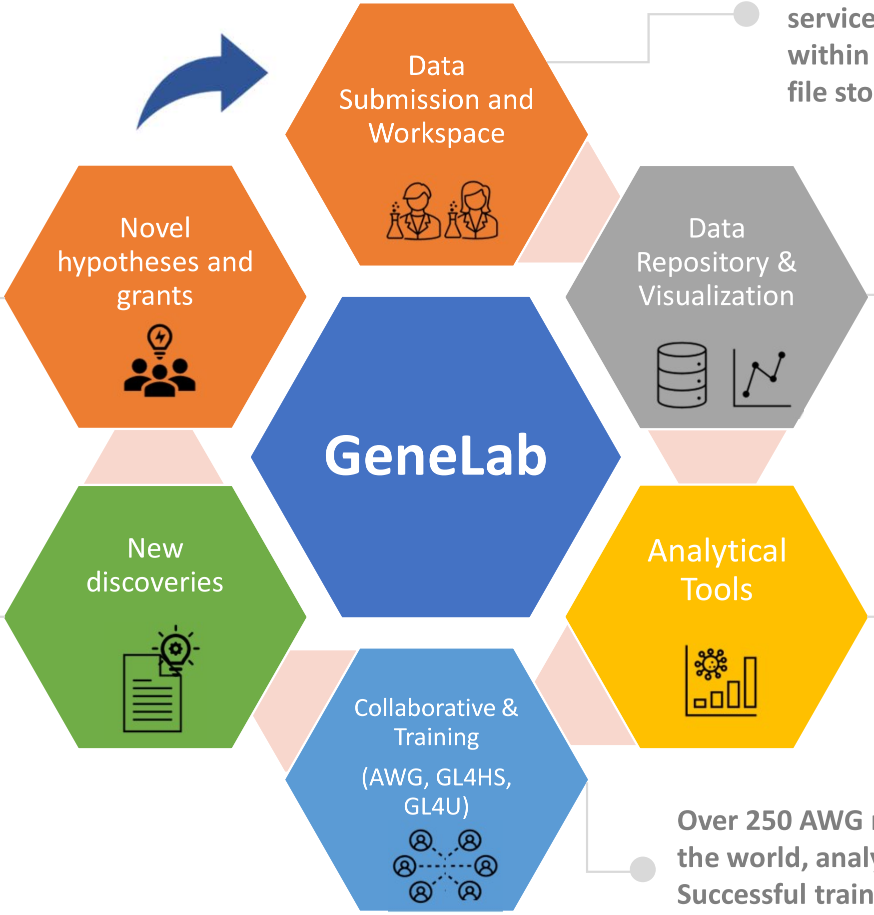
National Aeronautics and
Space Administration

Biological and Physical Sciences

NASEM: GeneLab & Open Science

Sylvain Costes
Open Sciences Data Repository Project
Manager: GeneLab & ALSDA
SCR Branch Chief

Overview



Web-based submission portal to support self-service metadata curation and data submission within FAIR Guidelines. Workspace providing users file storage in S3 and sharing features.

Over 370 public studies from various model organisms from microbes to plants to humans covering the full range of *omics* technologies. Interactive visualization portal to enable knowledge discovery.

Toolshed of bioinformatics tools with user-friendly interface for data analysis at any level (students, citizen scientists, PIs).

Over 250 AWG members from around the world, analyzing open science data. Successful training programs developed for high school and university students.

GeneLab has enabled *40 new publications* re-using data and performing meta-analysis.

Open access data enables discovery of new hypotheses and new ideas for grant proposal. Data from those new research experiments are generated and deposited back into GeneLab.

371
Studies

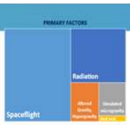
422
Datasets

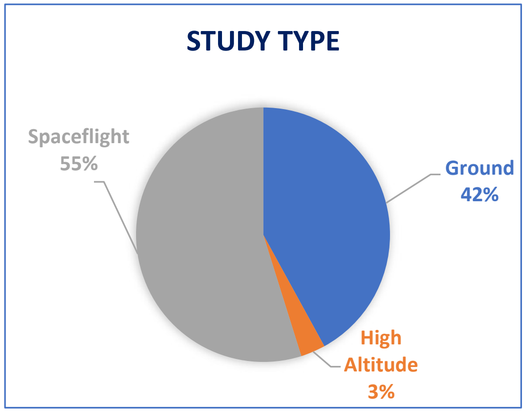
45
Species

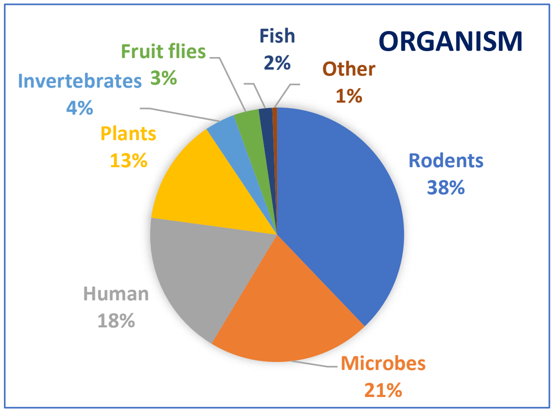
>10
Assays

>135TB
Data

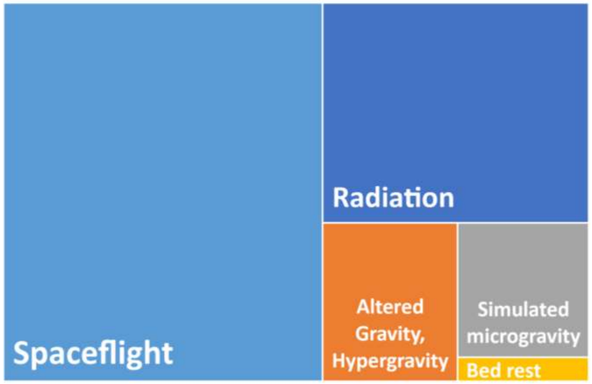
GeneLab Data Repository

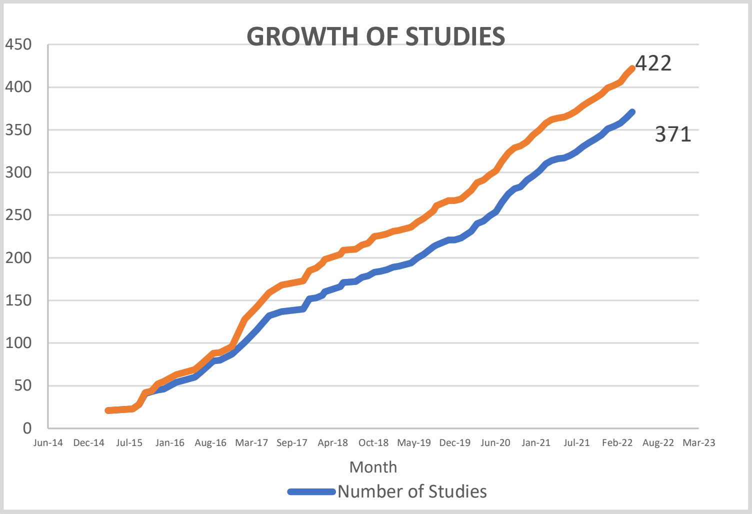


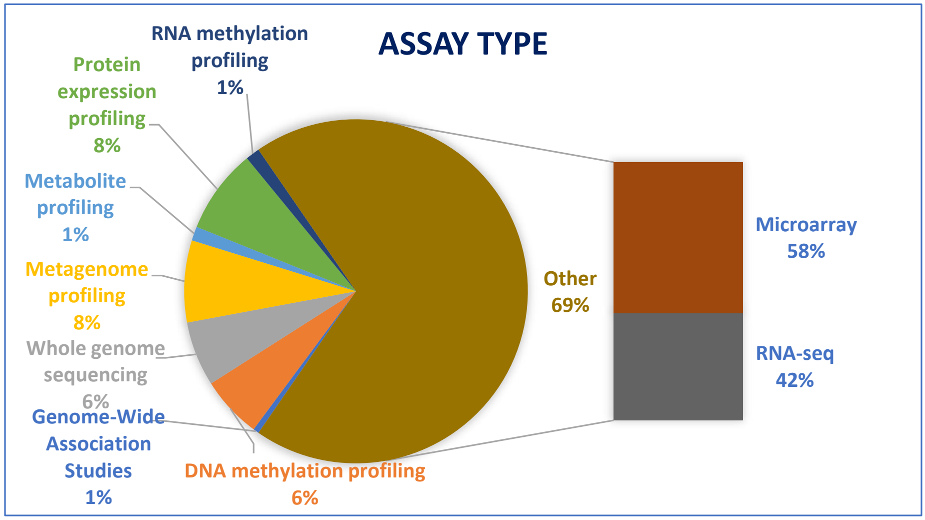

STUDY TYPE


ORGANISM

PRIMARY FACTORS




GROWTH OF STUDIES


ASSAY TYPE

Re-use of Data and Enabling New Discoveries

40 enabled publications (**10 publications produced by the AWGs**) using data available in GeneLab.

Mammalian and Invertebrate Models as Complementary Tools for Gaining Mechanistic Insight on Muscle Responses to Spaceflight

by Thomas Cahill [1], Henry Cope [2], Joseph J. Bass [3], Eliah G. Overbey [4], Rachel Gilbert [5,6], Willian Abraham da Silveira [1,7], Amber M. Paul [5,8,9], Tejaswini Mishra [10], Raúl Herranz [11], Sigrid S. Reinsch [5], Sylvain V. Costes [5], Gary Hardiman [1,12], Nathaniel J. Szewczyk [3,13] and Candice G. T. Tahimic [5,14,*]

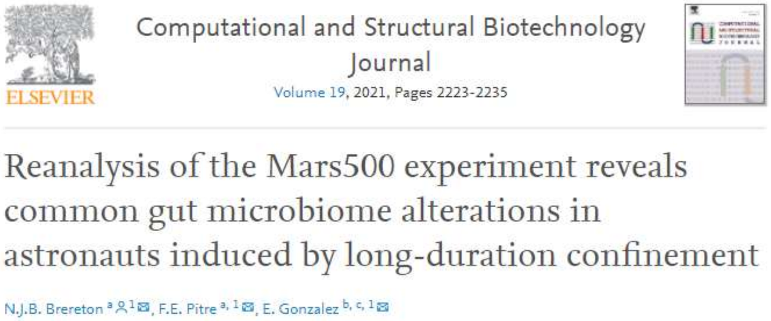
An Integrative Network Science and Artificial Intelligence Drug Repurposing Approach for Muscle Atrophy in Spaceflight Microgravity

Vidya Manian*, Jairo Orozco-Sandoval and Victor Diaz-Martinez

Article

Knowledge Network Embedding of Transcriptomic Data from Spaceflown Mice Uncovers Signs and Symptoms Associated with Terrestrial Diseases

Charlotte A. Nelson [1], Ana Uriarte Acuna [2,3], Amber M. Paul [2,4], Ryan T. Scott [2,3], Atul J. Butte [5,6], Egle Cekanaviciute [2], Sergio E. Baranzini [1,5,7,*] and Sylvain V. Costes [2,*]



ELSEVIER

Computational and Structural Biotechnology Journal

Volume 19, 2021, Pages 2223-2235

Reanalysis of the Mars500 experiment reveals common gut microbiome alterations in astronauts induced by long-duration confinement

N.J.B. Brereton [a, 1], F.E. Pitre [a, 1], E. Gonzalez [b, c, 1]

Rad-Bio-App: a discovery environment for biologists to explore spaceflight-related radiation exposures

Richard Barker, Sylvain V. Costes, Jack Miller, Samrawit G. Gebre, Jonathan Lombardino & Simon Gilroy

npj Microgravity **7**, Article number: 15 (2021) | Cite this article

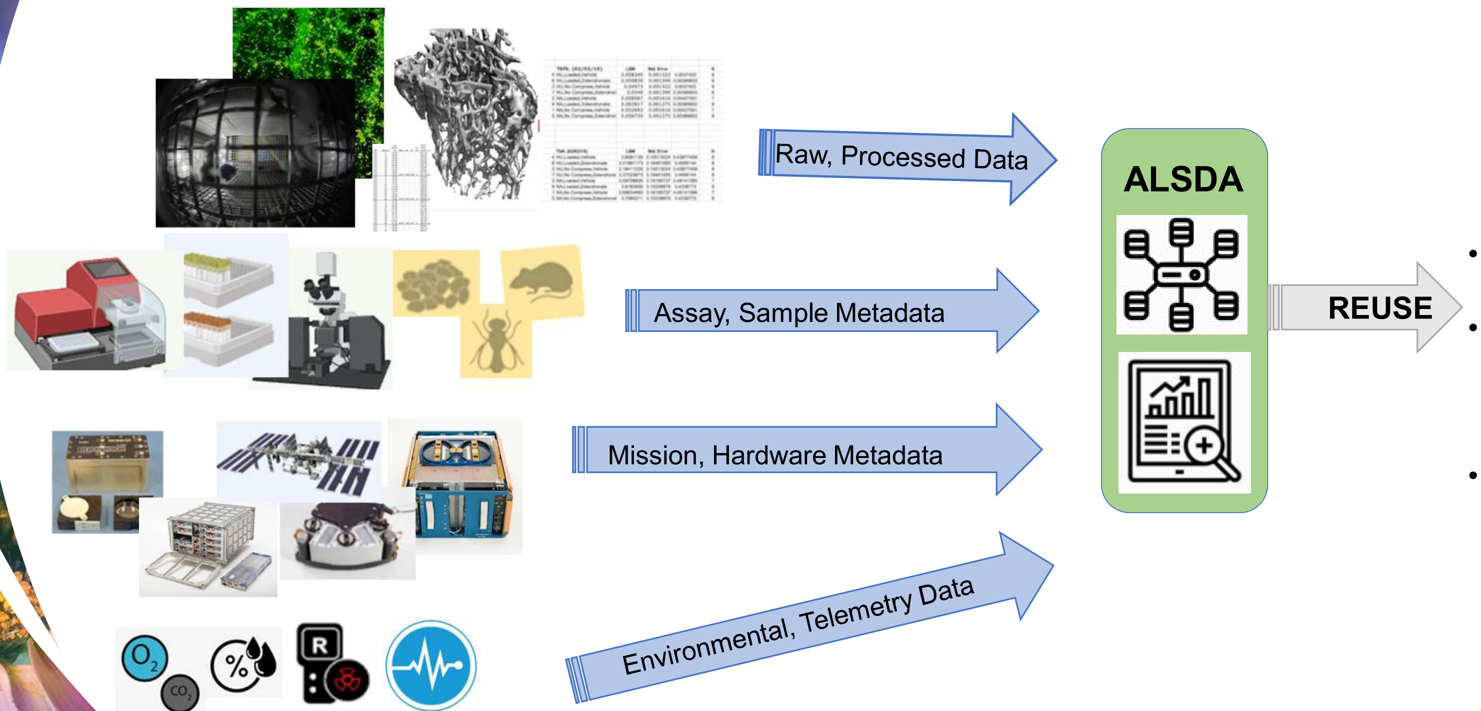
Cell: The biology of spaceflight package

A coordinated package of 29 scientific papers published in five *Cell Press* journals featuring **9** papers utilizing data or resources in GeneLab. *High impact research highlights:*

- Comparative Transcriptomics Identifies Neuronal and Metabolic Adaptations to Hyper gravity and Microgravity in Caenorhabditis elegans, *iScience*
- Comprehensive Multi-omics Analysis Reveals Mitochondrial Stress as a Central Biological Hub for Spaceflight Impact, *Cell*
- NASA GeneLab RNA-seq consensus pipeline: standardized processing of short-read RNA-seq data, *iScience*

Integrating data beyond *omics*

In 2021, the Ames Life Sciences Data Archive (ALSDA) transitioned to use the GeneLab Data Systems. The goal of this integration was to develop a multi-project submission portal to reduce the burden on PIs submitting data and enabling discovery of both omics and phenotypic data.



Raw, Processed Data

Assay, Sample Metadata

Mission, Hardware Metadata

Environmental, Telemetry Data

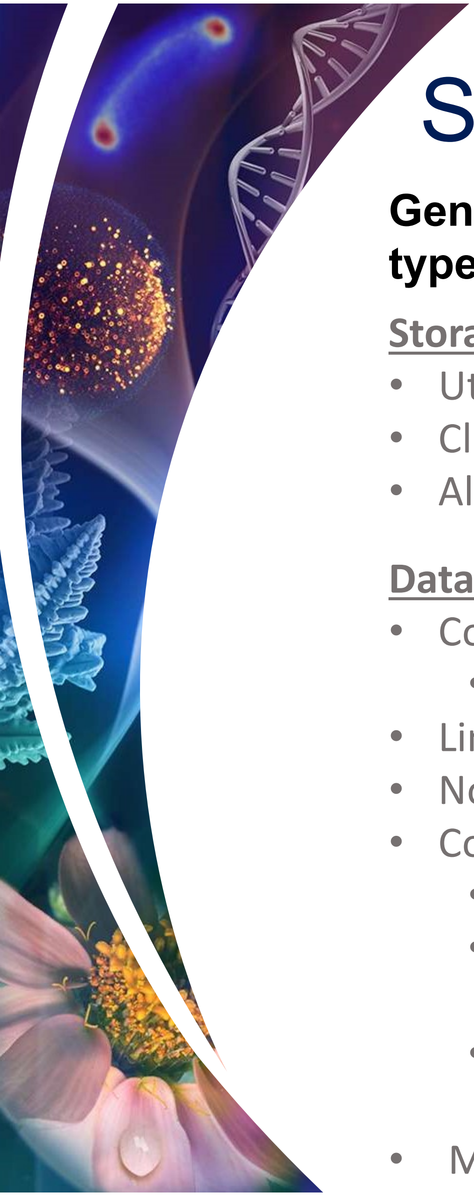
ALSDA

REUSE

Open Science Data Repositories

- Phenotypic-Physiological-Behavioral-Imaging-Level Data
- Mission Telemetry data from spacecraft and hardware associated to experimental studies
- Federated with GeneLab (Molecular Omics-Level Data)

(Images from Ronca et al., 2019 https://doi.org/10.1038/s41598-019-40789-y; Cells, Bone, RR Habitat NASA-ARC)

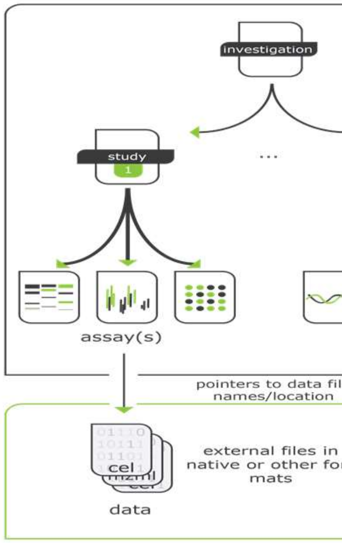


Scalability of Data

GeneLab was developed to be scalable – both for data storage and new data types.

Storage:
- Utilizing cloud for data systems development and data storage
- Cloud provides instant increase in storage
- Allows any data file type

Data:
- Configurable data model to capture any type of experimental data
  - Investigation/Study/Assay (ISA) tab-delimited (TAB) format
- Link multiple assays by sample name
- Not limited to *-omics assays*
- Configure metadata templates to include required fields
  - Qualitative or quantitative measurements (data)
  - Space-relevant fields (for example, radiation dosimetry data per sample)
  - Meets the minimum required information for assays (MIAME, MIxS, MIAPE)
- Machine-readable format – JSON



Omics – new technologies and data types in constant development

In the recent years, new omics technologies have matured such as single cell and spatial omics. Metadata standards were already available and GeneLab was easily able to curate the metadata and organize the files.

GLDS-404

Single cell transcriptional profiling of peripheral blood mononuclear cells (PBMCs) from mice flown on Rodent Research Reference Mission-2 (RRRM-2)

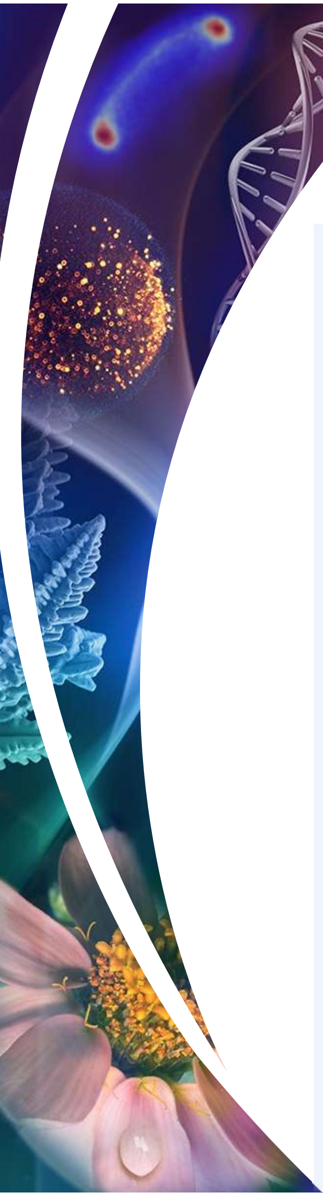
Organisms	Factors	Assay Types	Release Date	Description
Mus musculus	Spaceflight Age	transcription profiling	12-Aug-2021	In the Rodent Research Reference Mission (RRRM-2), forty female C57BL/6NTac mice were flown on the International Space Station. To assess differences in outcomes due to age, twenty 12 week-old and two...

GLDS-270

Spatially resolved transcriptional analysis of hearts from mice flown on the RR-3 mission

Organisms	Factors	Assay Types	Release Date	Description
Mus musculus	Spaceflight	transcription profiling	18-Mar-2020	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 coun...

As new technologies emerge, the GeneLab curation team can create new assay configuration to capture the minimum requirement metadata for each technology. Data standards are provided through standards consortiums and/or scientific community consensus.



Community standards

Standards Consortiums

For omics, many standards for the minimum information about a specific assay experiment exist. For example:

- MIAME - Minimum Information About a Microarray Experiment
- MIAPE – Minimum Information About a Proteomics Experiment
- MIxS – Minimum Information about any (X) Sequence
  - MIGS for genomes
  - MIMS for metagenomes
  - MIMARKS for marker genes
- ENCODE RNAseq experiments

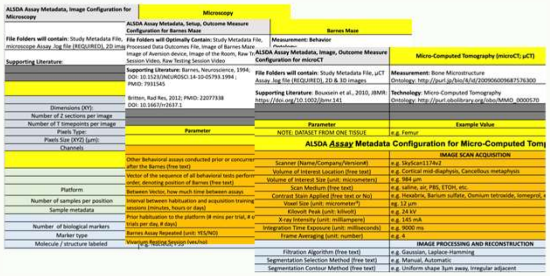
GeneLab uses these standards to ensure data is well curated and complies to the FAIR principles (Findable, Accessible, Interoperable, and Reusable)

Scientific Community Consensus

With the support from our Analysis Working Groups (AWGs), we have developed metadata standards:

- Spaceflight metadata fields by organism type
- Radiation specific metadata fields, including co-developing the Radiation Biology Ontology

ALSDA AWG has contributed their expertise to establish a consensus on standards for phenotypic experiments including assay, sample, and study design metadata which must be collected from PIs to **ensure data reusability.**



ALSDA Assay Metadata, Image Configuration for Microscopy | Microscopy

File Folders will contain: Study Metadata File, microscope Assay .log file (REQUIRED), 2D imag

Supporting Literature:

Dimensions (XY):
Number of Z sections per image
Number of T timepoints per image
Pixels Type:
Pixels Size (XYZ) (µm):
Channels
Platform
Number of samples per position
Sample metadata
Number of biological markers
Marker type
Molecule / structure labeled

ALSDA Assay Metadata, Setup, Outcome Measure Configuration for Barnes Maze | Barnes Maze

File Folders will Optimally Contain: Study Metadata File, Processed Data Outcomes File, Image of Barnes Maze Image of Aversion device, Image of the Room, Raw Tr Session Video, Raw Testing Session Video

Measurement: Behavior

Supporting Literature: Barnes, Neuroscience, 1994; DOI: 10.1523/JNEUROSCI.14-10-05793.1994 ; PMID: 7931545

Britten, Rad Res, 2012; PMID: 22077338 DOI: 10.1667/rr2637.1

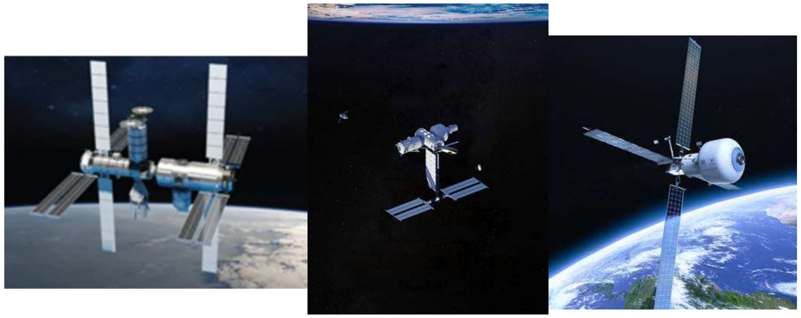
Parameter

Other Behavioral assays conducted prior or concurrer after the Barnes (free text)
Vector of the sequence of all behavioral tests perforr order, denoting position of Barnes (free text)
Between Vector, how much time between assays
Interval between habituation and acquisition training sessions (minutes, hours or days)
Prior habituation to the platform (# mins per trial, # o trials per day, # days)
Barnes Assay Repeated (unit: YES/NO)
Vivarium Resting Session (yes/no)

ALSDA Assay Metadata, Image, Outcome Measure Configuration for microCT	**Micro-Computed Tomography (microCT; µCT)**
File Folders will contain: Study Metadata File, µCT Assay .log file (REQUIRED), 2D & 3D images	**Measurement:** Bone Microstructure Ontology: http://purl.jp/bio/4/id/200906009687576300
Supporting Literature: Bouxsein et al., 2010, JBMR: https://doi.org/10.1002/jbmr.141	**Technology:** Micro-Computed Tomography Ontology: http://purl.obolibrary.org/obo/MMO_0000570
Parameter	**Example Value**
NOTE: DATASET FROM ONE TISSUE	e.g. Femur
ALSDA *Assay* Metadata Configuration for Micro-Computed Tom	
	IMAGE SCAN ACQUISITION
Scanner (Name/Company/Version#)	e.g. SkyScan1174v2
Volume of Interest Location (free text)	e.g. Cortical mid-diaphysis, Cancellous metaphysis
Volume of Interest Size (unit: micrometers)	e.g. 984 µm
Scan Medium (free text)	e.g. saline, air, PBS, ETOH, etc.
Contrast Stain Applied (free text or No)	e.g. Hexabrix, Barium sulfate, Osmium tetroxide, Iomeprol, e
Voxel Size (unit: micrometer³)	eg. 12 µm
Kilovolt Peak (unit: kilivolt)	e.g. 24 kV
X-ray Intensity (unit: milliampere)	e.g. 145 mA
Integration Time Exposure (unit: milliseconds)	e.g. 9000 ms
Frame Averaging (unit: number)	e.g. 4
	IMAGE PROCESSING AND RECONSTRUCTION
Filtration Algorithm (free text)	e.g. Gaussian, Laplace-Hamming
Segmentation Selection Method (free text)	e.g. Manual, Automatic
Segmentation Contour Method (free text)	e.g. Uniform shape 3µm away, Irregular adjacent

Proprietary data

Currently all the data that is published, is openly accessible worldwide. GeneLab has already in place a mechanism for account-based access, for example our Collaborative workspace. This capability can be expanded in the future for:



Astronaut/Human space-relevant data

- Develop a controlled access data portal
- Create an automatic data access request workflow
- Scientists will be able to translate their findings from model organisms to human outcomes

Commercial Space Industry

- Develop a controlled access data portal and an automatic data access request workflow for "closed" data
- Utilize GeneLab infrastructure to collect and host space-relevant data for biological research

Commercial and International Partners

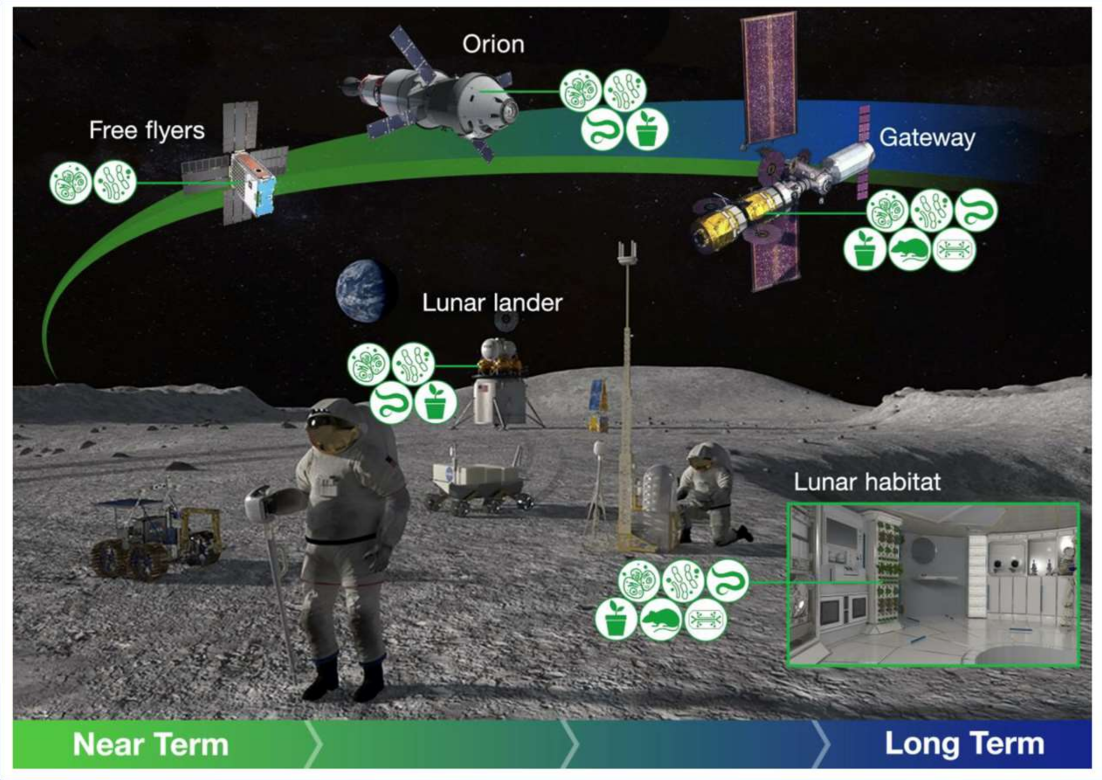
Open access data in GeneLab, **accelerates the pace of scientific discovery** and thus **enables exploration and development of countermeasures** by using systems biology approaches to identify cross-species relevance, mechanisms, biomarkers and potential health risks for LEO and beyond LEO (Lunar and Mars Exploration).

To increase usability and accessibility, space biological research should be available through a common portal. It’s important to work closely with our commercial and international partners to ensure data across agencies and platforms are harmonized and comparable. In addition, systems already developed can be utilize not duplicating efforts and costs for data sharing.

For example, GeneLab already hosts datasets from multiple space agencies (ESA, JAXA, CSA) and from CASIS funded experiments.

In order to continue maximizing the return of spaceflight experiments, we encourage commercial and international partners to utilize the GeneLab Data Systems for their research data, both for open and proprietary data.

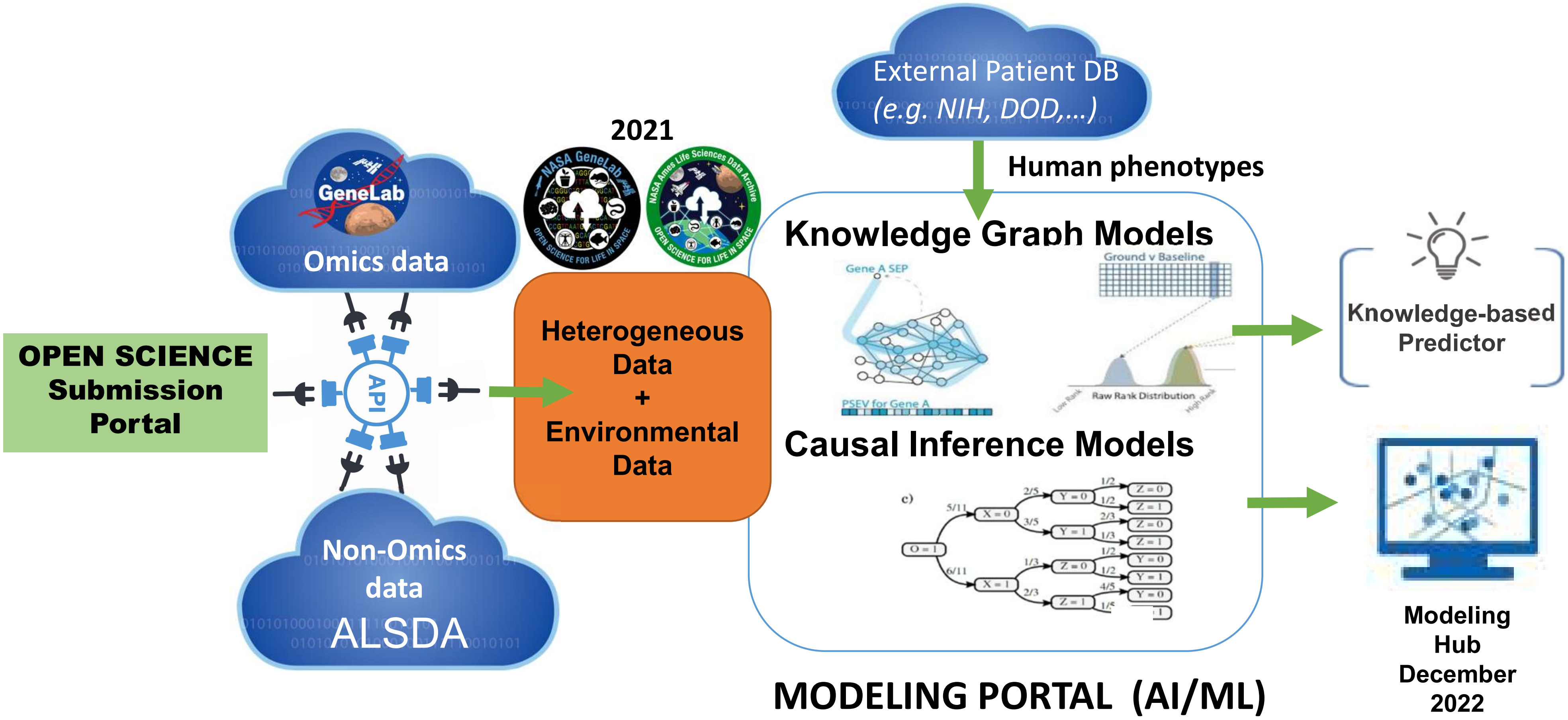
Beyond LEO - Lunar



With limited sample return for various platforms, we are preparing new metadata templates and data streams to host and publish data from future lunar experiments and beyond.

(Credit: NASA Biological and Physical Science Division; Beyond LEO Instrumentation & Science Series Science Working Group, 2021 Report, https://ntrs.nasa.gov/api/citations/20210023324/downloads/BLISS%20SWG%202021%20Report%20Final.pdf)

From multiple databases to a knowledge-based system



External Patient DB
(e.g. NIH, DOD,...)

Human phenotypes

GeneLab
Omics data

2021

OPEN SCIENCE Submission Portal

Heterogeneous Data + Environmental Data

Non-Omics data
ALSDA

Knowledge Graph Models

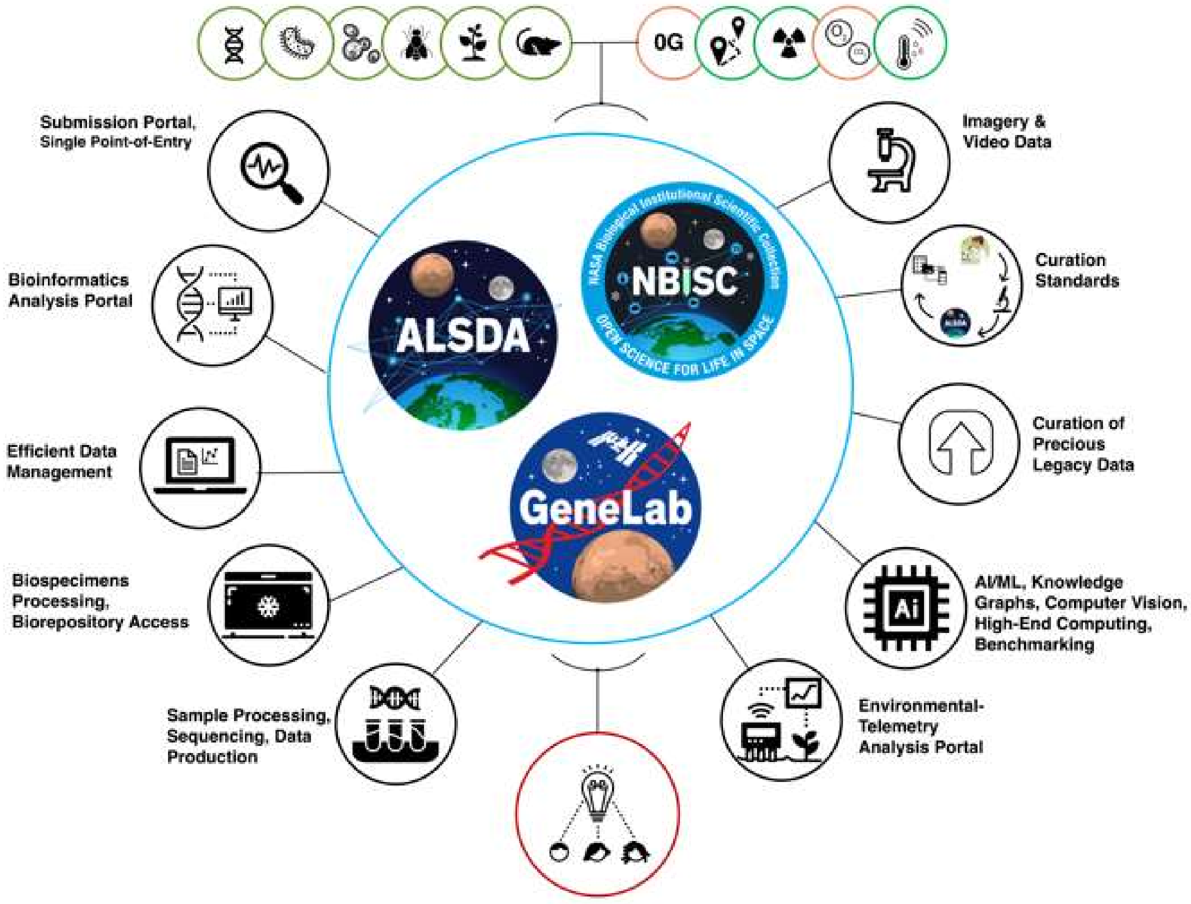
Causal Inference Models

MODELING PORTAL (AI/ML)

Knowledge-based Predictor

Modeling Hub December 2022

Open Science Data Repositories



Submission Portal, Single Point-of-Entry

Bioinformatics Analysis Portal

Efficient Data Management

Biospecimens Processing, Biorepository Access

Sample Processing, Sequencing, Data Production

Imagery & Video Data

Curation Standards

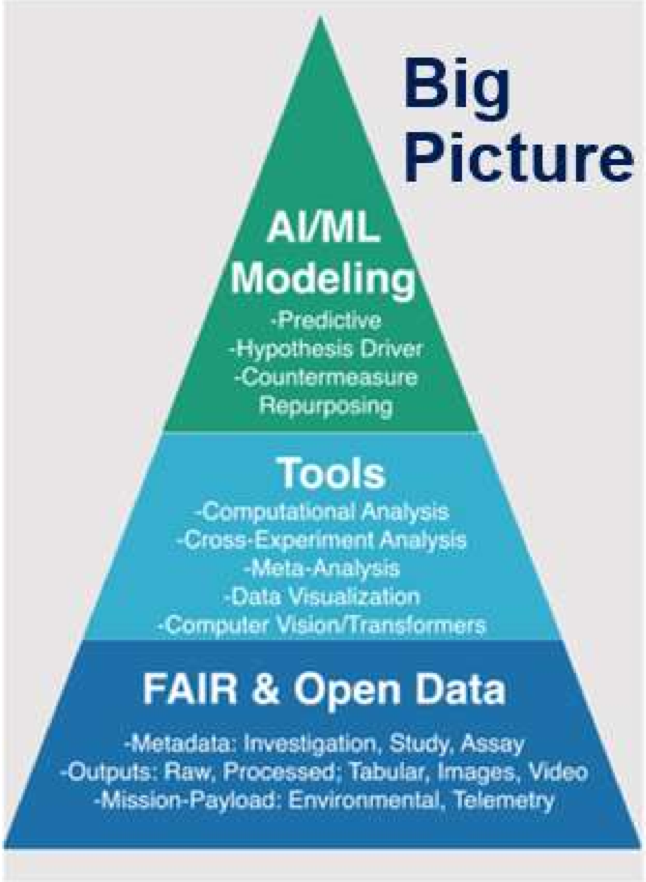
Curation of Precious Legacy Data

AI/ML, Knowledge Graphs, Computer Vision, High-End Computing, Benchmarking

Environmental-Telemetry Analysis Portal

New Knowledge; Faster Pace; Inclusive & Diverse Access

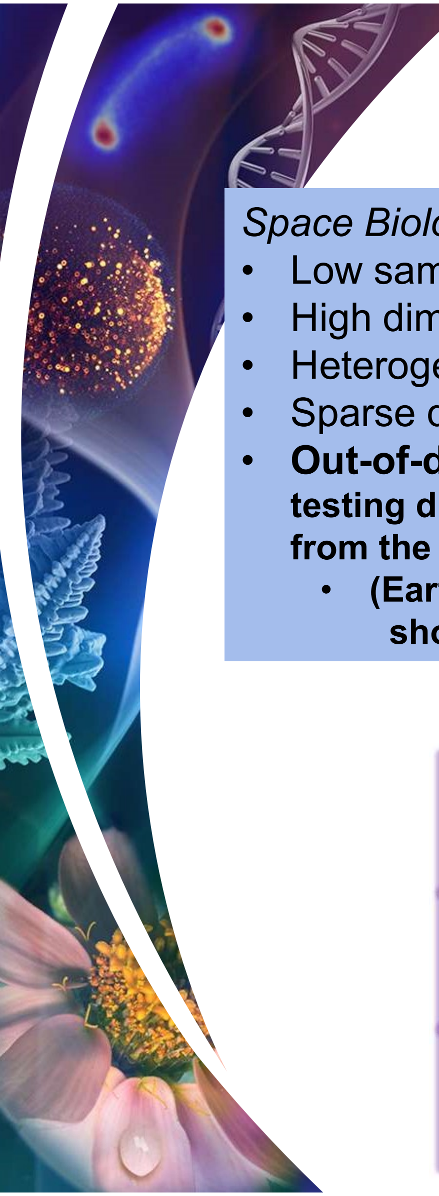
Big Picture



AI/ML Modeling
-Predictive
-Hypothesis Driver
-Countermeasure Repurposing

Tools
-Computational Analysis
-Cross-Experiment Analysis
-Meta-Analysis
-Data Visualization
-Computer Vision/Transformers

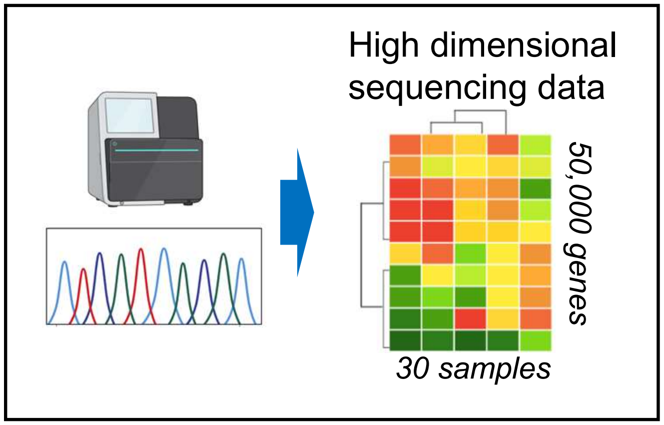
FAIR & Open Data
-Metadata: Investigation, Study, Assay
-Outputs: Raw, Processed; Tabular, Images, Video
-Mission-Payload: Environmental, Telemetry

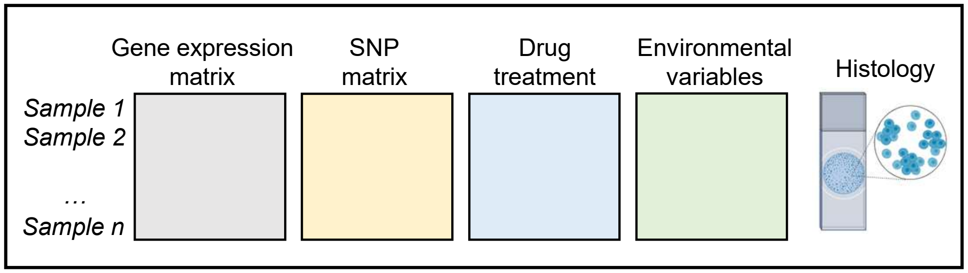


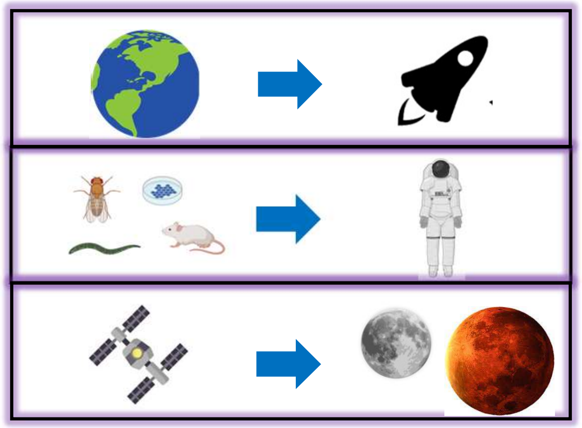
Challenges for Machine Learning in Space Biology

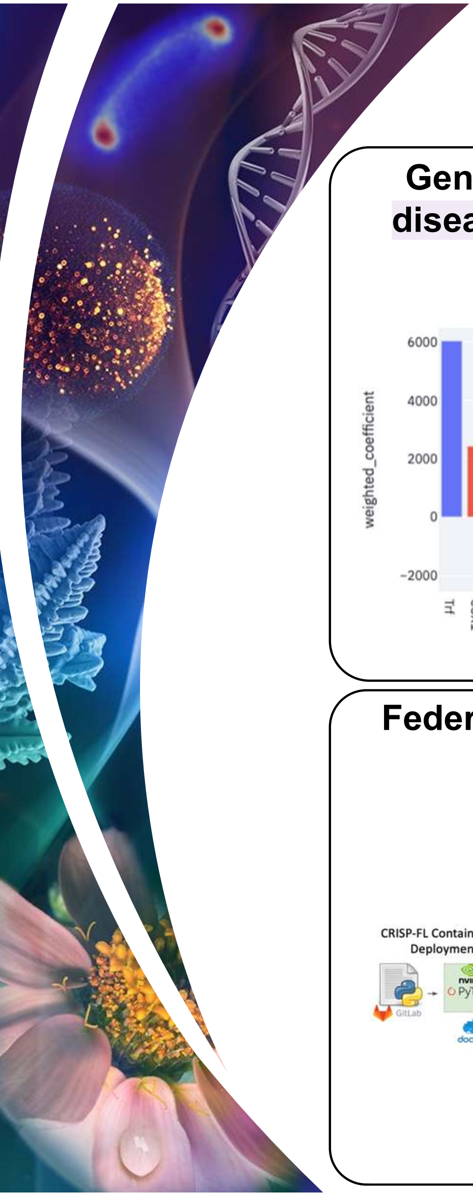
Space Biology Challenges

- Low sample size *n*
- High dimensionality *D*
- Heterogeneous data
- Sparse data
- **Out-of-distribution generalization - the testing distribution is unknown and different from the training**
  - **(Earth -> space, mouse -> human, short term -> long duration spaceflight)**







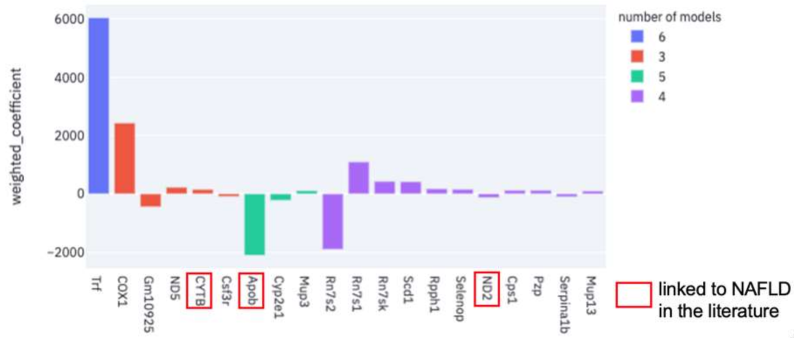


Causal inference in biological systems

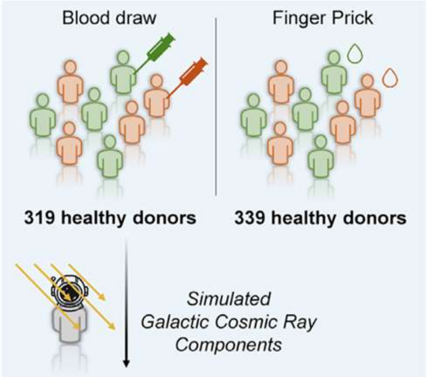
Causal Relation Inference and Search Platform (CRISP)

Genes with a causal relationship to liver disease phenotype in spaceflown rodents

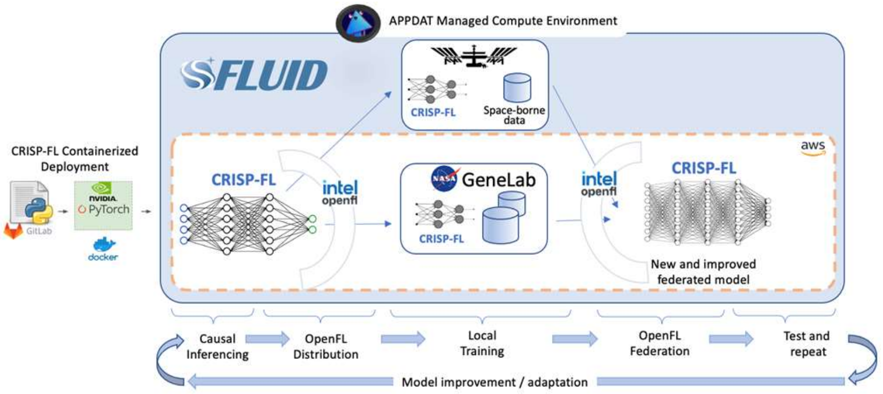
GLDS-47 GLDS-137
GLDS-48 GLDS-168



Genetic variants with a causal relationship to DNA damage and radiation sensitivity in human irradiated immune cells



Federated causal inference between Earth data and spaceborne data



2021 FDL Astronaut Challenge

A novel paradigm for generating human-relevant biomedical insights from observational datasets with limited size by leveraging and augmenting with animal model data

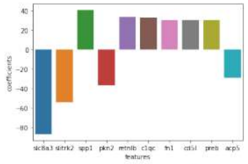


Figure 1: Top-10 IRM features according to feature coefficients with all human and mice gamma-radiation data.

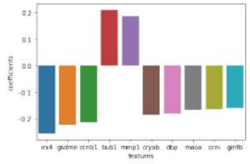
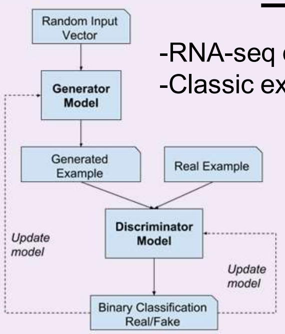


Figure 2: Top-10 IRM features according to feature coefficients with all human and mice heavy-ion radiation data.

AI-readiness and formatting standards: Benchmark datasets for space biology

RNA sequencing dataset



-RNA-seq data quantifies all expressed genes in a sample
-Classic example of high-D (~50k genes), low-N dataset

Approach:
1. Start with real RNA-seq data from GeneLab
2. Generate synthetic RNA-seq data using generative adversarial network (GAN)
3. Benchmark dataset will be high-D and high-N (synthetic)

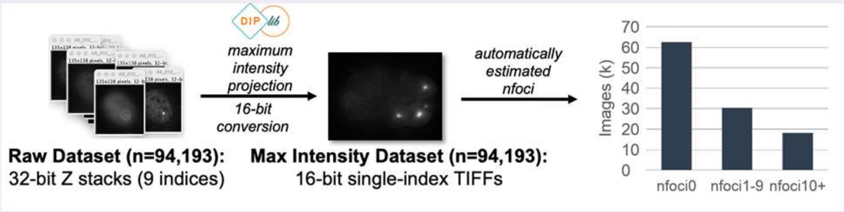
ML applications: e.g. causal inference to identify causal genes with relation to a pathogenic target variable

Microscopy dataset

-Huge amounts of microscopy data in space biology are time consuming to manually annotate through expert review

Approach:

-Mouse radiation exposure microscopy dataset with DNA damage events as distinct foci (PI: Sylvain Costes)



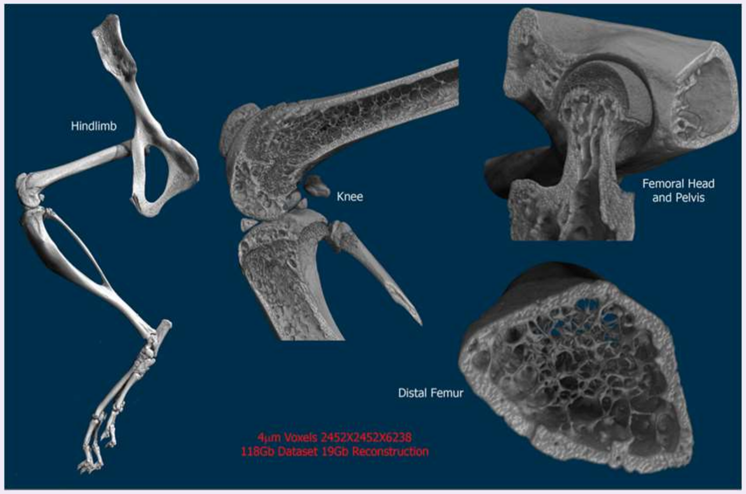
ML applications: e.g. train a self-supervised classifier to detect number of DNA damage foci; or to detect radiation tracks through cells; or to classify images based on the type of radiation.

Bone Computed Tomography (CT) dataset

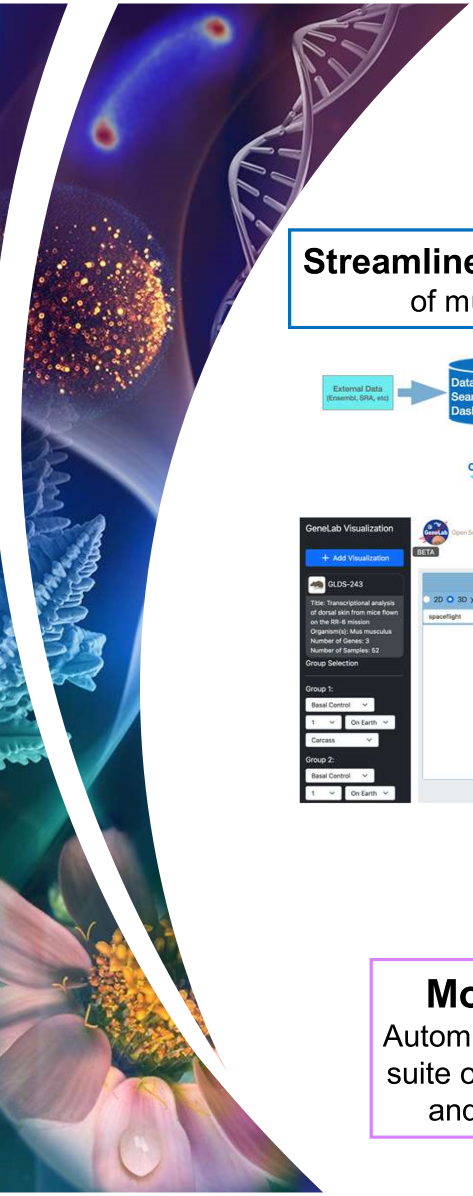
-CT scan is a key assay in space biology to assess bone changes in spaceflight

Approach:

-Mouse hindlimb CT dataset from spaceflight or hindlimb unloading (PI: Eduardo Almeida)

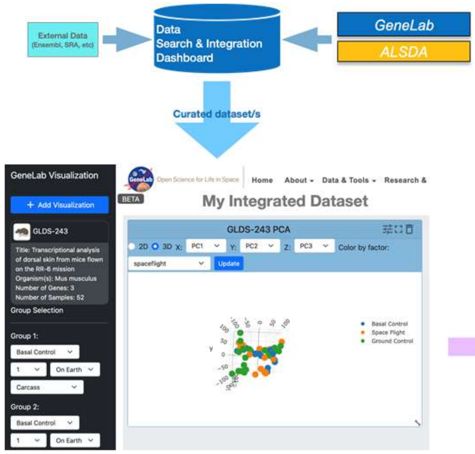


ML applications: e.g. train a classifier to detect the type of stressor based on bone loss, to predict future bone loss when exposed to that stressor.



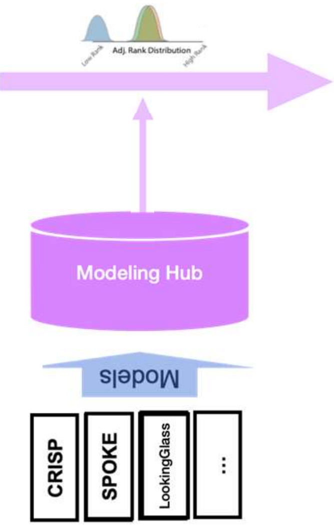
Space Biology Model Hub and Analysis Portal

Streamlined Data Integration
of multiple datasets

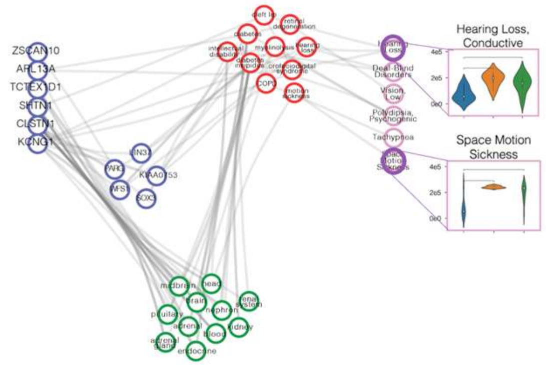


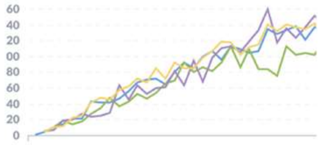
Title: Transcriptional analysis of dorsal skin from mice flown on the RR-6 mission
Organism(s): Mus musculus
Number of Genes: 3
Number of Samples: 52

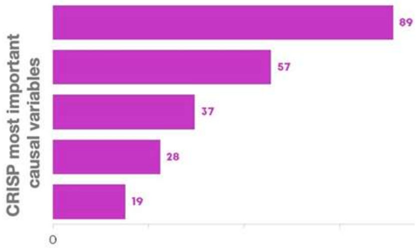
Modeling Hub
Automated pipelines for a suite of machine learning and modeling tools

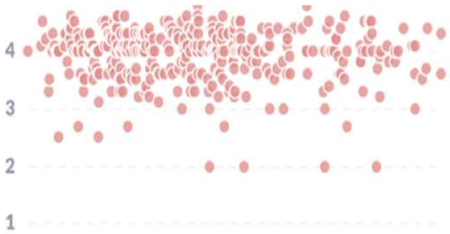


Analysis Portal
Interactive analysis dashboard of modeling and analysis results









Leading the Path to Open-Source Science

Transform to Open Science (TOPS) is a $40 million*
5-year NASA Science Mission Directorate mission

Objectives:

- ★ Increase understanding & adoption of open science.
- ★ Accelerate major scientific discoveries.
- ★ Broaden participation by historically underrepresented communities.

Year of Open Science

Goals for 2027:

- ★ 20K earn Open Science Badge
- ★ 5+ major discoveries
- ★ Increase participation of underrepresented groups by 2x

*pending appropriations

Training the Next Generation of Scientists

GeneLab for High Schools (GL4HS): A four-week intensive training summer program for rising high school juniors and seniors to learn bioinformatics and computational biology methods and techniques to analyze space omics data.

Learn more and apply at: https://www.nasa.gov/ames/genelab-for-high-schools

GeneLab for Colleges/Universities (GL4U): For educators and students to learn how analyze omics data using GeneLab standard pipelines and space-relevant data

Access to course materials: https://github.com/nasa/GeneLab-Training/tree/main/GL4U

Space Life Sciences Training Program (SLSTP): Provides undergraduate students entering their junior or senior years, and entering graduate students, with professional experience in space life science disciplines.

Learn more and apply at: https://www.nasa.gov/ames/research/space-life-sciences-training-program

Spaceflight Technology, Applications, and Research(STAR): The annual course targets principal investigators (PIs), senior research scientists, and postdoctoral scholars and aims to facilitate their entry to space biology and preparation for conducting spaceflight experiments using NASA and commercial platforms.

Applications open until May 30th: https://science.nasa.gov/biological-physical/programs/star

NASA Postdoctoral Program: If you're an early-career or senior scientist, apply to the NASA Postdoctoral Program to help pursue NASA's mission and experience the world's most diverse technology and expertise.

Learn more at: https://npp.orau.org/

Near-term Goals

Oct 1st, 2022

Release the Multi-Project Submission Portal

New Interface and curated phenotypic data (ALSDA)

FY 2023

Release Modeling Hub and Analysis Portal

Enable discovery of imaging data

Ease data ingest > 1 TB

FY 2024

Develop smart assist submission features

Automate data stream from lunar experiments

Participate in SMD-Source Science Initiatives – Present opportunities to the BPS scientific community

Continue to ingest and host experimental and mission telemetry from space-relevant experiments

Pending yearly budget

Thank you!

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

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

Open Science for Life in Space is funded by the NASA Space Biology program and NASA Human Research Program

BACK UP

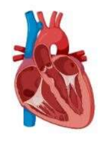
NASA Biological Open Science Resources

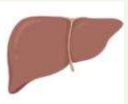
Biospecimen Sharing Program (BSP)

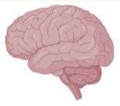
- *Dissects and preserves* rodent tissues from Flight and Ground investigations
- *Coordinates* internal tissue sharing

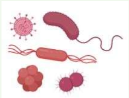
NASA Biological Institutional Scientific Collection (NBISC)

- *Collection* of non-human specimens and space microbial culture









Ames Life Sciences Data Archive (ALSDA)

- *Collects and curates physiological,* mission, project and imaging data

GeneLab (GL)

- *Collects and curates* omics data

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?

Visualize Data
Interact with GeneLab processed data

LATEST NEWS

NASA's GeneLab Develops RNA-seq Consensus Pipeline

Re-adaptation After Simulated Spaceflight

Common gut microbiome alterations in astronauts

GL4HS 2021 - Another Successful Year!

TRANSCRIPTOMICS

GENOMICS (including metagenomics, epigenomics)

PROTEOMICS / METABOLOMICS

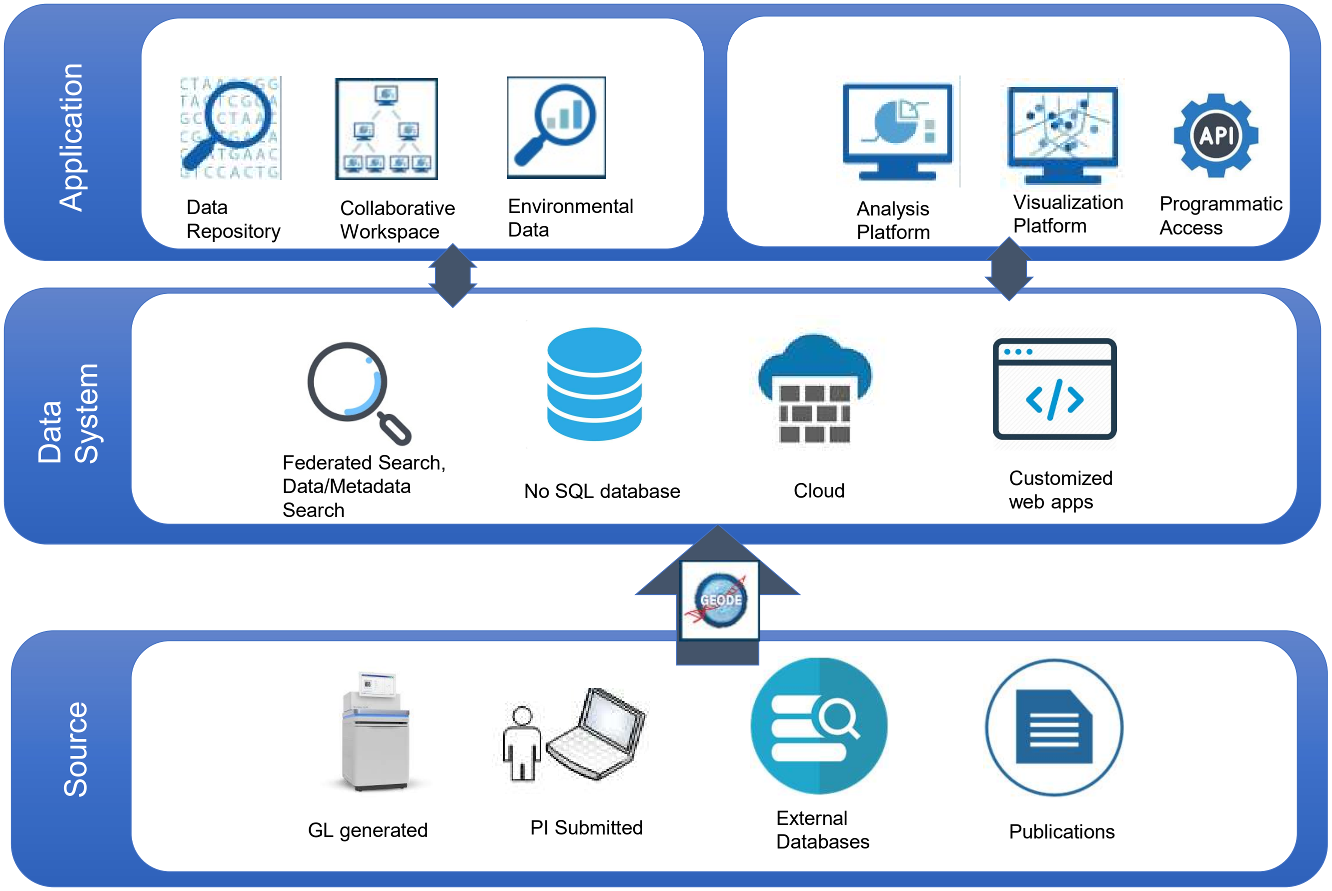
PROCESSED

NASA BPS Open Science Enterprise Solution: genelab.nasa.gov

- Open access data
- **FAIR (Findable, Accessible, Interoperable, Reusable)**
- Controlled access tools
- API - internal and external
- User Friendly Interface
- Tutorials
- Self-service Submission Portal

- Federated search – GEO, PRIDE, MG-RAST, **ALSDA**
- Database & Cloud – Scalable, easy access, fast
- Web apps
  - Data Access & Management
  - Security
  - Operation
  - Governance and Integration
- Open Source software – *no maintenance cost for software*

- Multiple data sources
  - Standard metadata organization
  - Open file formats



Application

Data Repository

Collaborative Workspace

Environmental Data

Analysis Platform

Visualization Platform

Programmatic Access

Data System

Federated Search, Data/Metadata Search

No SQL database

Cloud

Customized web apps

GEODE

Source

GL generated

PI Submitted

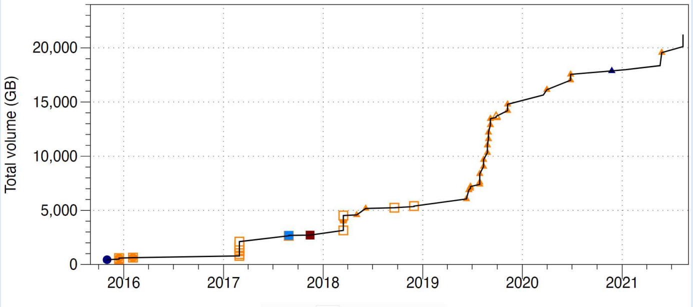
External Databases

Publications

Omics Data Generation

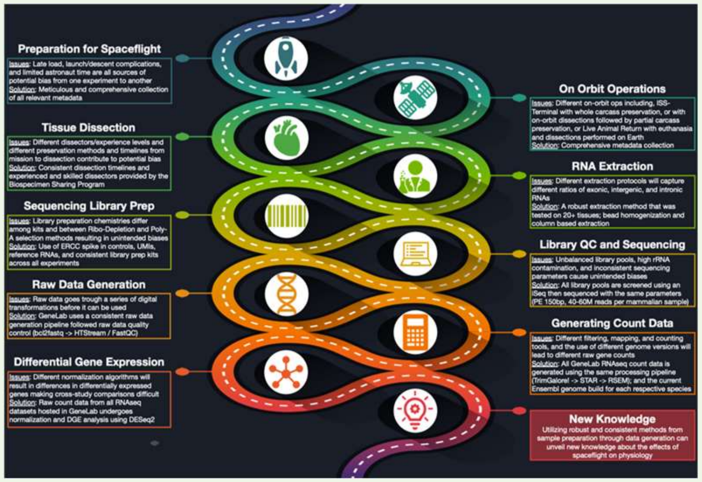
Maximizing spaceflight experiments by generating omics data without *__any propriety time__* for open science.

- Maximizing access to spaceflight data through tissue sharing efforts.
- Upon curation, these data are released *immediately* to the public through the GeneLab data system.
- To date, **59 studies** are available including data from: Rodent Research missions and Plant experiments. Assays include:
  - Transcriptomics
    - Bulk RNASeq
    - Single Cell RNASeq
    - Spatial Transcriptomics
  - Epigenomics
  - Proteomics
- Enabling meta-analysis publications



Standardizing Sample Processing and Sequencing for Spaceflight Samples

- GeneLab also works with NASA-funded principal investigators (PI's) to generate proprietary data using GeneLab standard assays.
- Optimized processing protocols and high-quality data outputs
- Data Processing services
- Request quote: https://genelab.nasa.gov/form/genelab-sequencing-services



Preparation for Spaceflight

Issues: Late load, launch/descent complications, and limited astronaut time are all sources of potential bias from one experiment to another
Solution: Meticulous and comprehensive collection of all relevant metadata

On Orbit Operations

Issues: Different on-orbit ops including, ISS-Terminal with whole carcass preservation, or with on-orbit dissections followed by partial carcass preservation, or Live Animal Return with euthanasia and dissections performed on Earth
Solution: Comprehensive metadata collection

Tissue Dissection

Issues: Different dissectors/experience levels and different preservation methods and timelines from mission to dissection contribute to potential bias
Solution: Consistent dissection timelines and experienced and skilled dissectors provided by the Biospecimen Sharing Program

RNA Extraction

Issues: Different extraction protocols will capture different ratios of exonic, intergenic, and intronic RNAs
Solution: A robust extraction method that was tested on 20+ tissues; bead homogenization and column based extraction

Sequencing Library Prep

Issues: Library preparation chemistries differ among kits and between Ribo-Depletion and Poly-A selection methods resulting in unintended biases
Solution: Use of ERCC spike in controls, UMIs, reference RNAs, and consistent library prep kits across all experiments

Library QC and Sequencing

Issues: Unbalanced library pools, high rRNA contamination, and inconsistent sequencing parameters cause unintended biases
Solution: All library pools are screened using an iSeq then sequenced with the same parameters (PE 150bp, 40-60M reads per mammalian sample)

Raw Data Generation

Issues: Raw data goes trough a series of digital transformations before it can be used
Solution: GeneLab uses a consistent raw data generation pipeline followed raw data quality control (bcl2fastq -> HTStream / FastQC)

Generating Count Data

Issues: Different filtering, mapping, and counting tools, and the use of different genome versions will lead to different raw gene counts
Solution: All GeneLab RNAseq count data is generated using the same processing pipeline (TrimGalore! -> STAR -> RSEM); and the current Ensembl genome build for each respective species

Differential Gene Expression

Issues: Different normalization algorithms will result in differences in differentially expressed genes making cross-study comparisons difficult
Solution: Raw count data from all RNAseq datasets hosted in GeneLab undergoes normalization and DGE analysis using DESeq2

New Knowledge

Utilizing robust and consistent methods from sample preparation through data generation can unveil new knowledge about the effects of spaceflight on physiology

GeneLab Power Users

GeneLab Analysis Working Groups (AWGs) *consist of* ***250+ scientists*** *from multiple space agencies, international institutions, and industry. Scientists meet monthly with each group to analyze data in the GeneLab repository.*
We invite you to join - https://genelab.nasa.gov/awg/join!

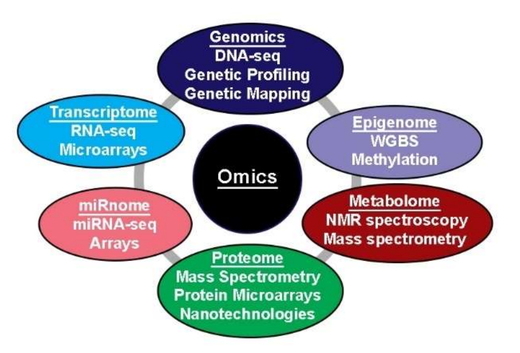
ANIMAL

68 members

Facilitates the use of omics in understanding basic mechanisms by which animals and constituent tissues and cells adapt to the spaceflight environment.

MULTI-OMICS

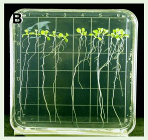
128 members



Interactions between the different omics to provide complete understanding of the entire system begin studied.

PLANTS

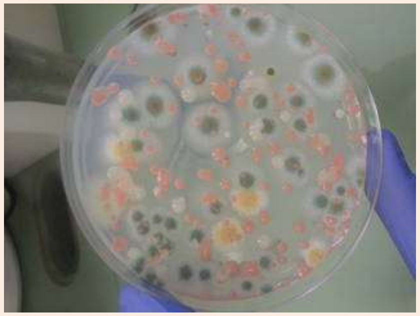
58 members



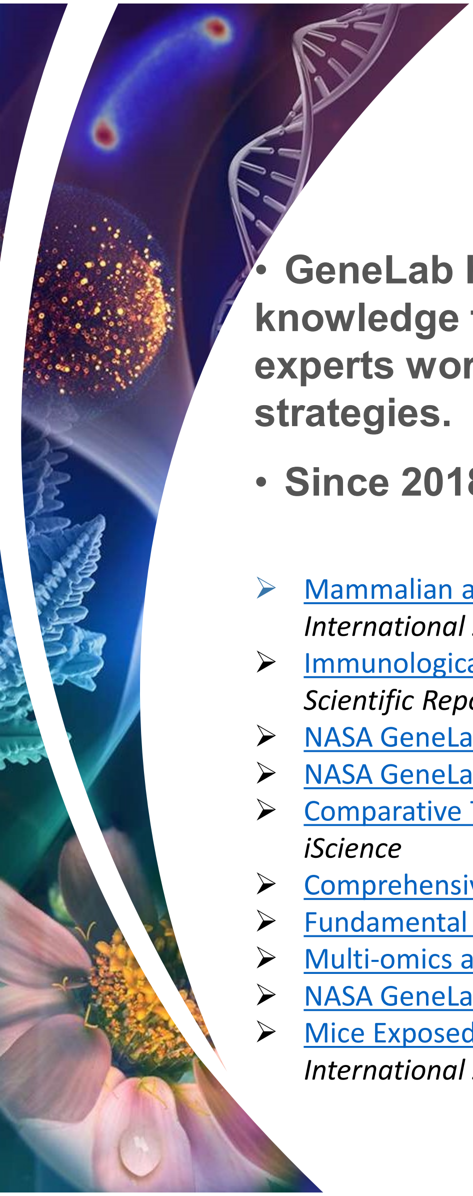
Share and discuss the latest developments in ***Astrobotany*** *– the discipline of botany concerned with interactions between plant biology and space environment.*

MICROBES

50 members



Focuses on analyzing microbial datasets within GeneLab that includes gene-expression, proteomic, metabolomic and environmental metagenomic datasets.



Accelerating the pace of scientific discovery through open data

- **GeneLab has established the AWGs with the goal of maximizing the generation of new knowledge from these rare and complex spaceflight datasets. With over 250+ scientists and experts worldwide the four working groups focus Animal, Plants, Microbe and Multi-omics strategies.**
- **Since 2018, the AWGs have published 10 peer-reviewed publication re-using data in GeneLab:**

- Mammalian and Invertebrate Models as Complementary Tools for Gaining Mechanistic Insight on Muscle Responses to Spaceflight, *International Journal of Molecular Sciences*
- Immunological and hematological outcomes following protracted low dose/low dose rate ionizing radiation and simulated microgravity, *Scientific Reports*
- NASA GeneLab RNA-seq consensus pipeline: standardized processing of short-read RNA-seq data, *iScience*
- NASA GeneLab RNA-seq consensus pipeline: standardized processing of short-read RNA-seq data, *Cell System*
- Comparative Transcriptomics Identifies Neuronal and Metabolic Adaptations to Hypergravity and Microgravity in Caenorhabditis elegans, *iScience*
- Comprehensive Multi-omics Analysis Reveals Mitochondrial Stress as a Central Biological Hub for Spaceflight Impact, *Cell*
- Fundamental Biological Features of Spaceflight: Advancing the Field to Enable Deep-Space Exploration, *Cell*
- Multi-omics analysis of multiple missions to space reveal a theme of lipid dysregulation in mouse liver, *Science Reports*
- NASA GeneLab Platform Utilized for Biological Response to Space Radiation in Animal Models, *Cancers*
- Mice Exposed to Combined Chronic Low-Dose Irradiation and Modeled Microgravity Develop Long-Term Neurological Sequelae, *International Journal of Molecular Sciences*