



Stacks

load_radtags.pl

load_radtags.pl takes a set of data produced by either the **denovo_map.pl** or **ref_map.pl** programs (or produced by hand) and loads it into the database. This allows the data to be generated on one computer, but loaded from another. Or, for a database to be regenerated without re-executing the pipeline.

Program Options

```
load_radtags.pl -D db -p path -b batch_id [-B -e desc] [-c] [-M pop_map] [-d]
[-t] [-W path] [-U] [-d] [-h]
```

- D** - Database to load data into.
- p** - Path to input files.
- b** - Batch ID.
- M** - If you have analyzed several populations, specify a population map.
- c** - Load the catalog into the database.
- B** - Load information into batch table.
- e** - batch dEscription.
- d** - perform a dry run. Do not actually load any data, just print what would be executed.
- W** - only load files found on this white list.
- U** - do not load stacks to unique_tags table to save database space.
- t** - pipeline type (either 'map' or 'population'), load_radtags.pl will guess based on the presence/absence of progeny file types.
- h** - display this help message.

Example Usage

```
% load_radtags.pl -D redsea_radtags -b 1 -p ~/redseq_experiment/stacks/ -B -e "This is our Red
```

Other Pipeline Programs

Raw Reads

```
process_radtags
process_shortreads
clone_filter
kmer_filter
```

Core

```
ustacks
pstacks
cstacks
sstacks
```

Execution control

```
denovo_map.pl
ref_map.pl
load_radtags.pl
```

Utilities

```
index_radtags.pl
export_sql.pl
sort_read_pairs.pl
exec_velvet.pl
```

genotypes
populations
rxstacks