sstacks

Sets of stacks, i.e. putative loci, constructed by the **ustacks** or **pstacks** programs can be searched against a catalog produced by **cstacks**. In the case of a genetic map, stacks from the progeny would be matched against the catalog to determine which progeny contain which parental alleles. In the case of a general population, all samples in the population would be matched against the catalog with **sstacks**.

Program Options

```
sstacks [--aligned] -P dir [-b batch_id] -M popmap [-p n_threads]
sstacks [--aligned] -c catalog_path -s sample_path [-s sample_path ...] -o path [-p n_threads]
```

b — database/batch ID of the catalog to consider (default: guess).

P — path to the directory containing Stacks files.

M — path to a population map file from which to take sample names.

s — filename prefix from which to load sample loci.

c — path to the catalog.

g,--aligned — base matching on alignment position, not sequence identity.

p — enable parallel execution with num_threads threads.

o — output path to write results.

x — don't verify haplotype of matching locus.

Gapped assembly options:

--gapped — preform gapped alignments against the catalog loci.

Example Usage

Match each of three samples of progeny from a genetic map against the catalog, one at a time:

```
% sstacks -b 1 -c ./stacks/batch_1 -s ./stacks/progeny_01 -p 15
% sstacks -b 1 -c ./stacks/batch_1 -s ./stacks/progeny_02 -p 15
% sstacks -b 1 -c ./stacks/batch_1 -s ./stacks/progeny_03 -p 15
```

Match each of three samples in a population against the catalog in a single command (saving the time of having to reload the catalog each exectution):

```
% sstacks -b 1 -c ./stacks/batch_1 -s ./stacks/sample_01 -s ./stacks/sample_02 -s ./stacks/sampl
```

Specify a directory containing all of the Stacks files generated with `ustacks` or `pstacks`, and `cstacks`. Then specify the path to a population map that contains all of the samples you

would like to match against the catalog (see here for information on population maps).

```
% sstacks –P ./stacks –M ./popmap –p 8
```

Other Pipeline Programs

Raw Reads
- process_radtags
- process_shortreads
- clone_filter
- kmer_filter

Core
- ustacks
- pstacks
- cstacks
- sstacks
- genotypes
- populations
- rxstacks

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