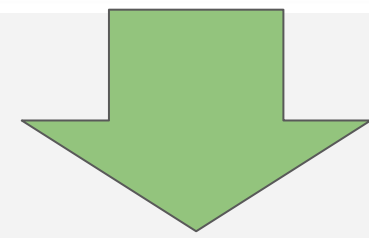
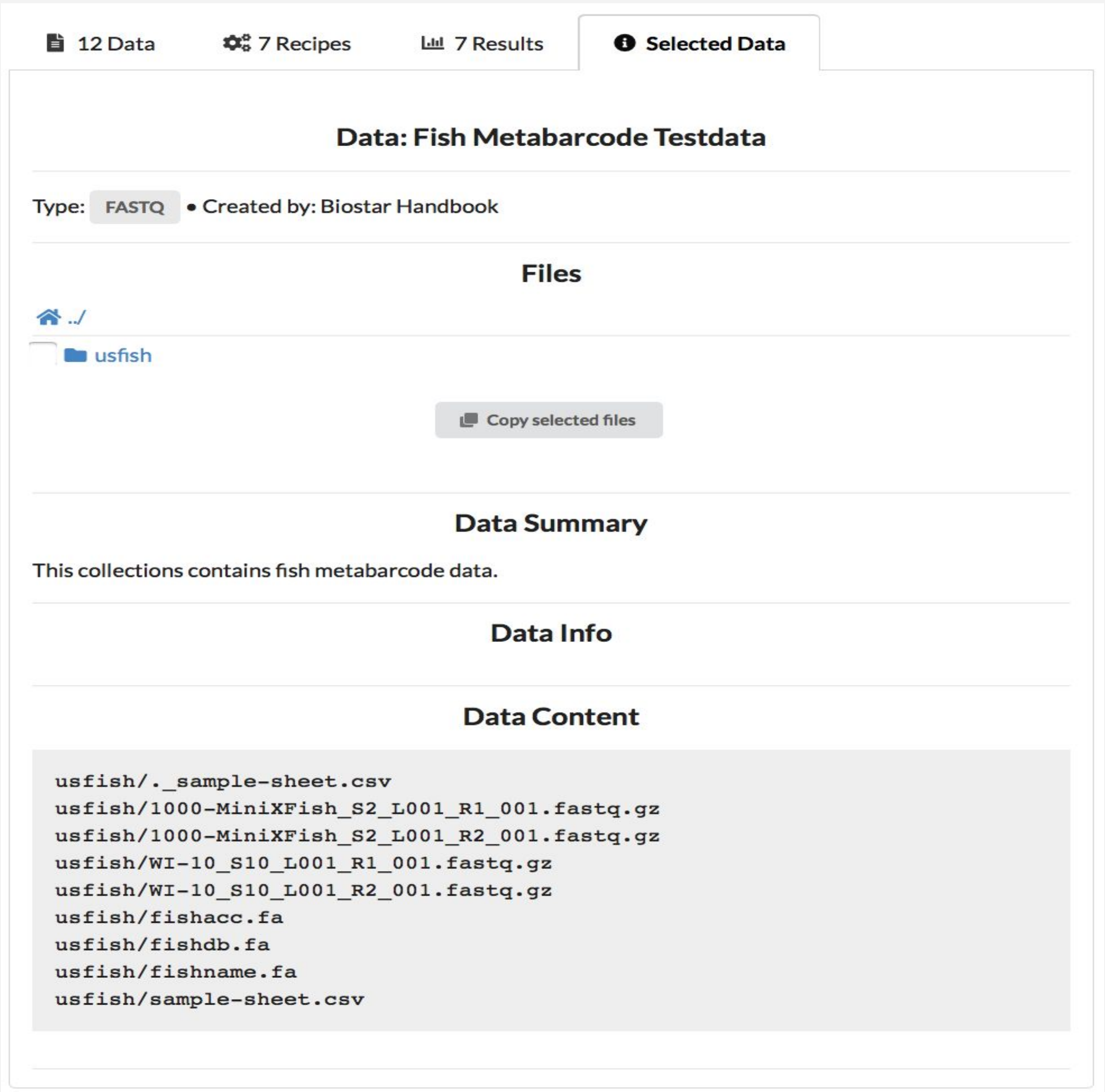


# Bioinformatics Recipes:

## A novel approach to sharing and disseminating bioinformatics protocols



Executing Recipe: Classify sequences using k-mer motifs

Classify paired end reads with a k-mer based approach using the Centrifuge software.

Sequencing Data Directory:

Fish Metabarcoding Testdata

Multiple paired-end sequencing reads.

Sample description:

Samplesheet for Fish Metabarcoding Testdata

The sample sheet that describes the data

Library layout:

Paired end

Specify the library type.

Reference Sequences:

Fish Sequences by Accession Number

The sequences to classify against

Minimum Length:

150

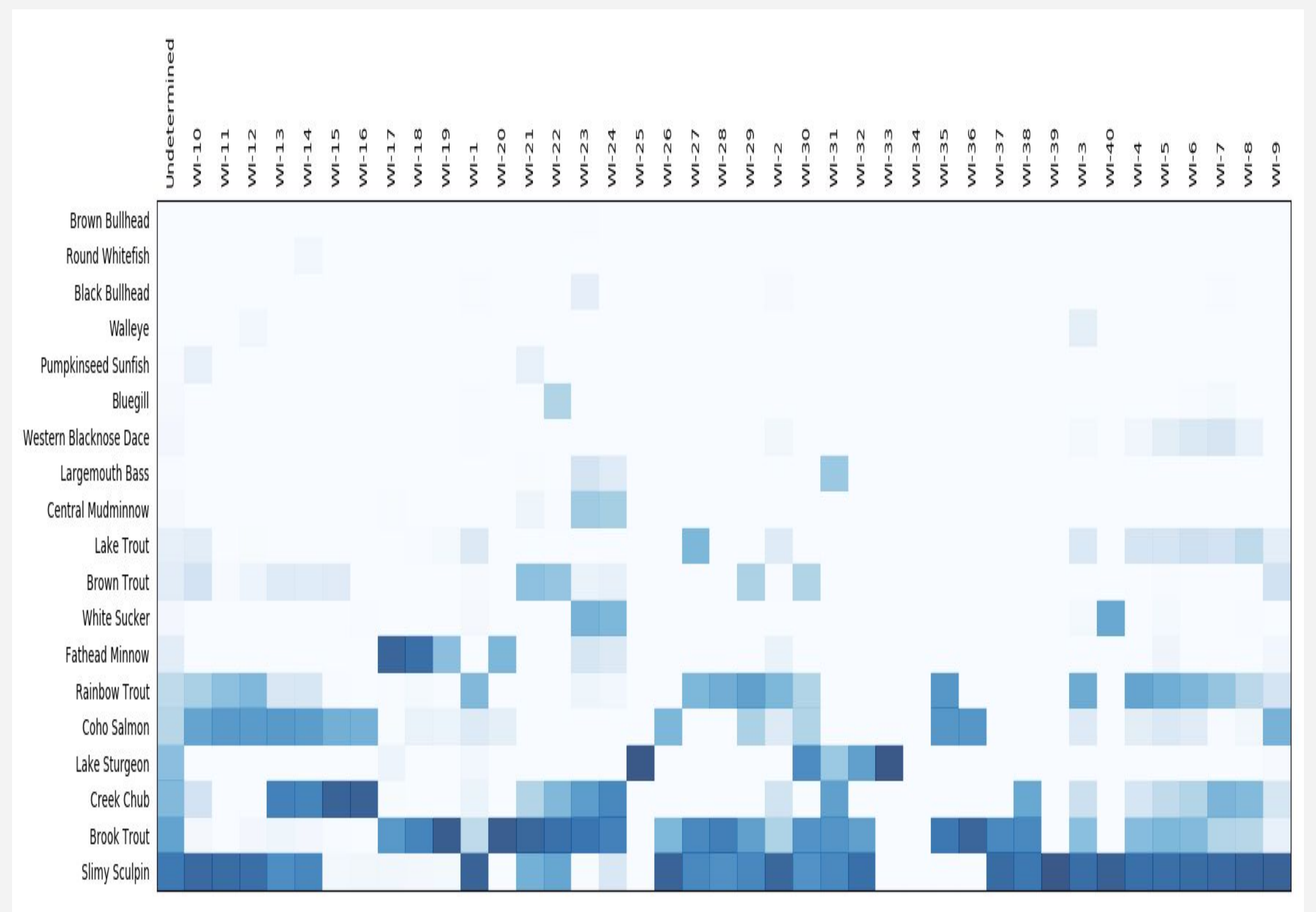
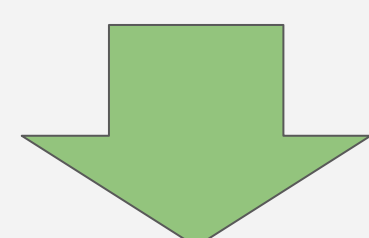
The minimum length of the match to accept the classification.

Report cutoff:

1

The minimal sum for each row in the final classification.

Run Back



**Problem :** Bioinformatics is experiencing a *reproducibility* crisis.

**Solution :** A web application allowing users to document, execute and share data analysis scripts.

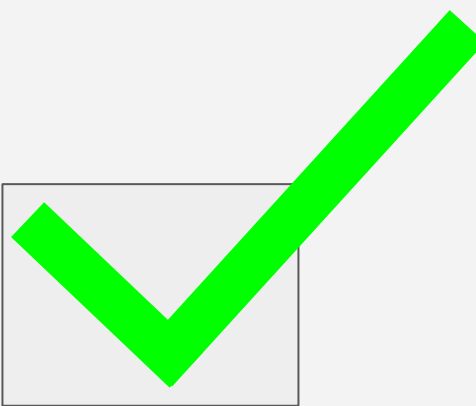
## What is a recipe?

Data analysis scripts + graphical user interface.

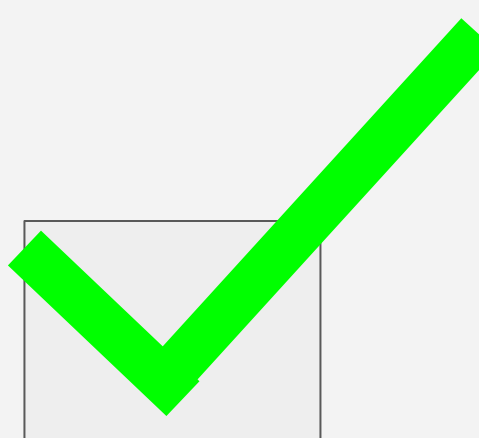
## What is the purpose of a recipe?

Recipes allow other people to run scripts that a bioinformatician has written.

## Can it run QIIME ?

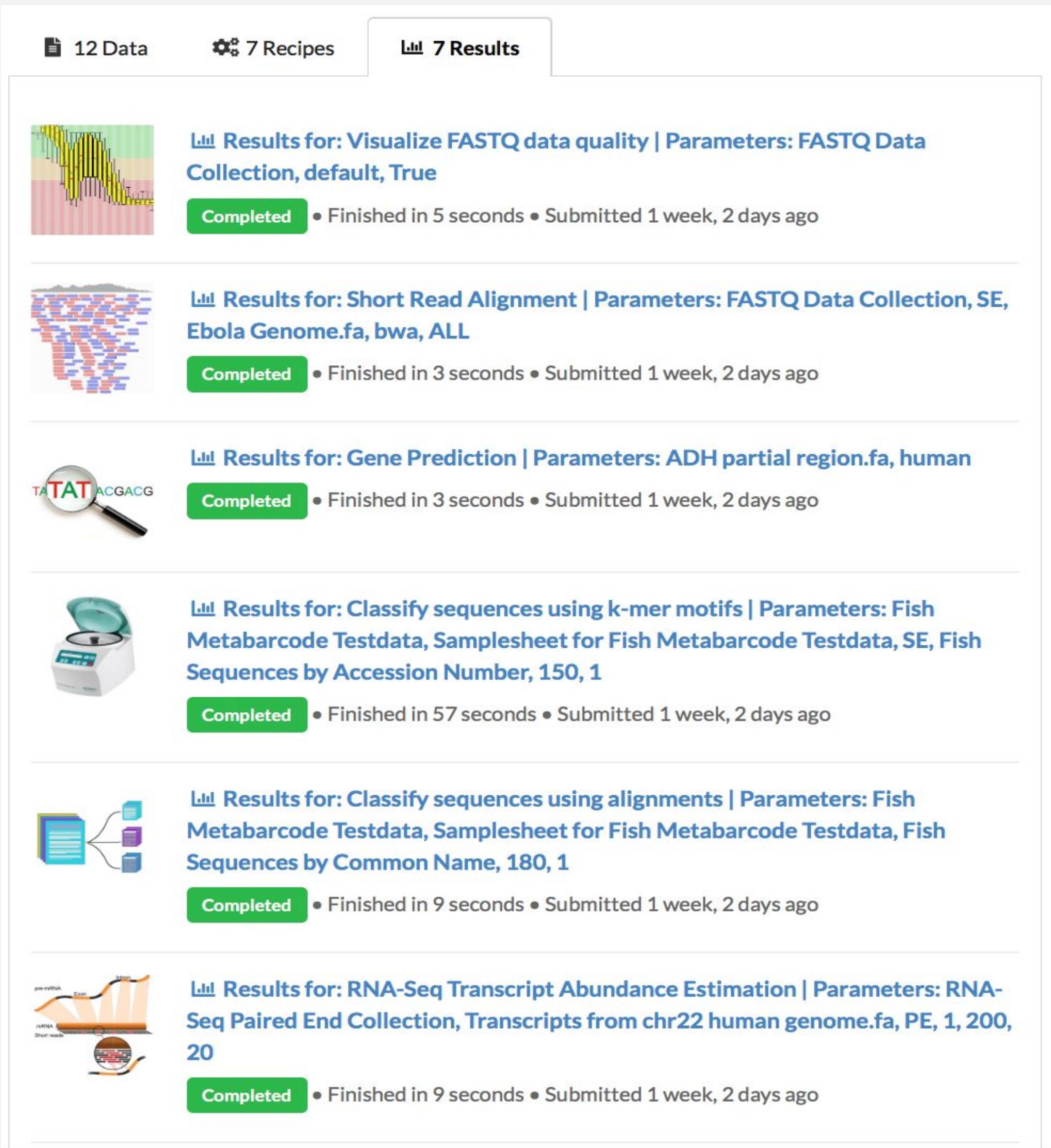


## Can it run MOTHUR ?



It can run any list of commands that can be executed in an environment.

## Results



## Sample plots

