
SCARF INSTALLATION

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This describes how to install all elements needed to run the SCARF software. It assumes installation is on a Mac OSX system. For Linux or Windows systems, you can attempt installation using these instructions as a guide. Please take detailed notes and email them to me, especially if you are successful! I will incorporate them into these instructions.

If not done already, download SCARF files:

1. Browse to <https://github.com/BradyLab/SCARF>
2. In upper-left area of screen, find drop-down box Branch:master, click to open it, and choose the "release" branch.
3. At bottom of right column on screen, click "Download ZIP" and choose a place to put it on your computer.
4. Unzip the zip file on your computer.
5. Rename the unzipped folder from "SCARF-release" to just "SCARF".

To install SCARF:

1. A variety of applications must be installed. Before installing them, it is helpful to prepare two text files for editing. There are two text files in the SCARF main directory that contain parameter settings for running SCARF:
 - allParameters.template is a template file containing sample settings for running SCARF on your genome data.
 - allParameters.test.template is a version of that same template, modified for testing SCARF.

Both files includes settings of paths where applications have been installed. Although you may make many copies of the allParameters.template file for running SCARF using different genomes or parameters, all will have the same application paths in them. You may as well put them in one time.

To run SCARF to generate markers after installation:

- Find file RUN.asciidoc in the SCARF folder on your computer and open it and follow the instructions.