
IGGPIPE

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Table of Contents

1. Download, Installation, and Running	1
1.1. Requirements	1
1.2. Download IGGPIPE files	1
1.3. Install IGGPIPE	1
1.4. Run IGGPIPE to generate markers after installation	2
1.5. For problems and help:	2
References	2

The BradyLab/IGGPIPE GitHub repository contains code and documentation for the software package called **IGGPIPE** (**IGG** Pipeline).

IGGPIPE 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 - an **IGG** marker.

IGG stands for *Indel Group in Genomes*.

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 IGGPIPE files

1. Browse to <https://github.com/BradyLab/IGGPIPE>
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 "IGGPIPE-master" to just "IGGPIPE".

1.3. Install IGGPIPE

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

1.4. Run IGGPIPE to generate markers after installation

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

1.5. For problems and help:

- Post an issue on GitHub under BradyLab/IGGPIPE repository
- Contact me, Ted Toal, twtoal@ucdavis.edu [<mailto:twtoal@ucdavis.edu>]

References

IGG markers and the IGGPIPE software are described in:

Toal, T.W., Burkart-Waco, D., Kuppu, S., Chetelat, R., and Brady, S.M. *InDel Group in Genomes (IGG): Molecular Genetic Markers Between Multiple Species Identified within Next Generation Sequencing Data by an in silico K-mer-based Pipeline* (Publication in process)