

Plan Overview

A Data Management Plan created using DMPTool

DMP ID: <https://doi.org/10.48321/D17352>

Title: CAREER: Defining cell cycle phases and quiescence in any cell type

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Template: NSF-BIO: Biological Sciences

Project abstract:

The long-term goal of this research and education plan is to seamlessly integrate single-cell experimental profiling and computational modeling to characterize the cell cycle and quiescence and introduce high school students to the power of computational modeling in biomedical applications. The cell cycle is a highly conserved biological process that culminates in a cell dividing into two daughter cells. Cells can exit the cell cycle into a quiescent G0 state, and re-enter the cell cycle to divide with the proper signals 1,2. Actively proliferating cell populations are not synchronized to the same cell cycle phase, leading to all cell cycle states being present in the population at any given time. Early studies characterizing the cell cycle used population-level transcriptomic profiling of forcibly synchronized cells to observe the tightly regulated transcriptional programs of the cell cycle 3. A significant limitation of the synchronized population-level experiments is that they do not capture the signature or marker genes for quiescent-like G0 states. The lack of a transcriptional signature and marker genes for quiescent cells is a gap in the field that affects all single-cell studies that are confounded by the biological signal produced by the cell cycle and quiescence. Single-cell RNA-seq (scRNA-seq) has solved this problem by allowing the characterization of all the cell cycle and quiescent states in a population of cells without synchronization. The PI's first publication as an independent researcher used

scRNA-seq to characterize all the cell cycle phases of human neural stem cells (hNSCs) and discovered a quiescent-like transcriptional state called Neural G0 4. Gaps in our knowledge about quiescence are the focus of this proposal and will be addressed by: Isolating, characterizing, and classifying quiescent-like G0 cells from each dermal layer. Creating a causal and mechanistic transcriptional regulatory network from scRNA-seq profiles of hNSCs to discover regulators of the Neural G0 transcriptional signature. Use Boolean network modeling to predict the dynamics of TF regulatory networks for quiescent-like G0 states and validate them experimentally.

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CAREER: Defining cell cycle phases and quiescence in any cell type

Data and Materials Produced

Describe the types of data, physical samples or collections, software, curriculum materials, and other materials to be produced in the course of the project. (For collaborative proposals, the DMP must cover all the various data types being collected by each collaborator.)

The projects from this proposal will produce:

- Flow cytometry data
- scRNA-seq profiles
- Software
 - Single-cell classifier of cell cycle phases and G0
 - Single-cell transcriptional regulatory network inference
 - Boolean network modeling
- Curriculum materials from educational outreach activities
 - High school STEM class unit
 - Online graduate class through ASU

Standards, Formats and Metadata

Describe the standards to be used for all the data types anticipated, including data or file format and metadata. [Note: Where existing standards are absent or deemed inadequate, this should be documented along with any proposed solutions or remedies.]

Standards for each include:

- Flow cytometry data - data and capture parameters will be recorded using the MIFlowCyt standards.
- scRNA-seq profiles - data and all relevant metadata will be recorded using the minSCe standards.
- Software will be developed with open-source standards, a GPLv3 license, the code will be placed in github and documented compliant with PEP 8, and tutorials and vignettes will be provided.
- Curriculum materials from educational outreach activities
 - High school STEM class unit - will be developed to meet the standards of the NGSS and deposited on OER.org.
 - Online graduate class through ASU - will be developed and deployed through ASU online.

Roles and Responsibilities

Describe the roles and responsibilities of all parties with respect to the management of the data

(including contingency plans for the departure of key personnel from the project).

The PI Dr. Plaisier will oversee the generation of data and the depositing of data and metadata into relevant repositories.

Dissemination Methods

Describe the dissemination methods that will be used to make data and metadata available to others during the period of the award, and any modifications or additional technical information regarding data access after the grant ends.

Standards for each include:

- Flow cytometry data - all data and metadata will be deposited into flowrepository.org.
- scRNA-seq profiles - all data and metadata will be submitted to SRA and GEO.
- Software - code will be placed in github and documented compliant with PEP 8, and tutorials and vignettes will be provided in github.com as well. Packages will be made available through CRAN and PyPI, and as preinstalled docker containers from DockerHub.
- Curriculum materials from educational outreach activities
 - High school STEM class unit - will be deposited on OER.org.
 - Online graduate class through ASU - will be developed and deployed through ASU online.

Policies for Data Sharing and Public Access

Describe the PI's policies for data sharing, public access and re-use, including re-distribution by others and the production of derivatives. Where appropriate, include provisions for protection of privacy, confidentiality, security, intellectual property rights and other rights.

All data and metadata will be made available alongside all analysis scripts. The PI has an open-source policy for all software that will be developed under GPLv3 software licenses.

Archiving, Storage and Preservation

Where relevant, describe plans for archiving data, samples, software, and other research products, and for on-going access to these products through their lifecycle of usefulness to research and education. Consider which data (or research products) will be deposited for long-term access and where. (What physical and/or cyber resources and facilities (including third party resources) will be used to store and preserve the data after the grant ends?)

The methods used to disseminate will also be used to archive, store, and preserve the data and metadata through public repositories:

- Flow cytometry data - all data and metadata will be deposited into flowrepository.org.
 - scRNA-seq profiles - all data and metadata will be submitted to SRA and GEO.
 - Software - code will be placed in [github](https://github.com) and documented compliant with PEP 8, and tutorials and vignettes will be provided in github.com as well. Packages will be made available through CRAN and PyPI, and as preinstalled docker containers from DockerHub.
 - Curriculum materials from educational outreach activities
 - High school STEM class unit - will be deposited on OER.org.
 - Online graduate class through ASU - will be developed and deployed through ASU online.
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Planned Research Outputs

Dataset - "Flow cytometry data"

Flow-cytometry will be used to observe single cells in various cell cycle phases based on four stains described in the project description.

Dataset - "scRNA-seq"

Single-cell RNA-seq data will be collected for multiple goals in this proposal

Software - "Software for single cell analysis"

We will develop multiple different software artifacts during the course of the grant to facilitate single cell analysis of the cell cycle.

Interactive resource - "Curriculum"

Curriculum will be developed to teach students about machine learning.

Planned research output details

Title	Type	Anticipated release date	Initial access level	Intended repository(ies)	Anticipated file size	License	Metadata standard(s)	May contain sensitive data?	May contain PII?
Flow cytometry data	Dataset	2027-12-31	Open	FlowRepository		Creative Commons Attribution 4.0 International	MIFlowCyt	No	No
scRNA-seq	Dataset	Unspecified	Open	NCBI Gene Expression Omnibus		None specified	minSCe	No	No
Software for single cell analysis	Software	Unspecified	Open	GitHub		None specified	None specified	No	No
Curriculum	Interactive resource	Unspecified	Open	OER Commons		None specified	None specified	No	No