**Jerby Lab: Documentation Guidelines**

**This document lays out the expectations for people working in the Jerby lab. Please read it thoroughly, and if there is ANYTHING that doesn’t make sense or that you think is in any way not the right expectation, then let me (Livnat) know – I am happy to discuss any aspect, individually or as a group. Nothing is unchangeable but I ask you to respect the process and abide by the expectations as written here unless we have had an explicit conversation that agrees to some changes.**

**1. General expectations.** Research methods and data are expected to be meticulously and faithfully recorded. Each lab member should keep a formal lab notebook to document each and every experiment they conduct in the lab. Your research is meant to move the entire field forward, which is impossible without reproducible and replicable procedures/results. Proper documentation and sharing of methodology are of outmost importance! Fabrication and/or falsification of results and plagiarism are wholly unacceptable and will not only affect your reputation but those of collaborators, the PI, the department, and the University. Concerns of academic misconduct should be brought to my attention immediately.

**2. Shared resource of protocols**

The Jerby lab maintains a share resource of protocols and lab/standard operating procedures. This is resource is meant to provide a detailed, stepwise, description that (if followed word-by-word) should allow each and every member of the lab to successfully conduct a wide range of experiments and techniques that we have optimized and mastered. Each member of the lab is expected to both use and contribute to the maintenance and update of this resource.

Contributing to the lab protocol resource: How does it work?

As we are now re-organizing this resource, each member of the lab is asked to add *ALL* of their protocols to the shared Oak directory:

smb://oak-smb-ljerby.stanford.edu/groups/ljerby/SharedResources/Protocols.

See “connection to Oak” below. If you are having issues connecting to Oak, please place your protocols in the lab’s Google drive [here](https://drive.google.com/drive/u/1/folders/16b3uy0EhsIYqsuU58Z88Xa9unLba4WPO), and ensure you can connect to the lab’s Oak repositories by mid-January.

The lab protocols’ resource should be as comprehensive as possible, but please avoid duplications of protocols and help us keep it organized.

Use the following nomenclature when naming the protocols you add: JLabProtocols\_XX\_ZZ\_VV.docx, XX denotes the serial number of the protocol (for now, keep it as XX, and it will modified by a designated member), ZZ is the protocol title (please use the minimal most informative title possible), VV denotes the version number of the protocol, as each protocol can be updated and have a several versions. Note that all previous version of the protocol will be saved, and files/protocols names will not be changed retrospectively.

Protocol updating. If you realize that a certain protocol is missing important information, it is extremally important that you will add that information to the protocol so that both you and other members of the lab will not waste time (and money) troubleshooting and trying to figure out what the missing information/parameters are. Every change to a protocol will result in a new version.

Please use the template provided [here](https://docs.google.com/document/d/14iyf307oGeTiyv_EaXctZjEluBcbFaV3/edit) when adding a new protocol to the lab resource.

When preforming an experiment, you should ALWAYs reference to the lab protocols used and the specific version used. You should also include information about any deviation from the protocol, as well as specific timing and quantities used, information about the specific cells/tissues/samples you applied the protocol to, etc.

Connection to oak: To mount Oak over SMB/CIFS, on Mac, use the Finder (command-K) and the following URL: smb://oak-smb-ljerby.stanford.edu/groups/ljerby

IMPORTANT: Please use [SUNetID@stanford.edu](mailto:SUNetID@stanford.edu) as login (and not only your SUNet ID)

If you are not on the Stanford wifi, then you'll need to connect first via VPN. Use the terminal to run code on Sherlock/SCG clusters – those have access to the lab Oak project directories to retrieve input data and save output files.

**3. Project directories**

Each lab member is expected to maintain a project directory with a full description of the experiments, experimental results, data generated, and (whenever relevant) code. A project directory should include all the information and data relevant for a particular project and can therefore be maintained by more than one lab member. In addition, a lab member may have more than one project directory if they are working on more than one project. All project directories are located on Oak (see “connection to Oak” above). Please confirm with me before adding a new project directory.

**4. Electronic and hardcopy lab notebooks**

You are expected to use both a hardcopy and an electronic lab notebook. Electronic lab notebooks are searchable and indexable, and can easily edited and include links to the data generated and protocols used, etc. However, as this notebook cannot be used to take notes, and document your experiments in real time (e.g., when you are in the TC handling cells or tissue samples) it is not a standalone document and can only complement the hardcopy notebook.

General guidelines are:

1. Use a separate notebook for each project.
2. **Date** every experiment.
3. Indicate the overall **purpose** of the experiment.
4. Record full details of **materials and methods** and point to the protocols used (each of the protocols used show be a part of the lab protocol resource; see section #2 above).
5. Include “back of the envelope” **calculations** (i.e., don’t use the back of an envelope, paper towel, etc.) so that these can be checked if there is a problem (ranging from how you made a 10 mM stock of some reagent to how you made a reaction mix).
6. Present the key **results** and/or refer to any electronic database with the results. Include all original data (e.g., gel photos, FACS plots, etc.).
7. Describe your **conclusions** – write this for your, my and future lab-workers’ benefit. Talk to us! State **lessons learned**, even if negative. Put models in to help you and others think about the work. It is also helpful to note which experiment/figures are in your papers and provide clear descriptions of how reagents such as strains, plasmids etc. were made, and which reagents were used for your published research.

Before you conduct an experiment, you should plan it and generate a word document outlining the step-by-step procedure you will conduct with pointers to the relevant protocols. These experimental planning documents should be a part of your electronic lab notebook. The document should include a placeholder for the results you will collect during the experiment. Planning your experiments will increase the likelihood that they will be successful and sufficiently comprehensive (e.g., allowing you to identify additional controls you may need to include, additional readouts, or alternatively ways to simplify your experimental design to avoid collection of redundant data).

Lab notebooks will be reviewed on the first weekend of every month and should be placed in a designated place for review. Current and past members’ notebooks are a crucial resource. We are required by the NIH to keep lab notebooks for several years and they must be usable for verifying data in any publication, should questions arise. You are welcome to make copies of your own notebooks to take with you when you leave but the original must remain here.

**Computational Resources/Storage**

Computational research and analysis of large datasets is a big part of the Jerby Lab. We strive to make this part of our research as well-documented and reproducible as possible, but we’re always improving. Below is a basic list of guidelines that you should follow for computational work.

1. **Use GitHub for version control**. Our lab uses GitHub for version control and software documentation. You can get free private github repositories by signing up for [GitHub education](https://education.github.com/students). We have a github repository for the lab at:

[https://github.com/Jerby-Lab](https://github.com/Sherlock-Lab)

If you still do not have a GitHub account, please create one, and we will add you as a member to the lab’s repository.

1. **Use a standard pipeline whenever possible.** If we have a developed workflow for a common tasks, re-use that workflow - there should be a very high bar to using something different, or writing something new to solve a problem we think is already solved. To aid in standardization of results and comparison between experiments, use one of these workflows when possible for your experiment. If the workflow doesn’t do what you need, consider talking to the author (if they are still here) about incorporating a new module. Better yet, write what you need, test it, and submit a pull request.
2. **Publish code that is well-documented, tested, easy to install and maintained.** If you publish a software tool, it is expected to be open source, installable as an R package or with Conda (if python based) and maintained for at least two years after publication. At minimum, the package should include a test dataset and expected output.
3. **Use the SCG cluster for data storage and computation.** More thorough instructions live at the [SCG Tools](https://github.com/bhattlab/scg_tools) repo.
4. **Ask questions on the #computing Slack channel.** Someone has probably had the same error as you, perhaps many times. If you can’t figure it out after a good faith effort (often googling an error message will lead you to an answer), reach out to others on Slack or in person. If there’s a problem with a workflow, you could also submit an issue on GitHub.

**\*\*Document History.** This document was initially based on a lab expectations documents from John Boothroyd, Gavin Sherlock, and Ami Bhatt’s labs, to which I made extensive revisions.