SCARF

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The BradyLab/SCARF GitHub repository contains code and documentation for the software package called **SCARF** (**SCAR F**inder).

SCARF analyzes two or more genomes for length-polymorphic regions bounded by unique sequences and designs PCR primers within these sequences. The primers can be used to amplify the region from genomic DNA of any of the species used to create the markers, and the amplicon size will indicate which species the DNA came from - a **SCAR** marker.

SCAR stands for *Sequence Characterized Amplified Regions*.

1. Download, Installation, and Running

1.1. Requirements

- The installation instructions are for Mac OSX. For other systems you are on your own, but please take copious notes and send them to me, and I'll update these instructions.

1.2. Download SCARF files

1. Browse to https://github.com/BradyLab/SCARF

2. At bottom of right column on screen, click "Download ZIP" and choose a place to put it on your computer.

3. Unzip the zip file on your computer.

4. Rename the unzipped folder from "SCARF-master" to just "SCARF".

1.3. Install SCARF

- Look inside the downloaded SCARF folder on your computer for file INSTALL.pdf or INSTALL.html and open either one and follow the instructions.

1.4. Run SCARF to generate markers after installation

- Find file RUN.pdf or RUN.html in the SCARF folder on your computer and open either one and follow the instructions.

1.5. For help, contact:

- Ted Toal, twtoal@ucdavis.edu [mailto:twtoal@ucdavis.edu]

References

SCAR markers were defined here:

Paran, I., and Michelmore, R. W. *Development of reliable PCR-based markers linked to downy mildew resistance genes in lettuce.* Theoretical and Applied Genetics 85.8 (1993): 985-993.

The SCARF software is described in:

Toal, T., Burkart-Waco, D., and Brady, S.M. *SCARF: In silico K-mer-based Pipeline Finds Candidate SCAR Genomic Markers and PCR Primers using NGS Data and Tomato/Potato/Pennellii Test Case* (Publication in process)