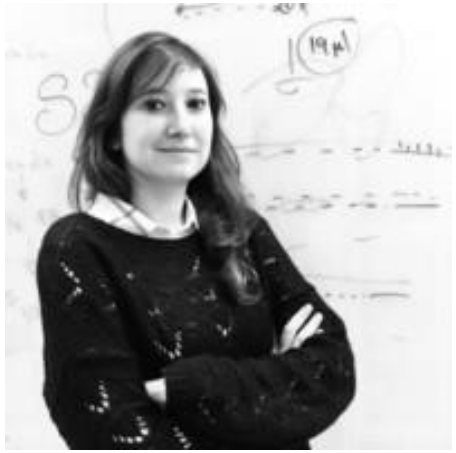
Tissue	Groups
Femur marrow (loaded bone)	n=4 of FLT, GC, LAR young and old
Humerus marrow (”unloaded” bone)	n=4 of FLT, GC, LAR young and old
Splenocytes	n=4 of FLT, GC, LAR young and old
PBMCs (peripheral blood mononuclear cells)	n=4 of FLT, GC, LAR young and old

Rodent Research Reference Mission-2 (RRRM-2) bulk RNA-seq and metagenomics:
Mesenteric lymph nodes, spleen, intestinal epithelia, brain endothelia, dorsal skin, adrenals, liver, kidney, brains, heart, eyes, lung

Single Cell and Spatially Resolved Multiomic Profiling of RR-3 Hearts and Brains

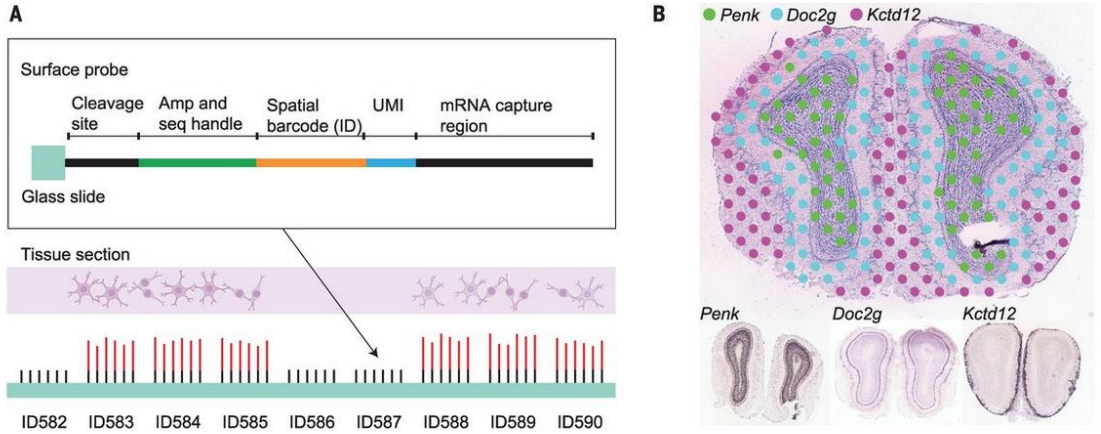
Background

- The human cardiovascular system changes during spaceflight.
- To better understand the molecular underpinning of these changes, hearts from the RR-3 mission are being analyzed using state-of-the-art profiling methods.
- Collaboration with Dr. Stefania Giacomello, SciLifeLab, Sweden



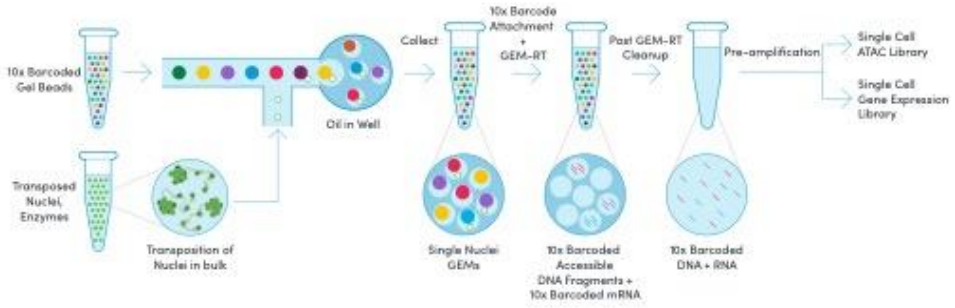
Dr. Stefania Giacomello

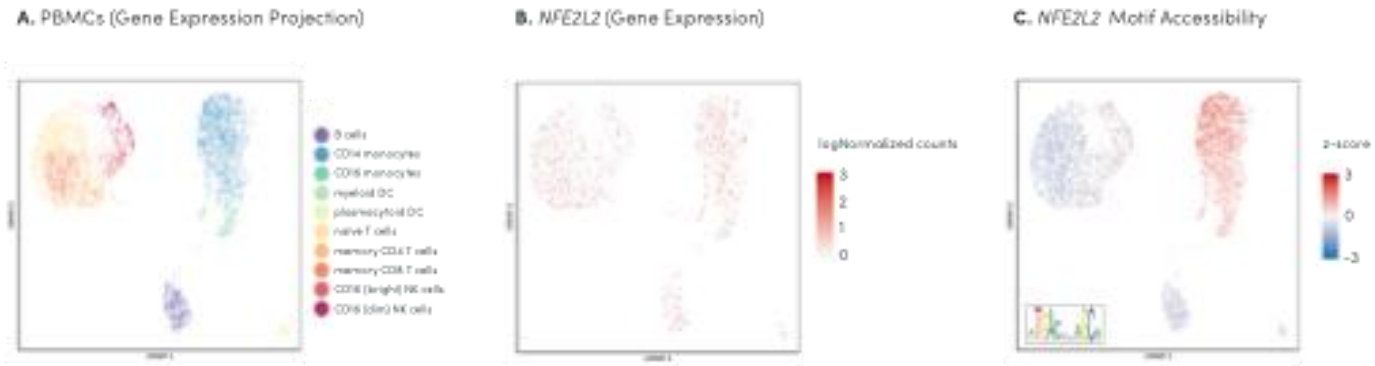
Spatially resolved transcriptomics



Tissue sections are placed over slides printed with a 2D grid barcoded adapters. mRNA diffused to the adapters for tagging. Sequencing of barcodes and mRNA generates spatially resolved transcriptional profiles. (Ståhl PL, Salmén F, Vickovic S, et al. Visualization and analysis of gene expression in tissue sections by spatial transcriptomics. Science. 2016).

Single cell profiling of gene expression and chromatin accessibility





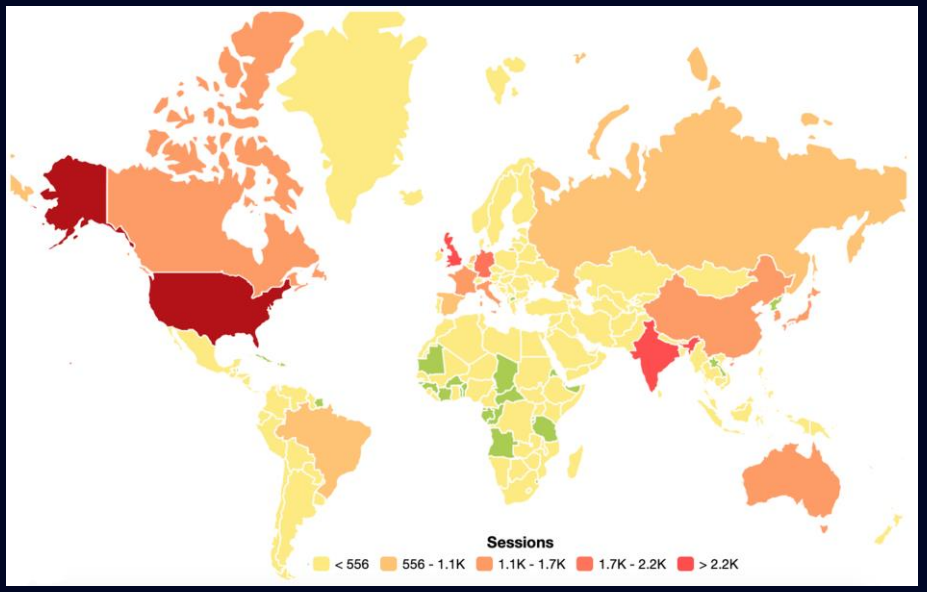
Single nuclei are capture within droplets to allow single-cell profiling of gene expression and chromatin accessibility. Here, the transcription factor NFE2L2 is expressed widely (B) in many cell types (A) but its motif is only accessible in a sub-set of cells (C) (Courtesy 10x Genomics).

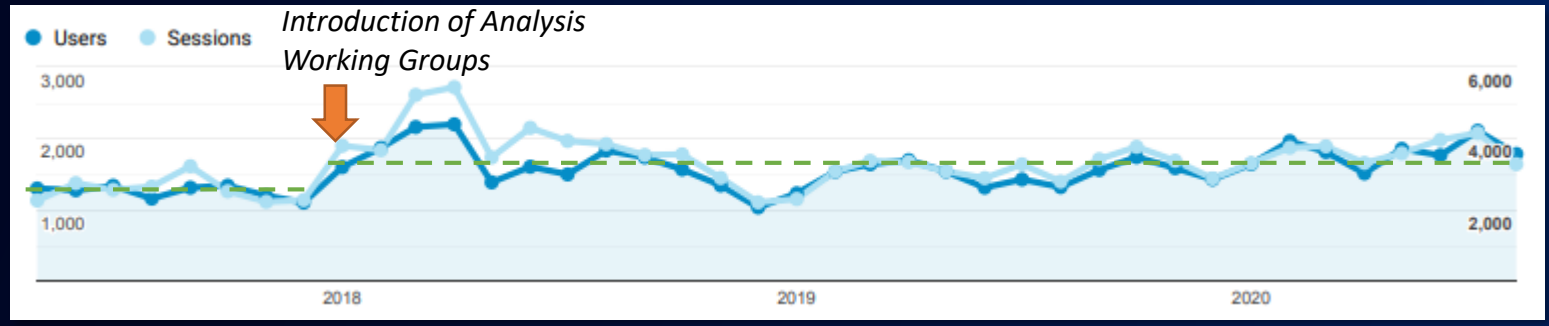
GeneLab User Growth

Usage: May 2017- Sept 2020

3327 Avg Monthly Sessions

1558 Avg Monthly Users





- **Downloads: Dec 2018 - Sept 2020**

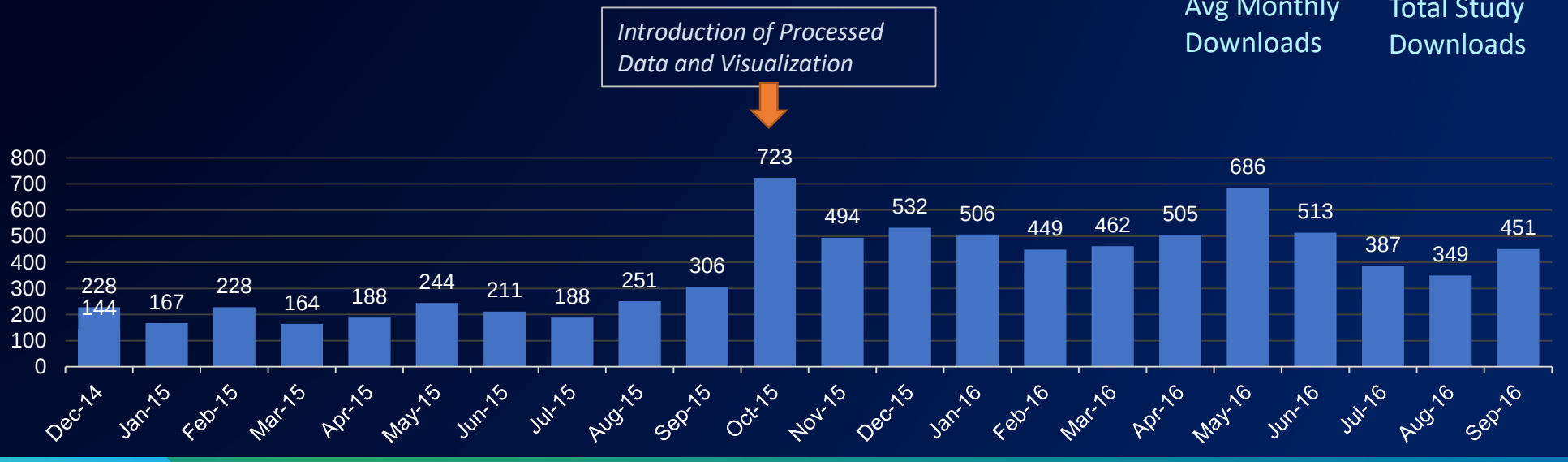
represents downloads per GLDS Study, not per file

360 Avg Monthly Downloads

7189 Total Study Downloads

Top 10 Countries – Sessions

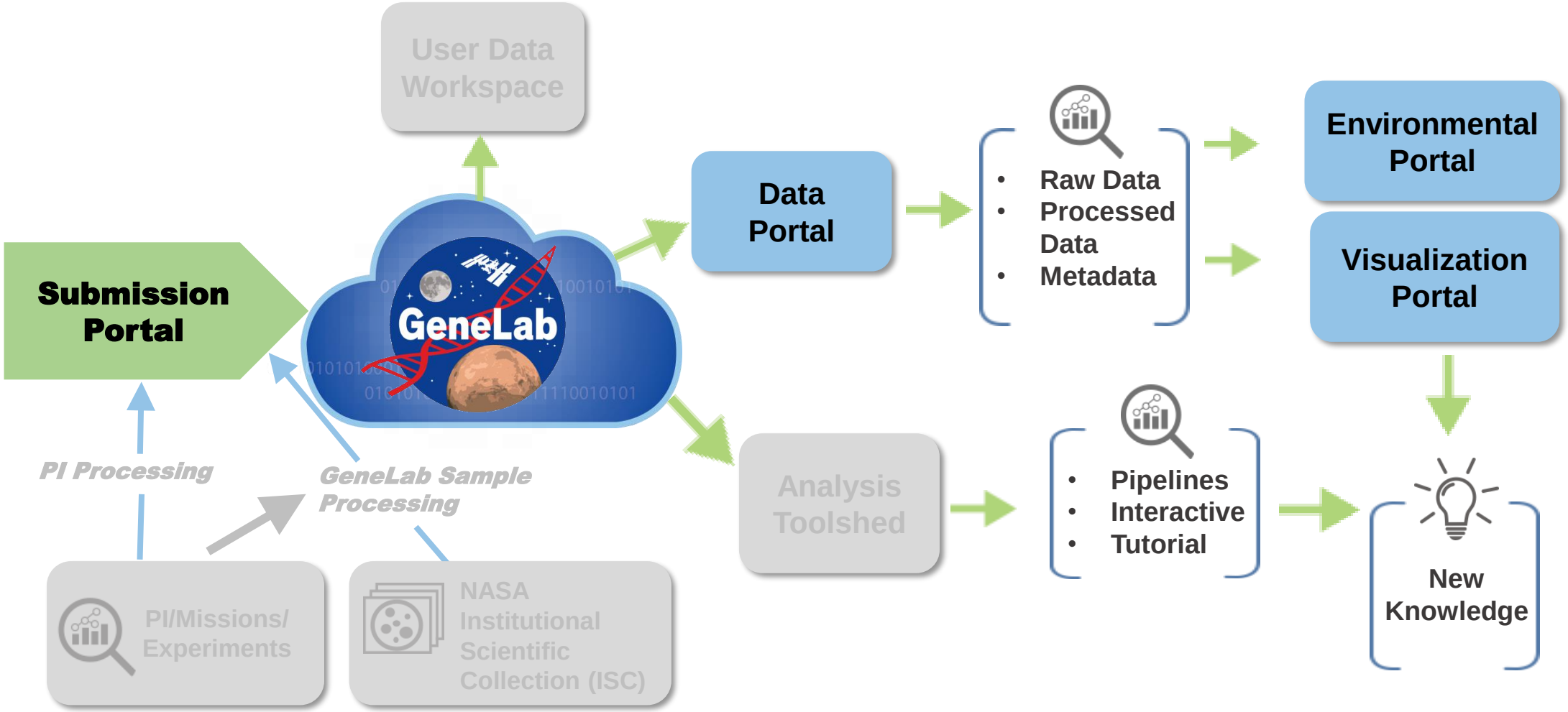
1. United States
2. India
3. United Kingdom
4. Germany
5. Canada
6. France
7. South Korea
8. Japan
9. China
10. Australia



DEMO



GeneLab Data Democratization



https://genelab.nasa.gov/

GeneLab Open Science for Life in Space

Home | About | Data & Tools | Research & Resources | Working Groups | Help

Keywords



Welcome to NASA GeneLab - the first comprehensive space-related omics database; users can upload, download, share, store, and analyze spaceflight and spaceflight-relevant data from experiments using model organisms.

Data Repository
Search and upload spaceflight datasets

Analyze Data
Perform large-scale analysis of biological omics data

Environmental Data
Radiation data collected during experiments conducted in space

Collaborative Workspace
Share, organize and store files

Submit Data
Have space-relevant data to submit to GeneLab?

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GLDS-329

Transcription profiling of atm mutant, adm mutant and wild type whole plants and roots of Arabidopsis after gamma ray irradiation in a time series

Organisms	Factors	Assay Types	Release Date	Description
Arabidopsis thaliana	Ionizing Radiation Genotype Organism Part Time	transcription profiling	30-Oct-2006	Whole seedlings of wild type (4d) and atm mutants (4d) have been analyzed after a gamma ray irradiation of 0.75h, 1.5h, 3h & 5h (time course). Roots of wt (4d), atm (3d) and atr (4d) mutants have been...



GLDS-326

Gene-metabolite network linked to inhibited bioenergetics in association with spaceflight induced loss of quadriceps muscle

Organisms	Factors	Assay Types	Release Date	Description
Mus musculus	Spaceflight	transcription profiling	23-Feb-2020	Prolonged residence of mice in spaceflight is a scientifically robust and ethically ratified model of muscle atrophy caused by continued unloading. Under the Rodent Research Program of NASA, we assaye...



GLDS-322

Comparative RNA-Seq transcriptome analyses reveal dynamic time dependent effects of 56Fe, 16O, and 28Si irradiation on the induction of murine hepatocellular carcinoma

Organisms	Factors	Assay Types	Release Date	Description
Mus musculus	Ionizing Radiation Time	transcription profiling	27-Aug-2020	One of the health risks posed to astronauts during deep space flights is exposure to high charge, high-energy (HZE) ions (Z>13) which can lead to induction of hepatocellular carcinoma (HCC). We perfor...

mouse AND liver x

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GLDS-329

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mouse AND liver x

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1

STS-135 Liver Metabolomics

https://genelab-data.ndc.nasa.gov/genelab/accession/GLDS-108



Mice were flown onboard STS-135 and returned to Earth for analysis. Livers were collected within 3-4 hours of landing and snap frozen in liquid nitrogen. Samples were shipped to Metabolon Inc. for analysis.

Organism: Mus musculus **Factor:** Microgravity Absorbe… **Assay Type:** metabolite profiling **Accession:** GLDS-108 **PI/Contact:** Michael Pecaut, Xiao …

Release/Publication Date: 28-Apr-2017

Rodent Research-3-CASIS: Mouse liver transcriptomic proteomic and epigenomic data

https://genelab-data.ndc.nasa.gov/genelab/accession/GLDS-137

mouse AND liver x

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Search results for: **mouse AND liver** using filter(s):

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1 2 3 4 Next >>

Transcriptional analysis of livers from mice preserved with the Rapid Freeze hardware

https://genelab-data.ndc.nasa.gov/genelab/accession/GLDS-273



Data from the NASA Rodent Research-1 (RR-1) mission showed that gene-expression levels in mouse livers are different depending on what tissue preservation protocol is used and that slow freezing is not an effective method for preserving signals in gene-expression data. In response to these and other observations the Rapid Freeze hardware was built for use on the International Space Station. The Rapid Freeze hardware freezes mouse tissues (Glovebox freezer) and whole carcasses (Cryochiller) at ra...

Organism: Mus musculus **Factor:** Dissection Condition ... **Assay Type:** transcription profiling **Accession:** GLDS-273 **PI/Contact:** Saravia-Butler, Galaz... **Release/Publication Date:** 25-Jun-2020

Efficient Identification of Multiple Pathways: RNA-Seq Analysis of Livers from 56Fe Ion Irradiated Mice

https://genelab-data.ndc.nasa.gov/genelab/accession/GLDS-294



Background: mRNA interactions with each other and other signaling molecules define different biological pathways and functions. Researchers have been investigating various tools to analyze these types of interactions. In particular gene co-expression network methods have proved useful in finding and analyzing these molecular interactions. Many different analytical pipelines to identify these interactions networks have been proposed with the aim of identifying an optimal partition of the network ...

Organism: Mus musculus **Factor:** Ionizing Radiation Time **Assay Type:** transcription profiling **Accession:** GLDS-294 **PI/Contact:** Anna Nia **Release/Publication Date:** 02-Mar-2020

RNA-seq data for: A conserved mito-cytoplasmic translational balance links two longevity pathways

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE122097



Slowing down mRNA translation in either the cytoplasm or the mitochondria are both conserved longevity mechanisms. Here, we found a non-interventional natural correlation of mitochondrial and cytoplasmic ribosomal proteins when looking at mouse population genetics, suggesting a mito-cytoplasmic translational balance. Additionally, inhibiting mitochondrial translation in C. elegans in turn reduced cytoplasmic translation and repressed growth pathways while upregulating stress responses at both pr...

Organism: Mus musculus,Caeno... **Accession:** GSE122097 **PI/Contact:** Georges Janssens **Release/Publication Date:** 11-Dec-2019

Expression data from mouse liver at the early phase of treatment with permethrin or clofibrate

http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE124081



Crlj:CD1(ICR) female mice were fed diets containing 0 ppm (control), 5000 ppm permethrin, and 5000 ppm clofibrate for periods of 2 weeks. We used microarrays to evaluate gene expression profiling in mouse liver at the early phase of treatment with permethrin or clofibrate.

Organism: Mus musculus **Accession:** GSE124081 **PI/Contact:** Takako Fukuda **Release/Publication Date:** 10-Dec-2019

mouse AND liver x

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Search results for: **mouse AND liver** using filter(s):

Total Search Results Found: **20**

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1

STS-135 Liver Metabolomics

https://genelab-data.ndc.nasa.gov/genelab/accession/GLDS-108



Mice were flown onboard STS-135 and returned to Earth for analysis. Livers were collected within 3-4 hours of landing and snap frozen in liquid nitrogen. Samples were shipped to Metabolon Inc. for analysis.

Organism: Mus musculus **Factor:** Microgravity Absorbe… **Assay Type:** metabolite profiling **Accession:** GLDS-108 **PI/Contact:** Michael Pecaut, Xiao …
Release/Publication Date: 28-Apr-2017

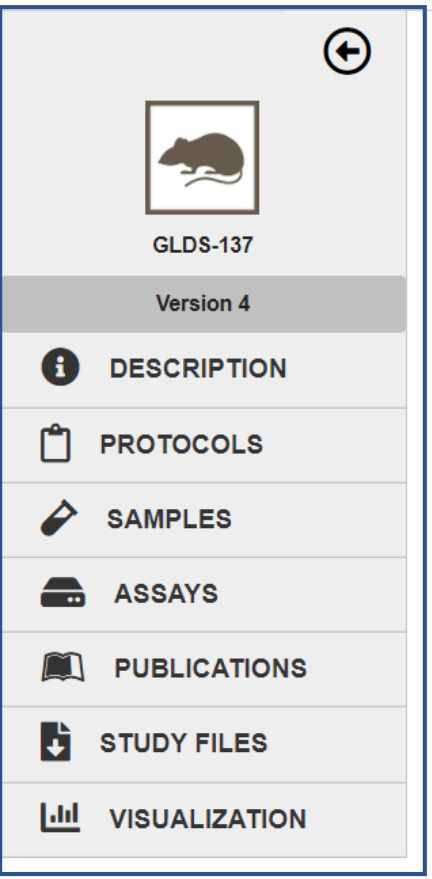
Rodent Research-3-CASIS: Mouse liver transcriptomic proteomic and epigenomic data

https://genelab-data.ndc.nasa.gov/genelab/accession/GLDS-137



The Rodent Research-3 (RR-3) mission was sponsored by the pharmaceutical company Eli Lilly and Co. and the Center for the Advancement of Science in Space to study the effectiveness of a potential countermeasure for the loss of muscle and bone mass that occurs during spaceflight. Twenty BALB/c 18-weeks old female mice (ten controls and ten treated) were flown to the ISS and housed in the Rodent Habitat for 39-42 days. Twenty mice of similar age sex and strain were used for ground controls housed ...

Organism: Mus musculus **Factor:** Spaceflight **Assay Type:** protein expression pr… **Accession:** GLDS-137 **PI/Contact:** Ruth Globus, Jonatha…
Release/Publication Date: 27-Aug-2017



Search Data

GLDS-137: Rodent Research-3-CASIS: Mouse liver transcriptomic, proteomic, and epigenomic data Version 4

Select a Version: 4

DOI: 10.26030/9k6w-4c28
Source Accession Number
Total Data Volume: 2.5 TB

Submitted Date: 04-Aug-2017
Release Date: 28-Aug-2017

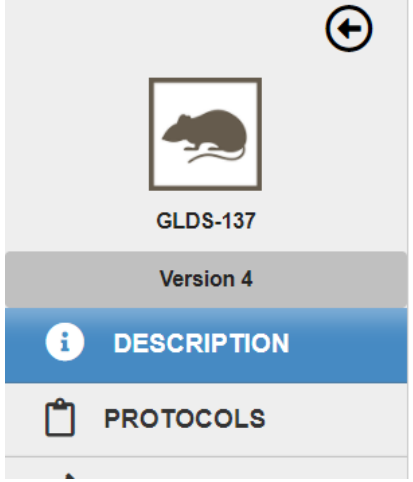
DESCRIPTION

Study Description

The Rodent Research-3 (RR-3) mission was sponsored by the pharmaceutical company Eli Lilly and Co. and the Center for the Advancement of Science in Space to study the effectiveness of a potential countermeasure for the loss of muscle and bone mass that occurs during spaceflight. Twenty BALB/c, 18-weeks old female mice (ten controls and ten treated) were flown to the ISS and housed in the Rodent Habitat for 39-42 days. Twenty mice of similar age, sex and strain were used for ground controls housed in identical hardware and matching ISS environmental conditions. Basal controls were housed in standard vivarium cages. Spaceflight, ground controls and basal groups had blood collected, then were euthanized, had one hind limb removed, and finally whole carcasses were stored at -80 C until dissection. All mice in this data set received only the control/sham injection.

Contacts

NAME	ROLE	ORGANIZATION	E-MAIL
Ruth Globus	Project Scientist	NASA Ames Research Center	ruth.k.globus@nasa.gov
Jonathan Galazka	Project Scientist	NASA GeneLab	jonathan.m.galazka@nasa.gov
Rosamund Smith	Principal Investigator	Eli Lilly and Company	



Mission

MISSION NAME	START DATE	END DATE
SpaceX-8	08-Apr-2016	11-May-2016

Acknowledgments

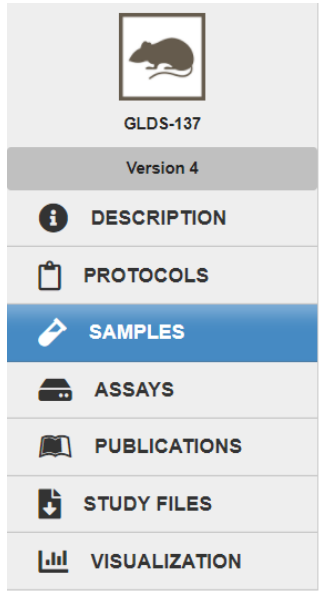
Funding for sample processing and sequencing was provided to the GeneLab project by the NASA Space Biology Program Office, Space Life and Physical Sciences Research and Applications Division. Samples from the RR-3 experiment were provided to GeneLab through the Biospecimen Sharing Plan of the NASA Life Sciences Data Archive.

Data Citation

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Smith R, Cramer M, Globus R, Galazka J. "Rodent Research-3-CASIS: Mouse liver transcriptomic, proteomic, and epigenomic data", GeneLab, Version 4, http://doi.org/10.26030/9k6w-4c28



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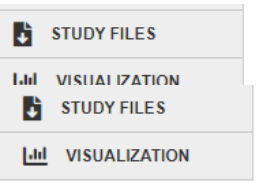
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- [x] Sample Name
- [x] Protocol REF
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- [x] Characteristics: Organism
- [x] Characteristics: Strain
- [x] Comment: Animal Source
- [x] Characteristics: sex
- [x] Characteristics: Age at Launch
- [x] Characteristics: Diet
- [x] Comment: Feeding Schedule
- [x] Parameter Value: Habitat
- [x] Factor Value: Spaceflight
- [x] Parameter Value: treatment
- [x] Parameter Value: Duration
- [x] Parameter Value: Euthanasia Chemical
- [x] Parameter Value: Carcass Weight
- [x] Parameter Value: Source Storage Temperature
- [x] Comment: Initiation Date
- [x] Comment: Completion Date
- [x] Comment: Dissection date
- [x] Protocol REF
- [x] Comment: Source description
- [x] Material Type
- [x] Comment: Original Submitted Sample Name
- [x] Comment: Sample Name Description
- [x] Comment: LSDA Biospecimen Source ID
- [x] Comment: LSDA Biospecimen Subject ID
- [x] Parameter Value: Sample Preservation Method
- [x] Parameter Value: Sample Storage Temperature

close select all unselect all

SAMPLES

Source Name	Sample Name	Protocol REF	Comment: Source description	Characteristics: Organism	Characteristics: Strain	Comment: Animal Source
CB1	Mmus_BAL-TAL_LVR_BSL_Rep1_B1	mouse habitation	previously dissected carcass	Mus musculus	BALB/c	Taconic Biosciences
CB2	Mmus_BAL-TAL_LVR_BSL_Rep2_B2	mouse habitation	previously dissected carcass	Mus musculus	BALB/c	Taconic Biosciences



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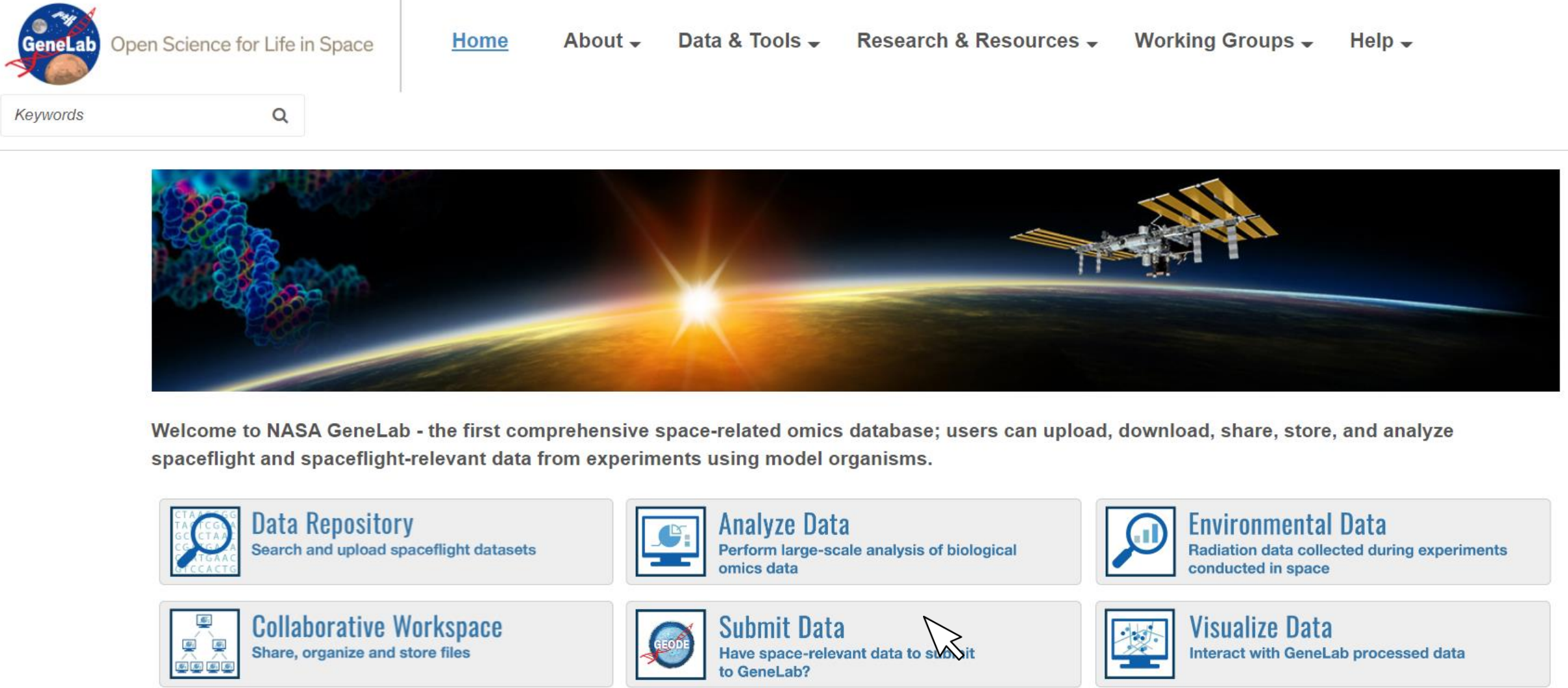
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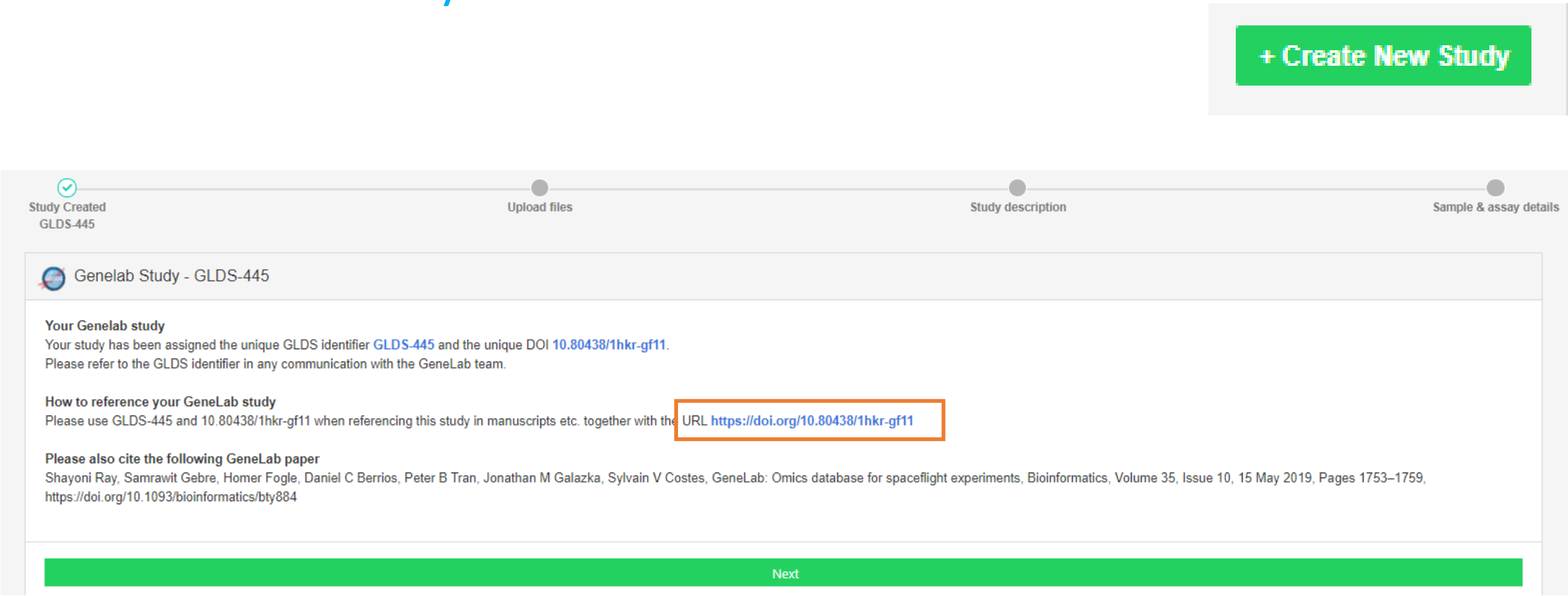
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    - Aligned sequence data
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    - Merged sequence data/FastQC reports
    - Aligned sequence data/Alignment logs
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    - Differential expression analysis data
    - Normalized counts data
    - Merged sequence data/MultiQC report
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    - Merged sequence data
    - Trimmed sequence data/Trimming reports
  - Study Metadata Files

	FILES	FILE SIZE	RESOURCE CATEGORY	RESOURCE DESCRIPTION
☑	GLDS-137_rna_seq_Mmus_BAL-TAL_LVR_FLT_Rep5_F5_SJ.out.tab	7.26 MB	Aligned sequence data	Data processed by the GeneLab Team, providing users high order data using standardized methods.
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☐	GLDS-137_rna_seq_Mmus_BAL-TAL_LVR_GC_Rep4_G5_R2_raw_fastqc.zip	456.51 KB	Merged sequence data/FastQC reports	Data processed by the GeneLab Team, providing users high order data using standardized methods.
☑	GLDS-137_rna_seq_Mmus_BAL-TAL_LVR_FLT_Rep2_F2_R2_raw_fastqc.html	636.29 KB	Merged sequence data/FastQC reports	Data processed by the GeneLab Team, providing users high order data using standardized methods.
☑	GLDS-137_rna_seq_Mmus_BAL-TAL_LVR_GC_Rep3_G3_R1_trimmed_fastqc.zip	434.84 KB	Trimmed sequence data/FastQC reports	Data processed by the GeneLab Team, providing users high order data using standardized methods.
☐	GLDS-137_rna_seq_Mmus_BAL-TAL_LVR_GC_Rep1_G1_R1_raw_fastqc.zip	449.76 KB	Merged sequence data/FastQC reports	Data processed by the GeneLab Team, providing users high order data using standardized methods.

https://genelab.nasa.gov/

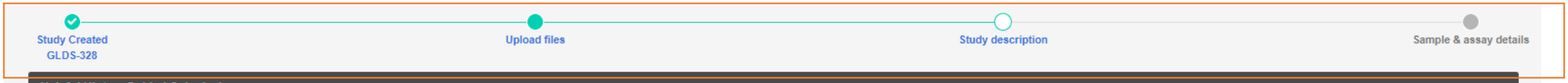


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Status Submitted Release Date 01-Sep-2021

Transcriptiome Profiles of mouse tissues after exposure to gamma-rays and HZE particles

Sam Gebre + Add person

Study to understand the effects of gamma-rays and HZE particles on mouse tissues. This experiment was conducted at BNL on 20 mice tissues. Radiation types studied included - Fe, Si, and X-ray at different doses and exposure times. The duration and dose for experiments varied: 0, 1, 3, Gy for 4, 8, 12, 24 hours. Total RNA was extracted and sequencing using the NovaSeq 6000.

Mus musculu

PUBLICATIO

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GeneLab: Omics database for spaceflight experiments
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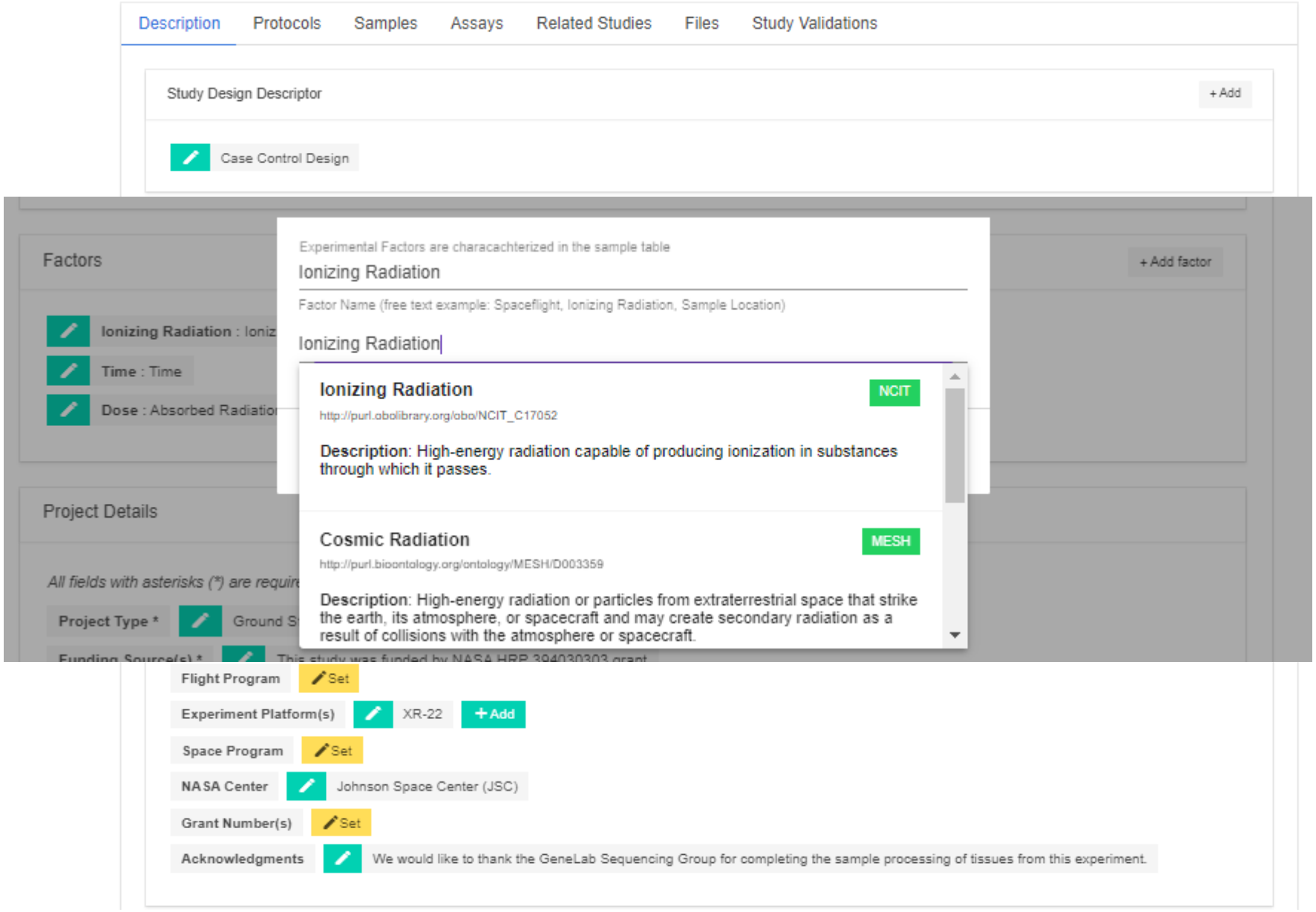
Ray Shayoni, Gebre Samrawit, Fogle Homer, Berrios Daniel C, Tran Peter B, Galazka Jonathan M, Costes Sylvain V
The authors who contributed to this publication. As appears in the publication, do not include affiliation

Publication abstract

MOTIVATION:To curate and organize expensive spaceflight experiments conducted aboard space stations and maximize the scientific return of investment, while democratizing access to vast amounts of spaceflight related omics data generated from several model organisms. RESULTS:The GeneLab Data System (GLDS) is an open access database containing fully coordinated and curated 'omics' (genomics, transcriptomics, proteomics, metabolomics) data, detailed metadata and radiation dosimetry for a variety of model organisms. GLDS is supported by an integrated data system allowing federated search across several public bioinformatics repositories. Archived datasets can be queried using full-text search (e.g. keywords, Boolean and wildcards) and results can be sorted in multifactorial manner using assistive filters. GLDS also provides a collaborative platform built on GenomeSpace for sharing files and analyses with collaborators. It currently houses 172 datasets and supports standard guidelines for submission of datasets, MIAME (for microarray), ENCODE Consortium Guidelines (for RNA-seq) and MIAPE Guidelines (for proteomics). AVAILABILITY AND IMPLEMENTATION:https://genelab.nasa.gov/.

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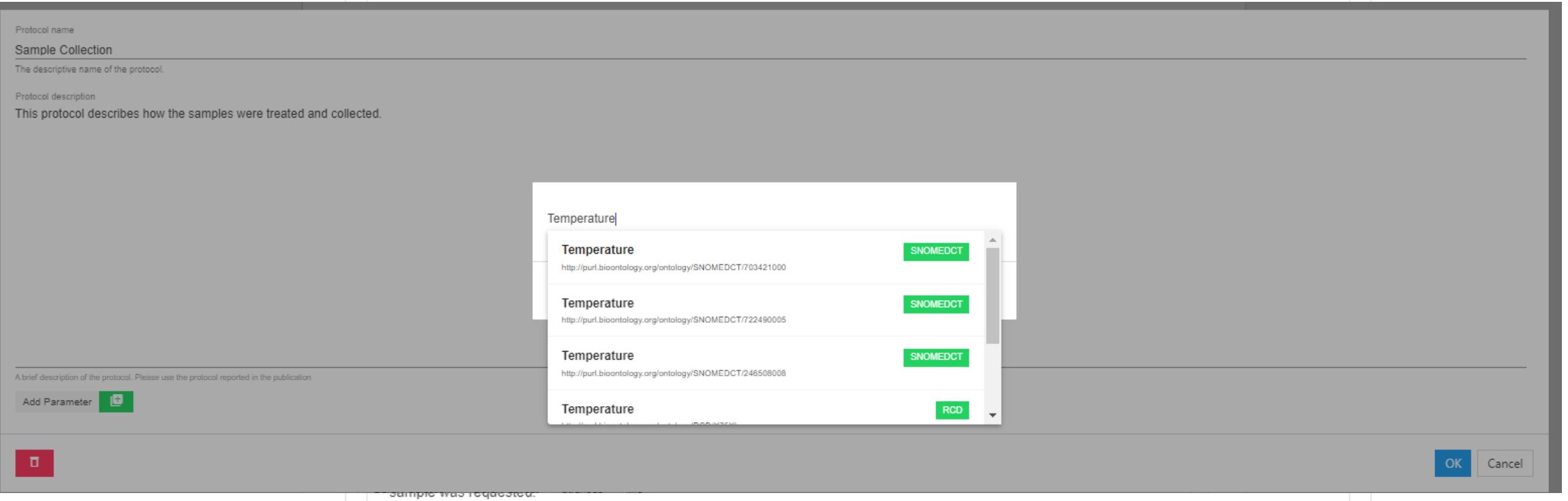
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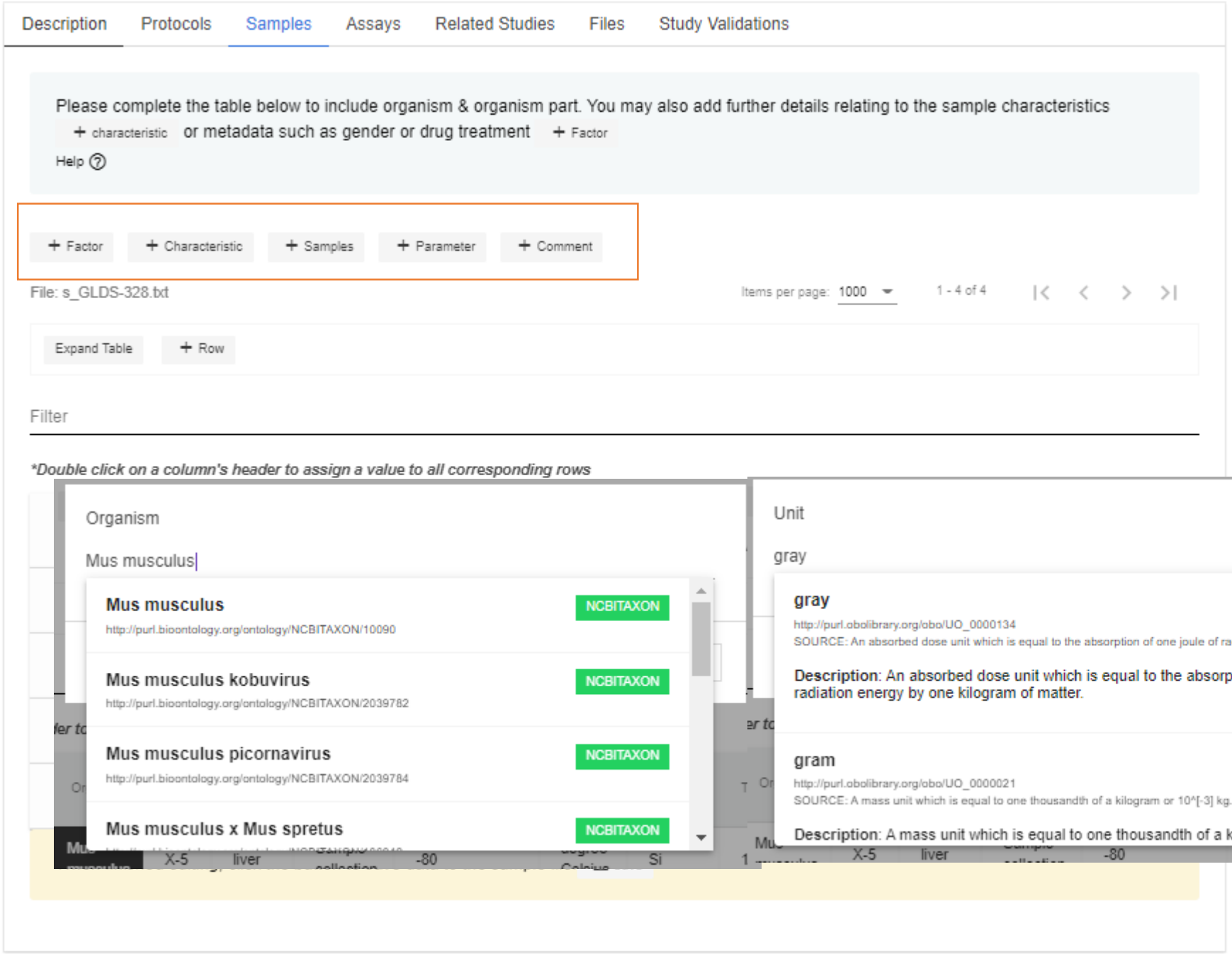
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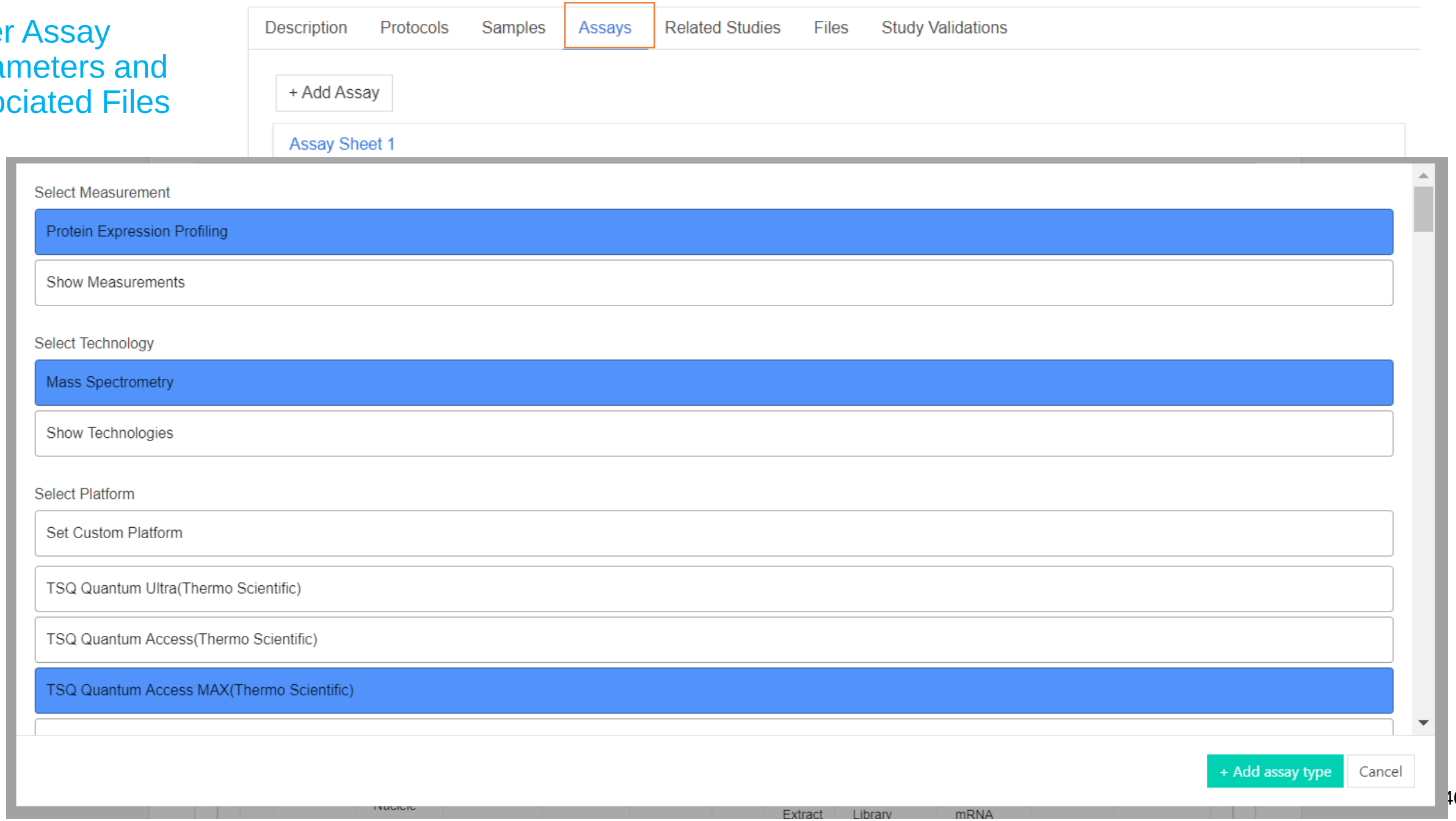
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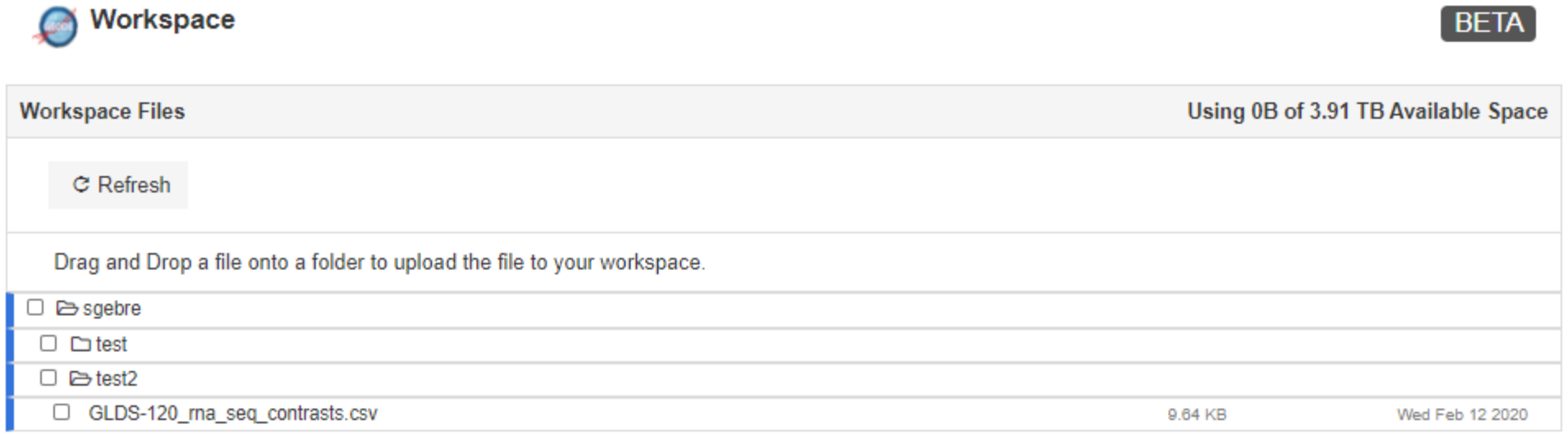
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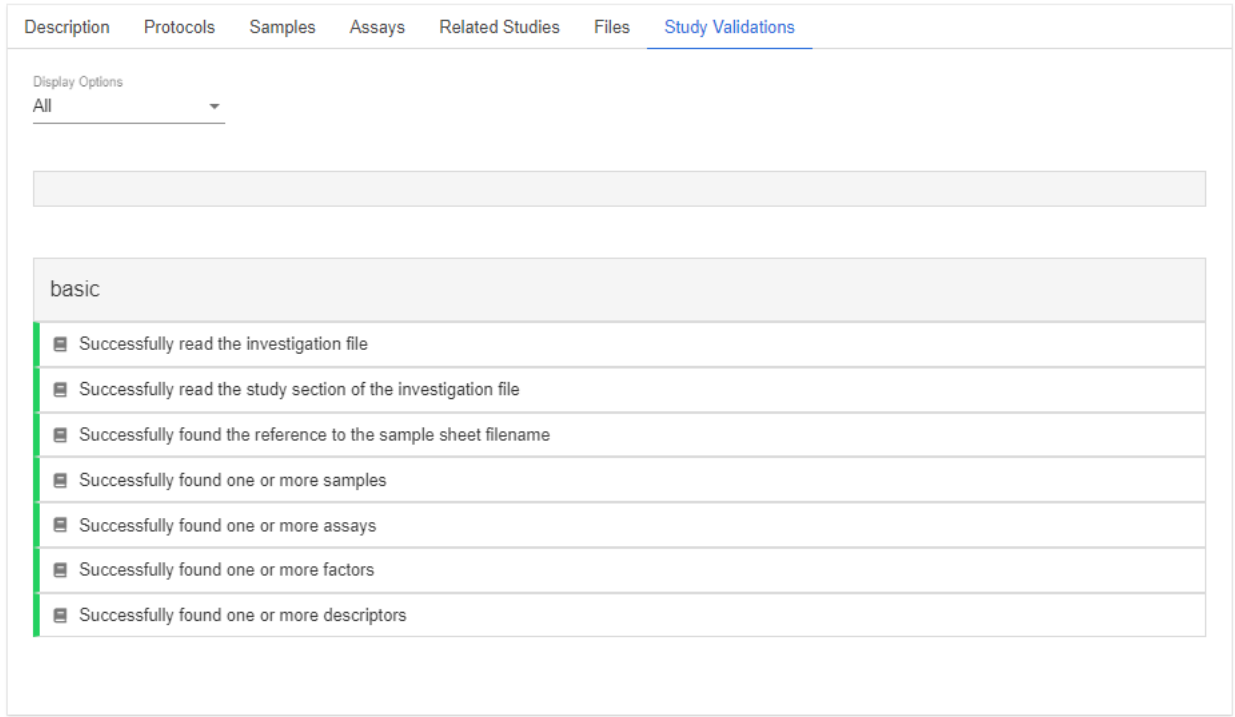
Enter Assay Parameters and associated Files



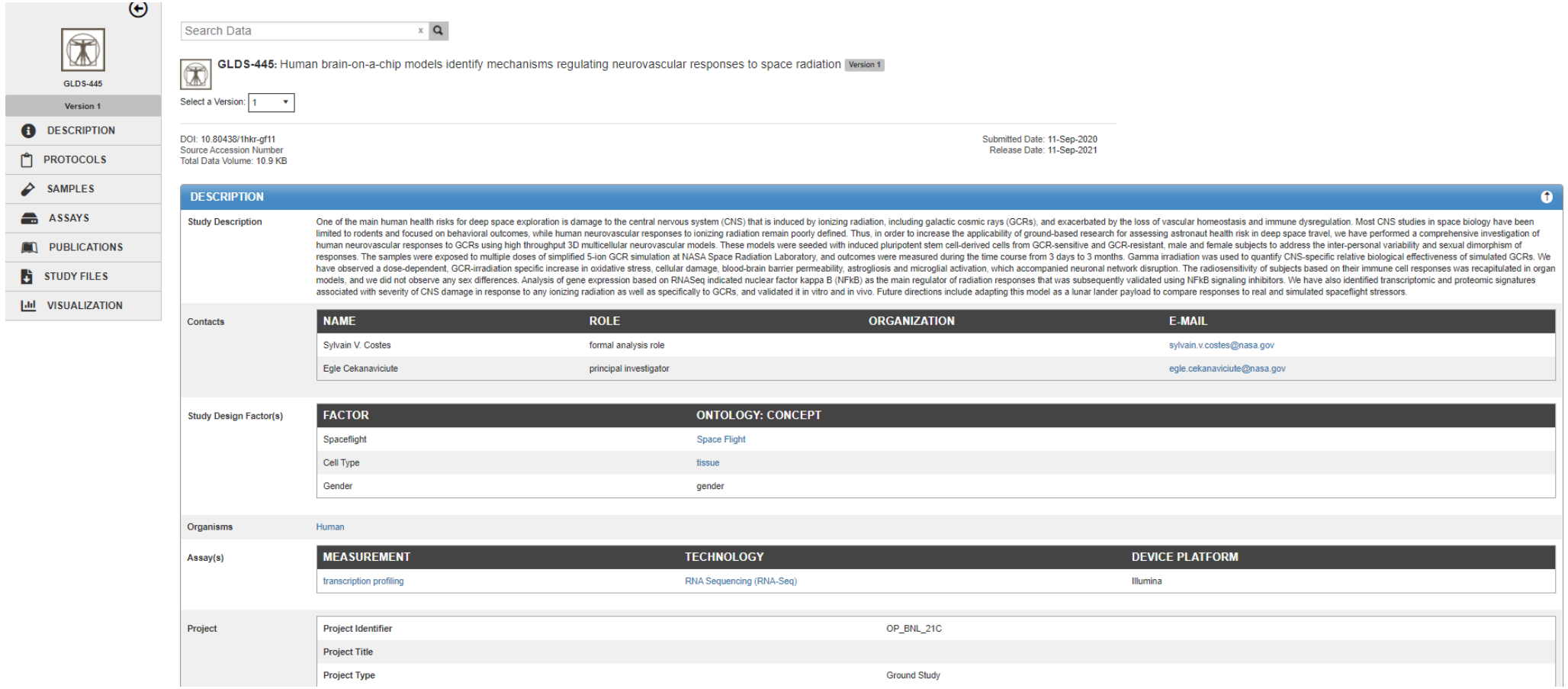
Workspace to store and associate data files



Study Validations



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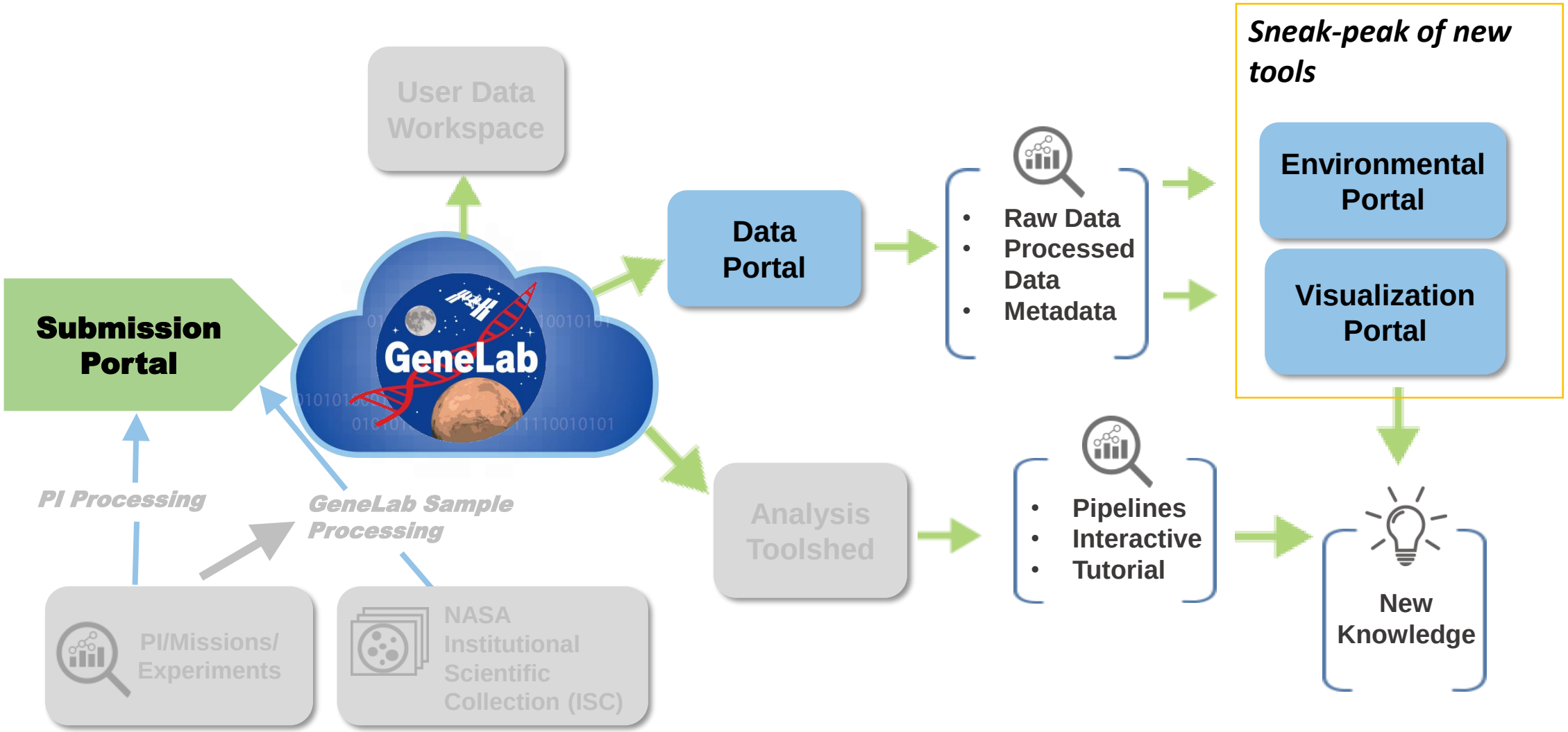
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GeneLab Data Democratization



Environmental Data

Supporting data for space flown experiments: Summarized STS and ISS Radiation dosimetry, ISS Cabin CO2, Temperature, Humidity



Environmental Data
Radiation data collected during experiments conducted in space

ENVIRONMENTAL DATA

- + Environmental Data for Spaceflight Experiments
  - › STS (Space Shuttle) Radiation Dosimetry
  - › BION-M1 Radiation Dosimetry
  - › Foton-M4 Radiation Dosimetry
  - › Shenzhou-8 Radiation Dosimetry
  - › ISS Radiation Dosimetry Data
    - › Rodent Research Radiation Dosimetry
    - › US Lab Radiation Dosimetry
    - › International Labs Radiation Dosimetry

Radiation Metadata for GLDS Studies

Table 1 contains information used to calculate the absorbed dose of radiation for STS ("space shuttle") experiments. The absorbed dose from ionizing radiation received by the specimens (animals, plants, cells) was estimated from data recorded by three passive radiation dosimeter (PRD) packages, designated DLOC1, DLOC2, and DLOC3, in the middeck of the space shuttle, where biological payloads were located. Each package contains a number of TLD-100 thermoluminescent detectors. The TLDs are passive detectors: they integrate dose and must be processed--in the case of TLDs, by heating. (As opposed to active detectors which are powered and can be read out continuously, in real-time.) The detectors are returned post-flight and the data analysed by the Space Radiation Analysis Group at NASA-Johnson Space Center. The reported dose for each PRD is the average over all the TLDs +/- the standard deviation, with appropriate background subtraction and error propagation. Correction for dose accumulated on the ground pre- and post-flight is done by subtracting the dose in identical detectors that remain on the ground, and a calibration factor is applied to convert dose in the TLDs to dose in water.

Radiation Metadata Table 1

GLDS Accession Number	GLDS-63	GLDS-21	GLDS-11 GLDS-15 GLDS-20	GLDS-4	GLDS-1 GLDS-3	GLDS-50	GLDS-17 GLDS-44 GLDS-121	GLDS-25 GLDS-54 GLDS-72 GLDS-87 GLDS-108 GLDS-116 GLDS-173 GLDS-222
Mission	STS-70	STS-108	STS-115	STS-118	STS-121	STS-126	STS-131	STS-135
Inclination	28.45	51.60	51.60	51.60	51.60	51.60	51.60	51.60
Launch/mission start	07-13-95	12-05-01	09-09-06	08-08-07	07-04-06	11-14-08	04-05-10	07-08-11

Environmental Data App

Coming soon!

Rodent Research-1

"This important first mission in NASA's rodent research project launched in 2014. It proved that the hardware system was effective and safe to use in space, and that critical research operations could be carried out by the space station crew. This first study showed that mice transported on the SpaceX Dragon capsule, then living in the habitat on the space station for a month, were both healthy and active. Rodent Research-1 also included a CASIS commercial research investigation dedicated to the study of muscle loss, or atrophy."

- NASA Ames Research Center on RR-1

Click here for more information on NASA's RR-1 mission

Overview

	mean	standard deviation	min	Q1	median	Q3	max
Temperature	22.579	0.295	21.8	22.4	22.6	22.8	24
Relative Humidity	43.291	3.974	31	42	43	46	56
CO2	3267.145	588.858	1862	2874	3374	3659	4667
Radiation: Total	0.204	0.008	0.189	0.198	0.203	0.208	0.231
Radiation: GCR	0.131	0.004	0.125	0.128	0.132	0.134	0.139
Radiation: SAA	0.073	0.009	0.059	0.067	0.072	0.077	0.097

Animal transfer : 9/25/2014 16:05
Sac1 : 10/12/2014 0:00
Sac2 : 10/13/2014 0:00
Return : 10/25/2014 19:36
Sac3 : 10/28/2014 0:01
Duration: 32 days

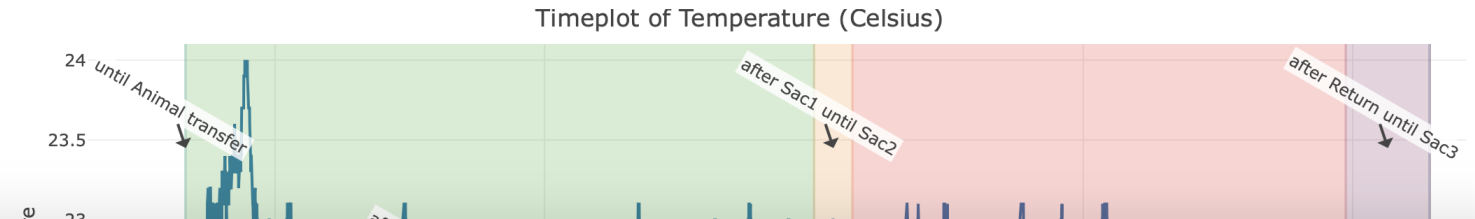
The Data

All Environmental Data | Radiation Data

Select which environmental factor to display on the plots
- [x] Temperature
- [ ] Relative Humidity
- [ ] CO2
- [ ] Radiation accumulated

Select to compare spaceflight data with ground control
- [ ] Display ground control

Timeplot | Column Chart



	mean	standard deviation	min	Q1	median	Q3	max
Temperature	22.579	0.295	21.8	22.4	22.6	22.8	24
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Sac3 : 10/28/2014 0:01
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The Data

All Environmental Data | Radiation Data

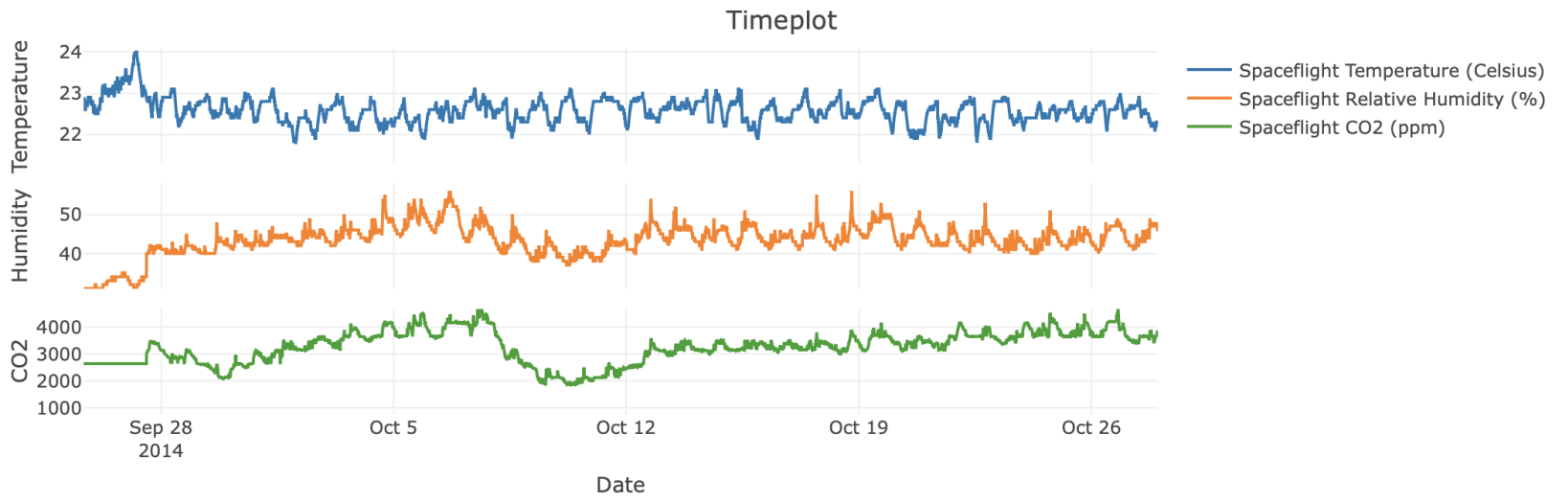
Select which environmental factor to display on the plots
- [x] Temperature
- [x] Relative Humidity
- [x] CO2
- [ ] Radiation accumulated

Select to compare spaceflight data with ground control
- [ ] Display ground control

Select to display on the timeplot the different periods of the mission (see the *Overview* section for landmark date/times)
- [ ] Display Periods

Select to display on the timpelot the durations that each light was switched on (Black regions are when the lights were switched on)
- [ ] Light 1
- [ ] Light 3

Timeplot | Column Chart



Select one or more missions.

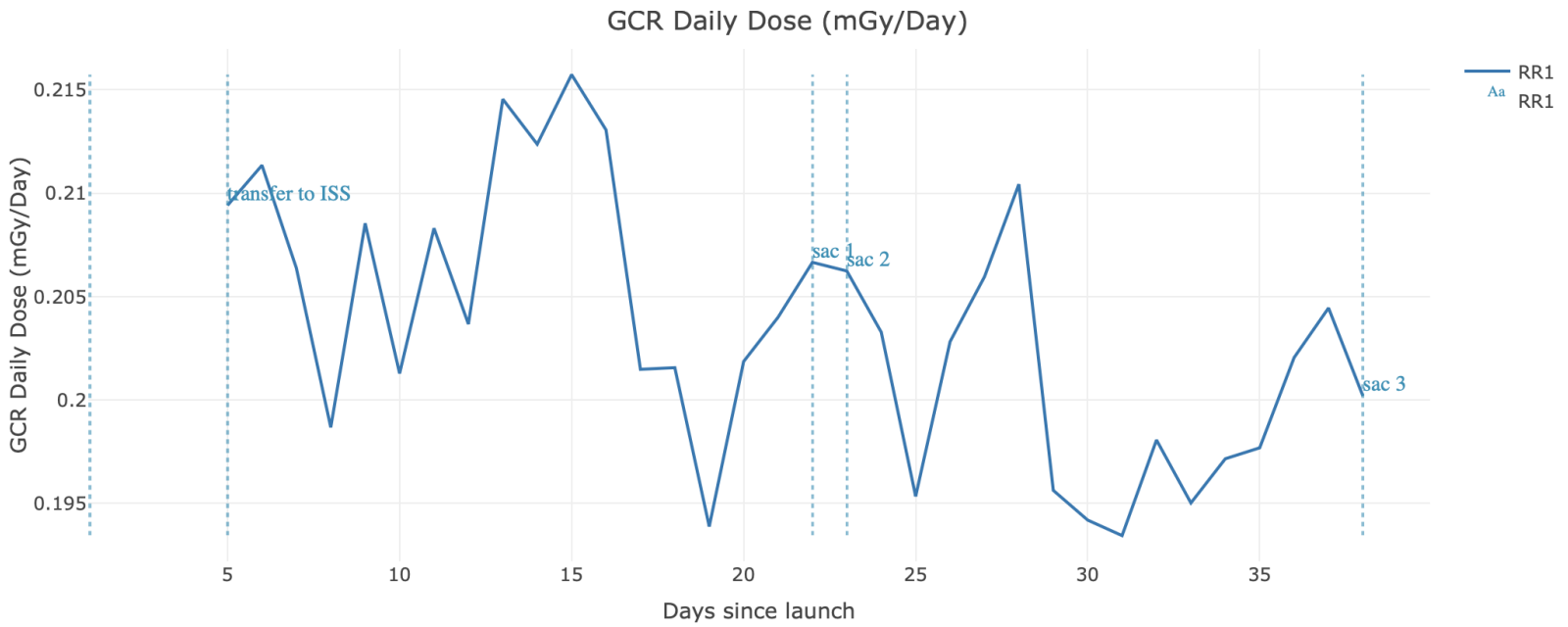
Mission	Date
RR1	2014-09-20 03:59:00
RR3	2016-04-08 04:00:00
RR5	2017-06-01 05:00:00
RR6	2017-12-06 15:06:00
RR7	2018-07-01 04:49:00
RR12	2019-04-17 19:19:00
RR19	0019-12-03 10:24:00

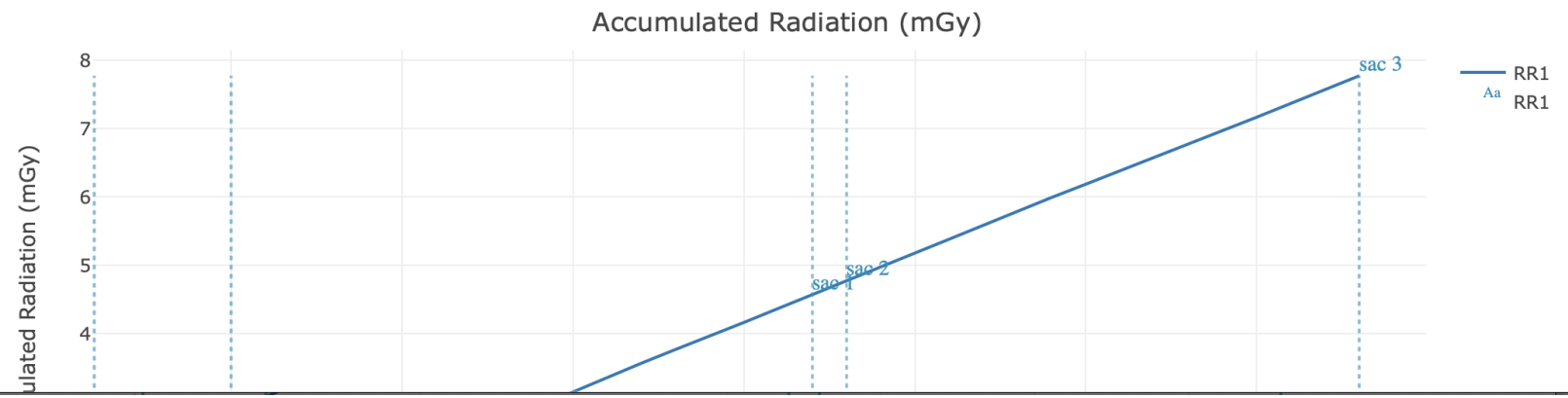
Select plots to display

- [x] Timeplot
- [ ] Boxplot
- [ ] Bar Chart

- [x] Show landmarks

Radiation | Temperature | Relative Humidity | CO2



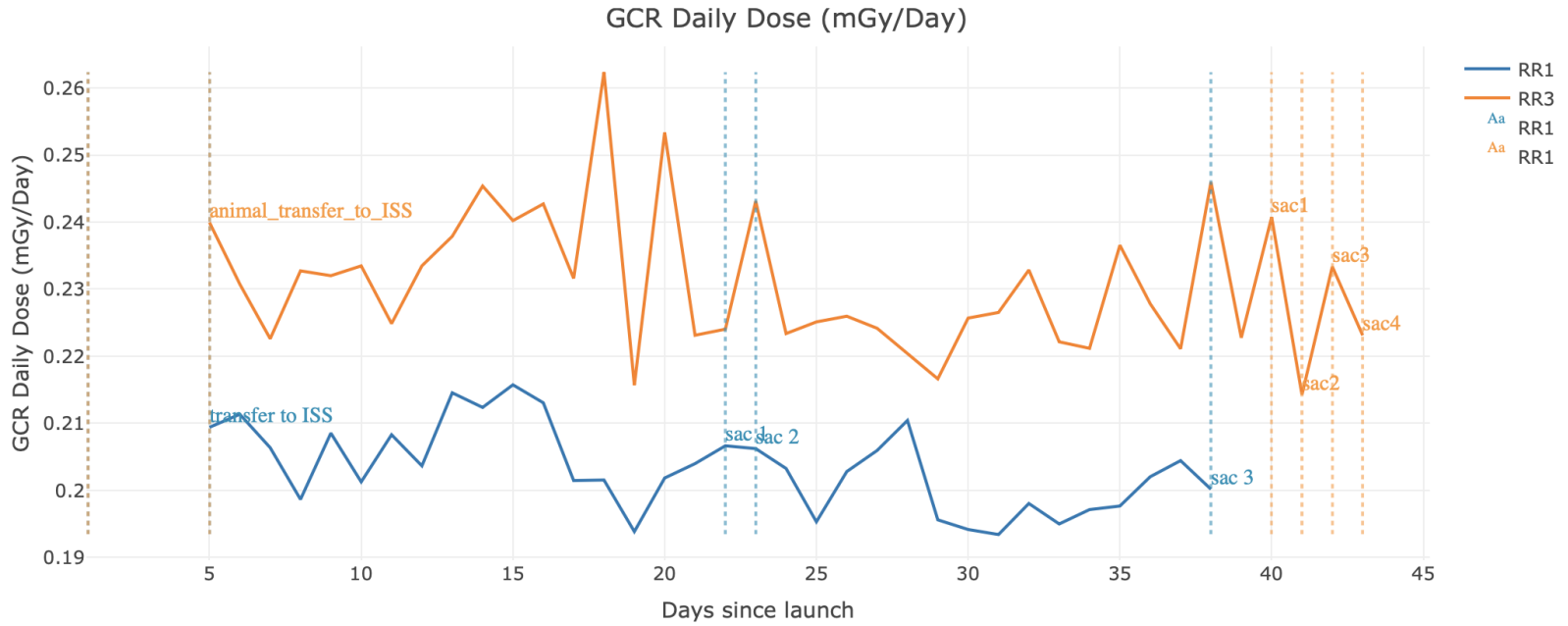


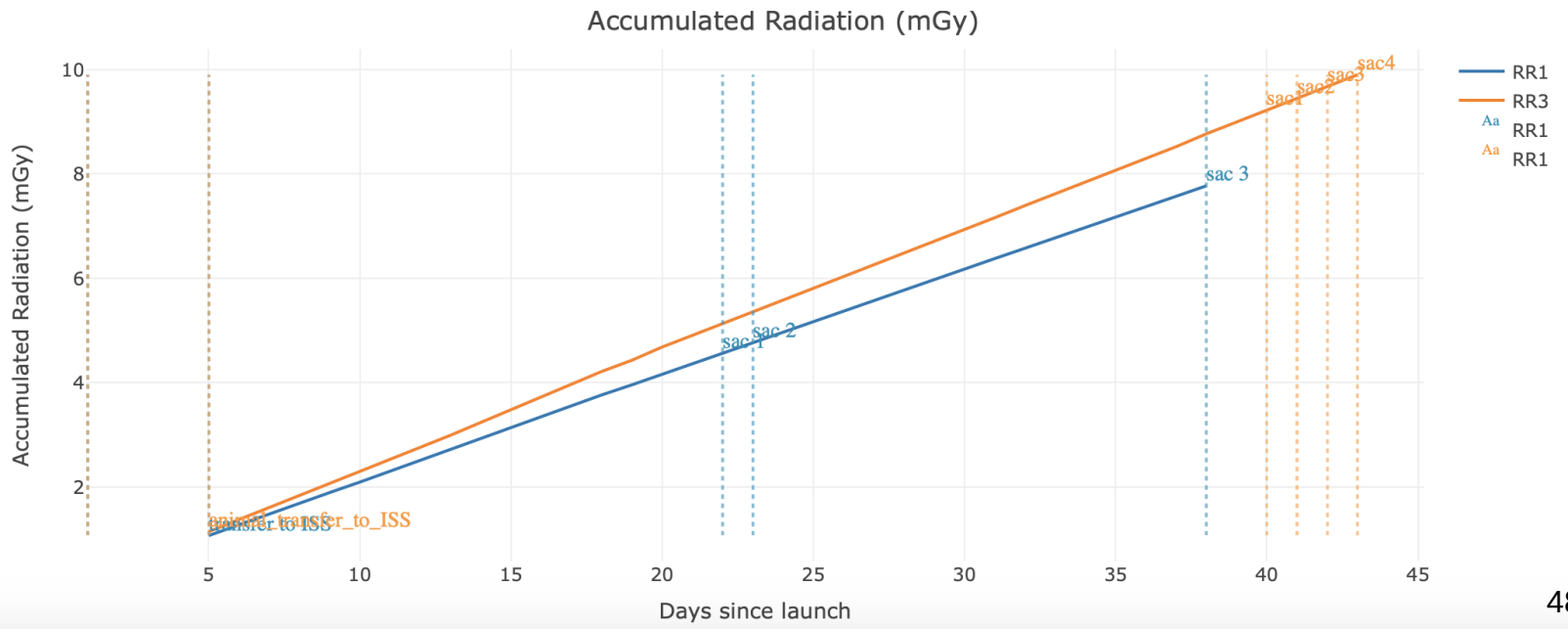
Mission	Date
RR1	2014-09-20 03:59:00
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RR5	2017-06-01 05:00:00
RR6	2017-12-06 15:06:00
RR7	2018-07-01 04:49:00
RR12	2019-04-17 19:19:00
RR19	0019-12-03 10:24:00

Select plots to display

- [x] Timeplot
- [ ] Boxplot
- [ ] Bar Chart

- [x] Show landmarks





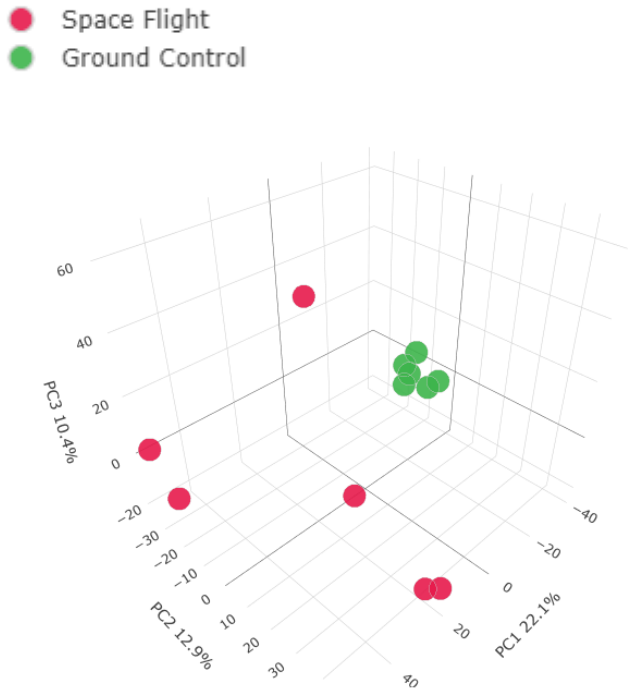
Data Visualization

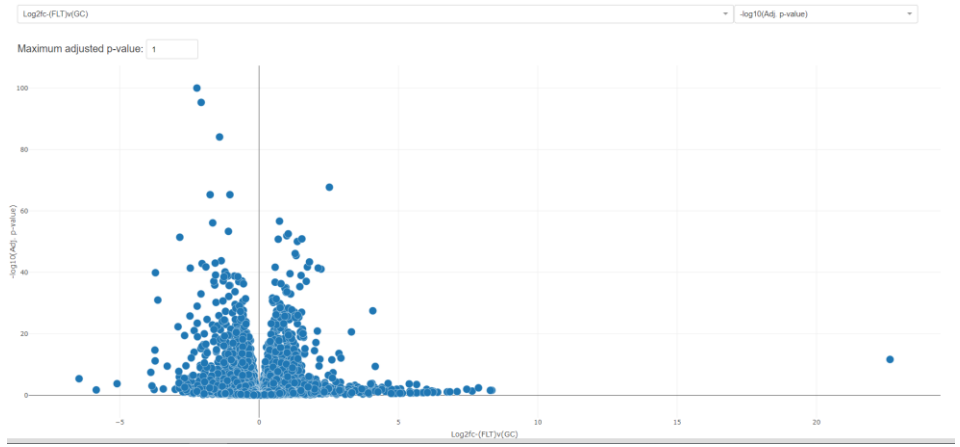
By study, users can visualize processed transcriptomics data in GeneLab

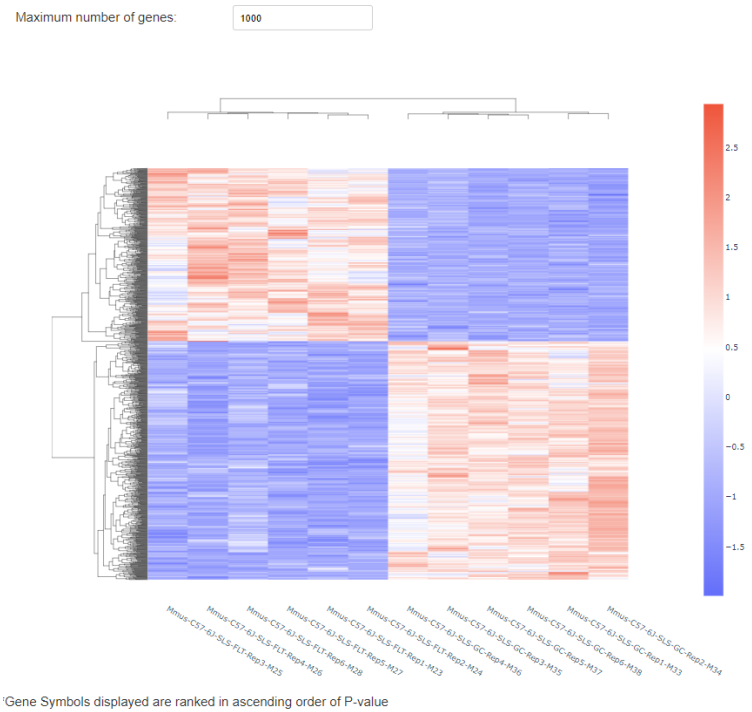
Visualize Data
Interact with GeneLab processed data

GLDS-104: Rodent Research-1 (RR1) NASA Validation Flight: Mouse soleus muscle transcriptomic and epigenomic data

PCA | QUERY DATA | PAIR PLOTS | VOLCANO PLOTS | DENDROGRAM | HEATMAP | SPLOT





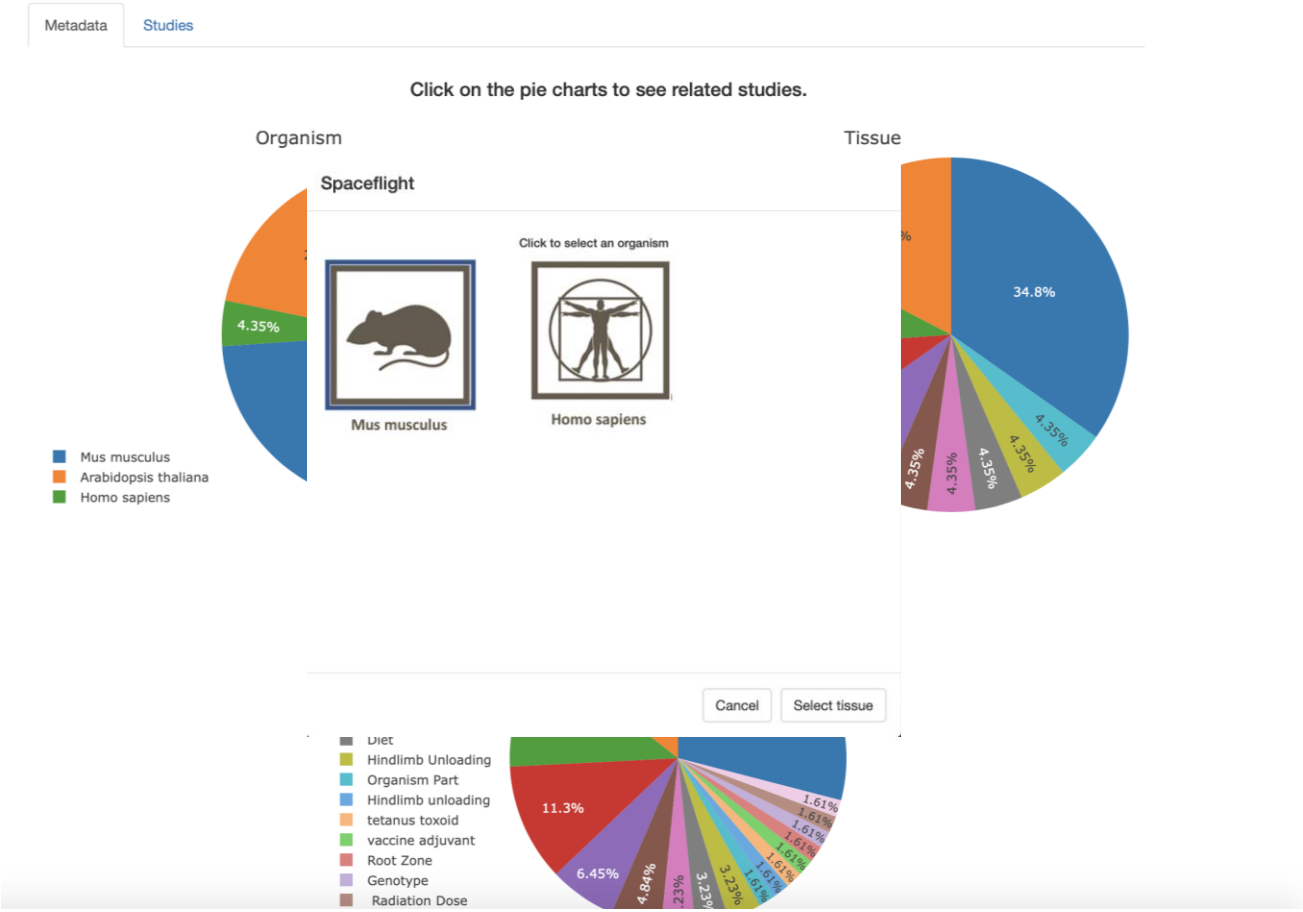


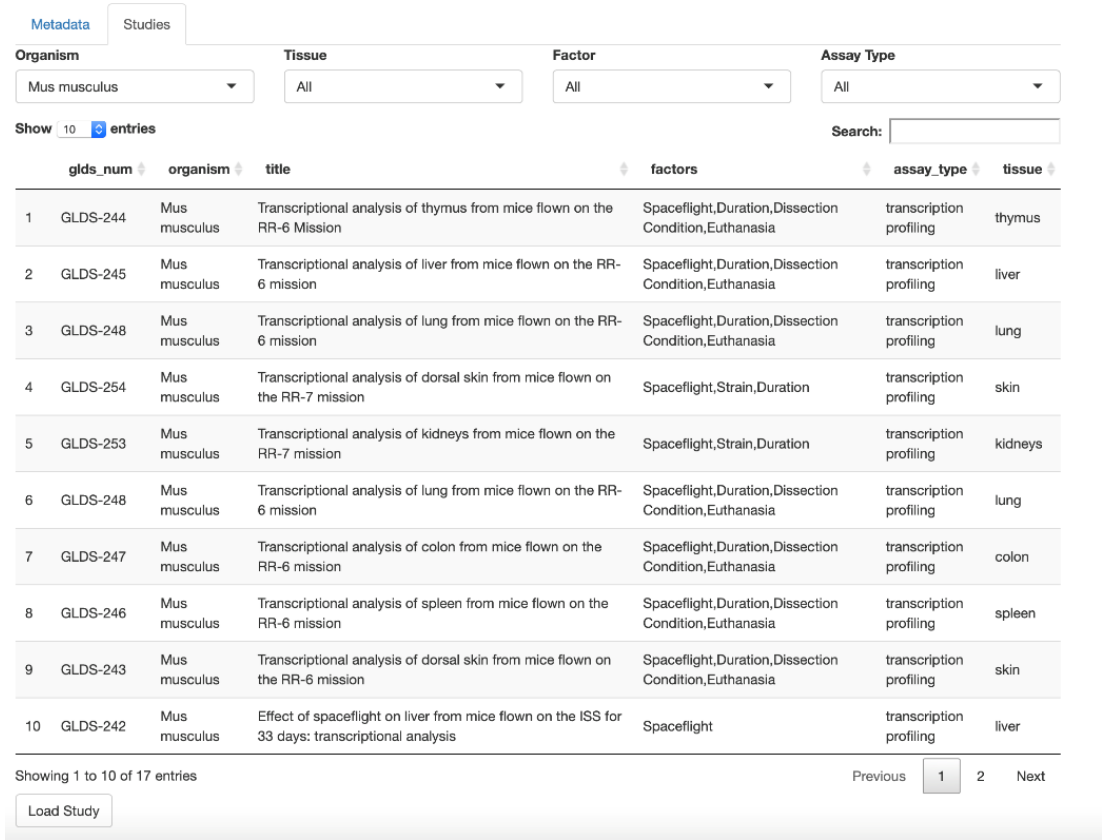
[1]Gene Symbols displayed are ranked in ascending order of P-value

Data Visualization 2.0

Add new types of visualization tools and extend the ability to visualize and compare multiple datasets.

Coming soon!





	glds_num	organism	title	factors	assay_type	tissue
1	GLDS-244	Mus musculus	Transcriptional analysis of thymus from mice flown on the RR-6 Mission	Spaceflight,Duration,Dissection Condition,Euthanasia	transcription profiling	thymus
2	GLDS-245	Mus musculus	Transcriptional analysis of liver from mice flown on the RR-6 mission	Spaceflight,Duration,Dissection Condition,Euthanasia	transcription profiling	liver
3	GLDS-248	Mus musculus	Transcriptional analysis of lung from mice flown on the RR-6 mission	Spaceflight,Duration,Dissection Condition,Euthanasia	transcription profiling	lung
4	GLDS-254	Mus musculus	Transcriptional analysis of dorsal skin from mice flown on the RR-7 mission	Spaceflight,Strain,Duration	transcription profiling	skin
5	GLDS-253	Mus musculus	Transcriptional analysis of kidneys from mice flown on the RR-7 mission	Spaceflight,Strain,Duration	transcription profiling	kidneys
6	GLDS-248	Mus musculus	Transcriptional analysis of lung from mice flown on the RR-6 mission	Spaceflight,Duration,Dissection Condition,Euthanasia	transcription profiling	lung
7	GLDS-247	Mus musculus	Transcriptional analysis of colon from mice flown on the RR-6 mission	Spaceflight,Duration,Dissection Condition,Euthanasia	transcription profiling	colon
8	GLDS-246	Mus musculus	Transcriptional analysis of spleen from mice flown on the RR-6 mission	Spaceflight,Duration,Dissection Condition,Euthanasia	transcription profiling	spleen
9	GLDS-243	Mus musculus	Transcriptional analysis of dorsal skin from mice flown on the RR-6 mission	Spaceflight,Duration,Dissection Condition,Euthanasia	transcription profiling	skin
10	GLDS-242	Mus musculus	Effect of spaceflight on liver from mice flown on the ISS for 33 days: transcriptional analysis	Spaceflight	transcription profiling	liver

PCA Plot

GeneLab

GLDS-244:Transcriptional analysis of thymus from mice flown on the RR-6 Mission
Organism: Mus musculus
Number of genes: 28067
Number of samples: 58

GLDS-245:Transcriptional analysis of liver from mice flown on the RR-6 mission
Organism: Mus musculus
Number of genes: 28067
Number of samples: 59

GLDS-248:Transcriptional analysis of lung from mice flown on the RR-6 mission
Organism: Mus musculus
Number of genes: 28067
Number of samples: 58

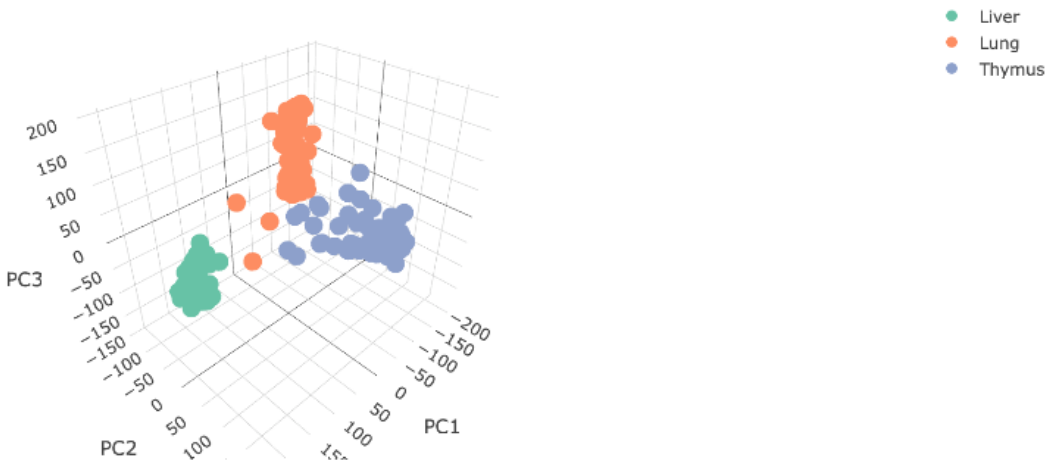
Metadata | Studies | PCA | Query data | Pair plots | Volcano plots | Heatmap

Factors:

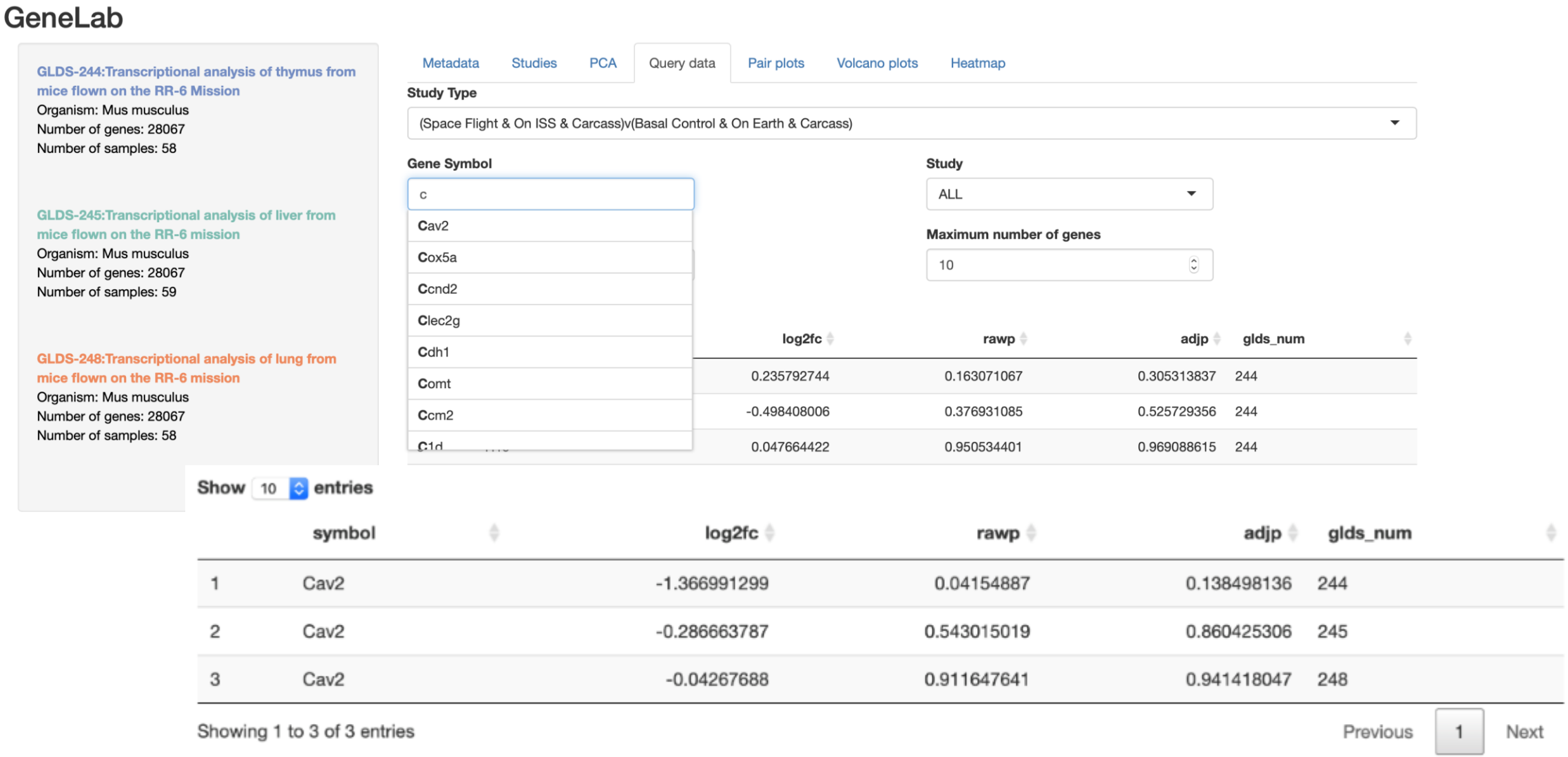
Tissue	Spaceflight	Dissection Condition	Euthanasia
All	All	All	All
☑ Use this factor as color	☐ Use this factor as color	☐ Use this factor as color	☐ Use this factor as color

X: PC1 | Y: PC2 | Z: PC3

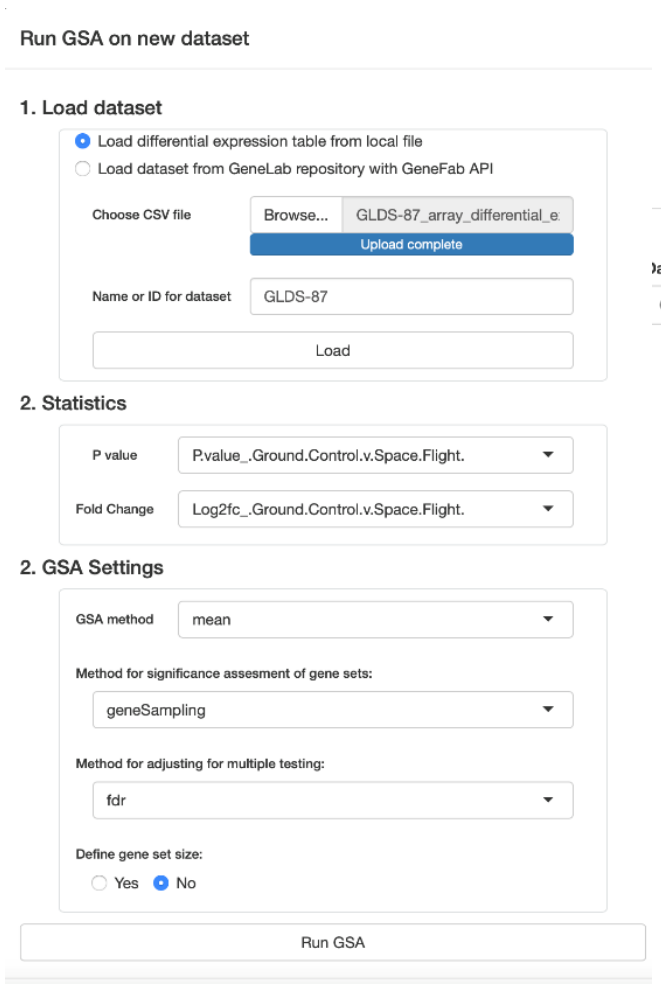
○ 2D ◉ 3D



Search by gene symbol



Pathway analysis by Gene set enrichment



Run GSA on new dataset

GSA Info | Network Plot | Heatmap | Consensus heatmap

Dataset :

GLDS-87

Show 10 entries

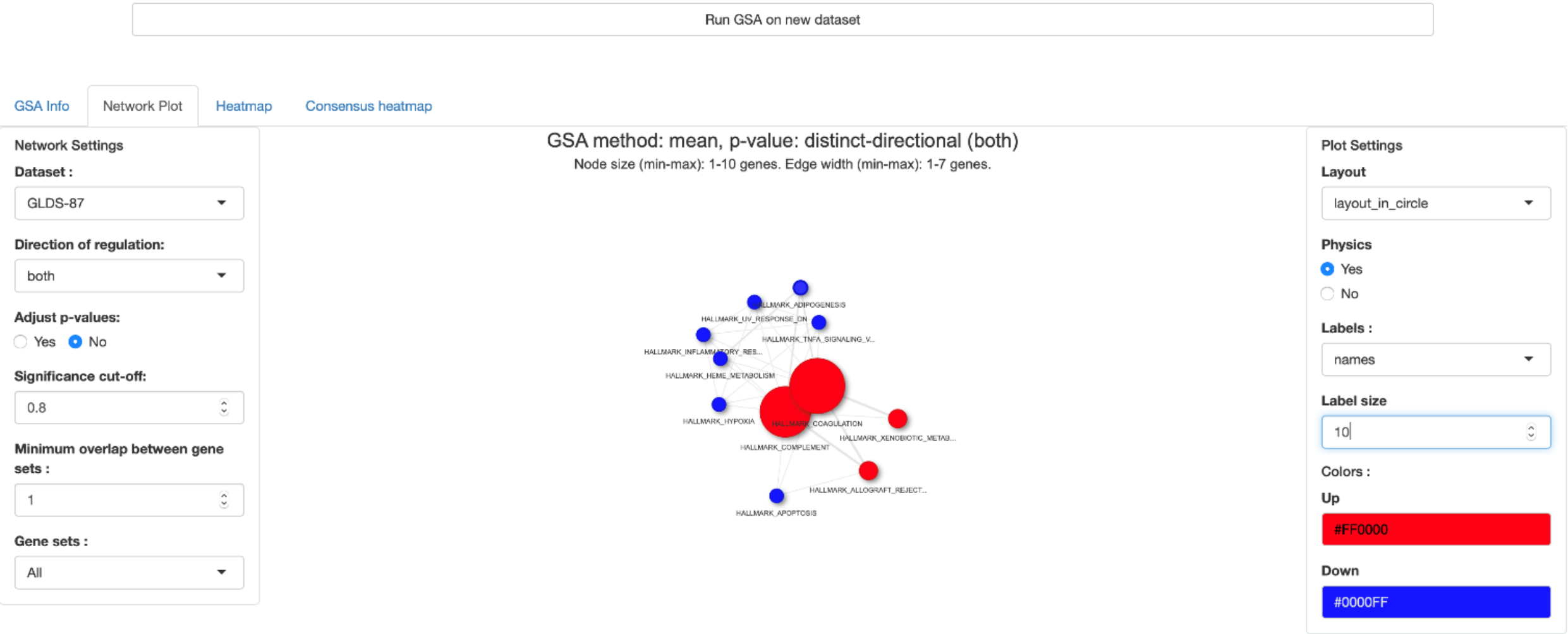
Search:

	Name	Genes (tot)	Stat (dist.dir.up)	p (dist.dir.up)	p adj (dist.dir.up)	Stat (dist.dir.dn)	p (dist.dir.dn)	p adj (dist.dir.dn)	Stat (non-dir.)	p (non-dir.)	p adj (non-dir.)	Genes (up)	Stat (mix.dir.up)	p (mix.dir.up)	(m
1	HALLMARK_TNFA_SIGNALING_VIA_NFKB	1	0.71194	0.67973	0.90044	0.28806	0.32037	0.50344	0.57613	0.54635	0.54635	0			
2	HALLMARK_HYPOXIA	1	0.71194	0.67973	0.90044	0.28806	0.32037	0.50344	0.57613	0.54635	0.54635	0			
3	HALLMARK_APOPTOSIS	1	0.76111	0.73673	0.90044	0.23889	0.26337	0.50344	0.47778	0.43946	0.54635	0			
4	HALLMARK_ADIPOGENESIS	1	0.89947	0.90091	0.90091	0.10053	0.09919	0.50344	0.20106	0.14819	0.54335	0			
5	HALLMARK_COMPLEMENT	9	0.505	0.34617	0.90044	0.495	0.65393	0.79925	0.47464	0.28917	0.54635	4	0.42022	0.16088	
6	HALLMARK_INFLAMMATORY_RESPONSE	1	0.71194	0.67973	0.90044	0.28806	0.32037	0.50344	0.57613	0.54635	0.54635	0			
7	HALLMARK_XENOBIOTIC_METABOLISM	2	0.13579	0.016298	0.17928	0.86421	0.9838	0.9838	0.27158	0.10559	0.54335	2	0.27158	0.072593	
8	HALLMARK_UV_RESPONSE_DN	1	0.71194	0.67973	0.90044	0.28806	0.32037	0.50344	0.57613	0.54635	0.54635	0			
9	HALLMARK_HEME_METABOLISM	1	0.89947	0.90091	0.90091	0.10053	0.09919	0.50344	0.20106	0.14819	0.54335	0			
10	HALLMARK_COAGULATION	10	0.43662	0.11969	0.65828	0.56338	0.88041	0.96845	0.45507	0.20838	0.54635	6	0.44026	0.15188	

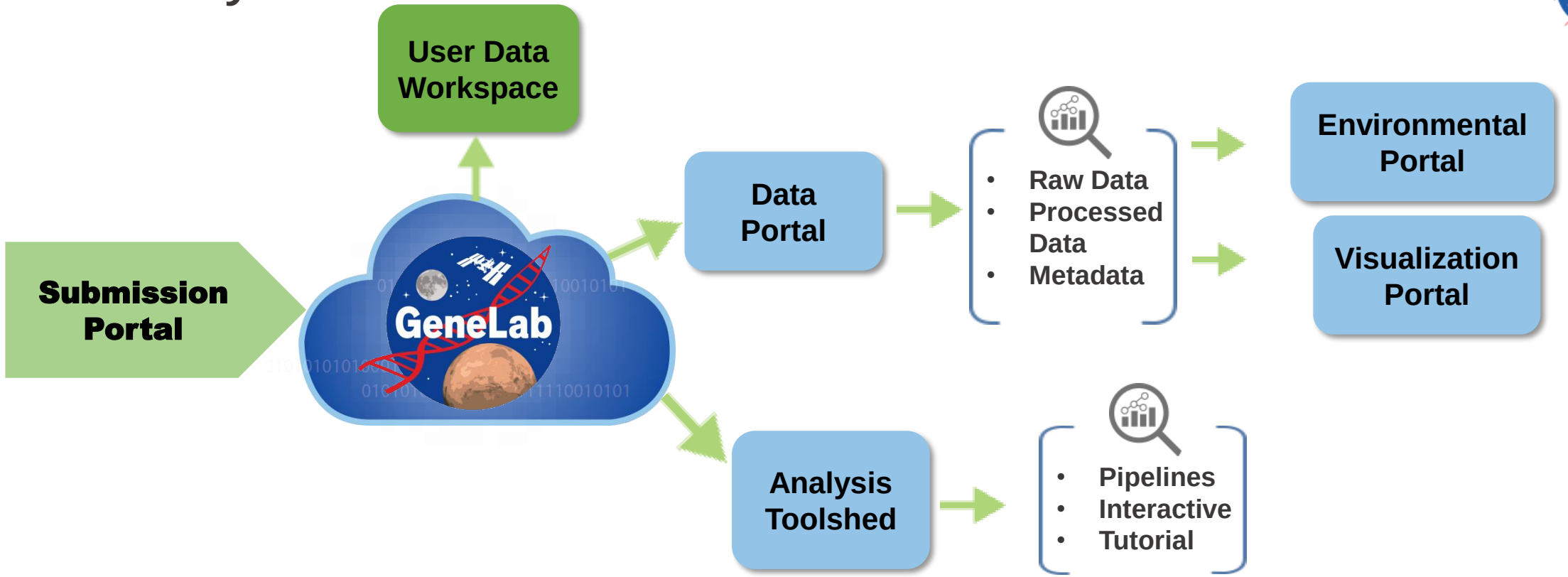
Showing 1 to 10 of 11 entries

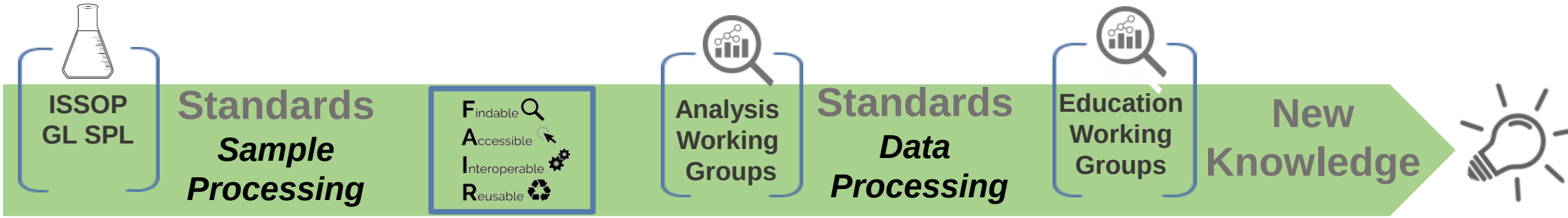
Previous 1 2 Next

Interactive Network Plot



In Summary:





55

Thank you!

Twitter: @NASAGeneLab
https://genelab.nasa.gov

2017-2018



2018-2019



GeneLab is funded by the NASA Space Biology program within the NASA Science Mission Directorate's (SMD) Biological and Physical Sciences (BPS) Division