

discoSnp

Reference-free detection of isolated SNPs

v1.2.3

User's guide – July 2014

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Publication

Publication is in preparation

discoSnp features at a glance

Software **discoSnp** is designed for extracting isolated Single Nucleotide Polymorphism (SNP) from raw set(s) of reads obtained with Next Generation Sequencers (NGS). Isolated means far away from any source of polymorphism, and far away means at least k bp, with k a user defined parameter.

Note that this tool is specially designed to use only a limited amount of memory (3 billions reads of size 100 can be treated with less than 6GB memory).

The software is composed of two independent modules. The first module, **kissnp2**, detects isolated SNPs from read sets. The second module, **kissreads**, enhances the kissnp2 results by computing per read set and for each found SNP i/ its mean read coverage and ii/ the average (phred) quality of reads generating the polymorphism.

Quick starting

After compiling programs (`./compile_kissnp_kissreads.sh`) the main script can be called as follows:

```
./run_discoSnp.sh -r "data_sample/reads_sequence1.fasta data_sample/reads_sequence2.fasta.gz"
```

This creates a fasta file called **discoRes_k_31_c_4_coherent.fa** containing the found SNPs.

Components

- *Licence and readme*
- *clear_kissnp_kissreads.sh* : cleaning the compiled tools. Useful when changing the k value
- *compile_kissnp_kissreads.sh* : compile all binaries and put them in a "tool" directory
- *data_sample* : directory containing two toy example read sets
- *kissnp2* : sources of the SNP detection module
- *kissreads* : sources of the read coverage and quality module
- *minia* : sources of the k-mer counting and datastructure
- *output_analyses* : directory containing third party tools for post processing discoSnp results.
- *run_discoSnp.sh* : main (hopefully user friendly) script running the both modules for searching SNPs from raw read sets and for counting their read coverage and quality

Download and install

Download from discoSnp web page – <http://colibread.inria.fr/discosnp/>. Please read and accept the CeCILL license before downloading.

- Unzip the downloaded package :
`# unzip discoSnp_versionnumber.zip`
- Get into the newly created *discoSnp* directory:
`# cd discoSnp`
- Compile the two modules (kissnp and kissreads) with the single command:
`# ./compile_kissnp_kissreads.sh k_value`

Note about the k value:

Replace *k_value* by the value of the kmer that you wish to use.

No need to recompile for any values below or equal to 31

No need to recompile for any values in [32,63]

No need to recompile for any values in [64,127]

...

By default, $k=31$ (value used both for compiling and in runtime).

- If you wish to recompile (for instance for changing the k value from any value below or equal to 31 to any value bigger or equal to 32) first clear the previously compiled executables:

```
# ./clear_kissnp_kissreads.sh
```

This installation process should generate the “tool” directory containing the two executables : *kissnp2* and *kissreads*.

Running discoSnp

- The main script ***run_discoSnp.sh*** automatically run the two modules (SNP detection and read coverage and quality computations). You will provide the following information:
 - ***-r (read_sets)*** “*readref.fasta readsnp.fastq.gz*”: localization of the read files. Note that these files may be in fastq, or fasta, gzipped or not. If there are more than one read file, then they must be surrounded by the “” character and they are separated by space. This is the only mandatory parameter.
 - ***-p prefix_name:*** all temp and final files will be written will start with this prefix default: “discoRes”
 - ***-k kmer_size:*** size of kmers (default: 31)
 - ***-b branching_strategy:*** branching filtering approach. This parameters influences the precision recall.
 - 0: SNPs for wich any of the two paths is branching are discarded (high precision, lowers the recal in complex genomes). Default value
 - 1: (smart branching) forbid SNPs for wich the two paths are branching (e.g. the two paths can be created either with a 'A' or a 'C' at the same position
 - 2: No limitation on branching (lowers the precision, high recall)”
 - ***-c minimal_coverage:*** minimal kmer coverage default 4
 - ***-d error_threshold:*** max number of errors per read (used by kissreads only). default 1
 - ***-g genome_size:*** estimated genome size. Used only to control kissnp2 memory usage. e.g. 3 billion (3000000000) uses 4Gb of RAM. Default 10000000 (uses a few MB of memory)
 - ***-w:*** If this option is called the waste files are not removed.
 - ***-h:*** show help.
- By default binaries are search in the current “tool” directory. You may change this default value by editing the *run_discoSnp.sh* script changing the *PATH_RS* line
- Additionally you may change some kissnp2 / kissreads options. In this case you may change the two corresponding lines in the *run_discoSnp.sh* file. To know the possible options, type *./tools/kissnp2* and/or *./tools/kissreads* without options. Note that usually, changing these options is not necessary.
- **Sample example:**
 - You can test discoSnp on a toy example containing 3 SNPs:

```
./run_discoSnp.sh -r "data_sample/reads_sequence1.fasta data_sample/reads_sequence2.fasta.gz"
```

Output

- **Final results are in *prefix_coherent_k_kval_c_cval.fa* file.** This is a simple fasta file composed of a succession of pairs of sequences. Each pair corresponds to a SNP. Let's look at an example :

```
>SNP_higher_path_2|high|left_unitig_length_472|right_unitig_length_261|left_contig_length_472|
right_contig_length_378|C1_8|C2_120|rank_0.88900
```

```
ttgcggataccgttgagacatcttataagtagacgcaatgcggaatctatagaatcgccgatagcgttggttggtggacacggctgattaccctctacccc
gcgctattagcttccataccacctgcggccatccattaagatccgctgctcctcacgaaaaaagaattaataagaagtcggtaacatgcggatttggtagtc
gttatagacaactttactggggcgaactaaaacgcttggtggacagaattttggcagtggaatcctcctaatgatgtgatattagggtctaaaatgtaagaa
ttcggtagttagattggacaaggggatccgaagatgttttggcgcagtttagtcacagggggagccctgcctacaaaaagcgcttactgttgactgtctag
ggatacagcgaaagcggcagtcgtgaagcaaaagtatatgtgcgacactgcatctagGCAGCGCAACAACGCAACAGCTCGAGG
TGTACTTCGCAGAGAAACCGCACGTCCAGTTCTAacactctcatatgtgctcgtcgtttatgctttcggcgtgaaaactgggtgcggcg
gtgtctggagaccatccttcttgcgtatgactccaaggacagccatcacggtttggtgggtcactgggactgtcacgcttaaccggacggaactcgagaagg
catacagctggtcgtgaagaccgctctgatccgacaccaccataacgcggcactcatgattatcatcacttttttagtccctattacagagctgcggggtggatg
actctctaccgcgctctgtggaagtgcacttgatcggtttgctgtagaaaaaacttaataacagaatgccgatgaaggcactactgtactaataggccggcg
ctacatgttaactac
```

```
>SNP_lower_path_2|high|left_unitig_length_472|right_unitig_length_261|left_contig_length_472|
right_contig_length_378|C1_118|C2_6|rank_0.88900
```

```
ttgcggataccgttgagacatcttataagtagacgcaatgcggaatctatagaatcgccgatagcgttggttggtggacacggctgattaccctctacccc
gcgctattagcttccataccacctgcggccatccattaagatccgctgctcctcacgaaaaaagaattaataagaagtcggtaacatgcggatttggtagtc
gttatagacaactttactggggcgaactaaaacgcttggtggacagaattttggcagtggaatcctcctaatgatgtgatattagggtctaaaatgtaagaa
ttcggtagttagattggacaaggggatccgaagatgttttggcgcagtttagtcacagggggagccctgcctacaaaaagcgcttactgttgactgtctag
ggatacagcgaaagcggcagtcgtgaagcaaaagtatatgtgcgacactgcatctagGCAGCGCAACAACGCAACAGCTCGAGG
TGTCTTCGCAGAGAAACCGCACGTCCAGTTCTAacactctcatatgtgctcgtcgtttatgctttcggcgtgaaaactgggtgcggcg
tgtctggagaccatccttcttgcgtatgactccaaggacagccatcacggtttggtgggtcactgggactgtcacgcttaaccggacggaactcgagaaggc
atacagctggtcgtgaagaccgctctgatccgacaccaccataacgcggcactcatgattatcatcacttttttagtccctattacagagctgcggggtggatga
ctctctaccgcgctctgtggaagtgcacttgatcggtttgctgtagaaaaaacttaataacagaatgccgatgaaggcactactgtactaataggccggcg
tacctgttaactac
```

- In this example a SNP A/T is found (underlined here). The central sequence of length 2k-1 (here $2*31-1=61$) is seen in upper case, while the two (left and right) extensions are seen in lower case.
- The comments are formatted as follow :

```
>SNP_higher/lower_path_id|high/low|left_unitig_length_int|right_unitig_length_int|
left_contig_length_int|right_contig_length_int|C1_int|C2_int|[Q1_int|Q2_int]|rank_float
```

- *higher/lower*: one of the two alleles
- *id*: id of the SNP: each SNP (couple of sequences) has a unique id, here 3.
- *high/low*: sequence complexity. If the sequence is of low complexity (e.g. ATATATATATATATAT) this variable would be *low*
- *left_unitig_length*: size of the full left extension. Here 472
- *right_unitig_length*: size of the right extension. Here 261
- *left_contig_length*: size of the full left extension. Here 472
- *right_contig_length*: size of the right extension. Here 378
- C1: number of reads mapping the central upper case sequence from the first read set
- C2: number of reads mapping the central upper case sequence from the second read set
- C3 [if input data were at least 3 read sets]: number of reads mapping the central upper case sequence from the third read set
- C4, C5, ...

- Q1 [if reads were given in fastq]: average phred quality of the central nucleotide (here A or T) from the mapped reads from the first read set.
- Q2 [if reads were given in fastq]: average phred quality of the central nucleotide (here A or T) from the mapped reads from the second read set.
- Q3 [if the data were at least 3 fastq read sets]: average phred quality of the central nucleotide (here A or T) from the mapped reads from the third read set.
- Q4, Q5, ...
- rank: ranks the predictions according to their read coverage in each condition favoring SNPs that are discriminant between conditions (Phi coefficient) (see publication)

Extensions: differences between unitig and contigs (from version 2.1.1.3)

By default in the pipeline, the found SNPs (of length 2k-1) are extended using a contiger. The output contains such contigs and their lengths are shown in the header (left_contig_length and right_contig_length). Moreover, a contig may hide some small polymorphism such as substitutions and/or indels. The output also proposes the length of the longest extension not containing any such polymorphism. These extensions are called unitigs (defined as « A uniquely assembleable subset of overlapping fragments »).

Output Analyze

- **From a fasta format to a csv format:** If you wish to analyze the results in a tabulated format:
 - `#python output_analyses/discoSnp_to_csv.py discoSnp_output.fa`
 - will output a .csv tabulated file containing on each line the content of 4 lines of the .fa, replacing the '|' character by spaces and removing the CX_
 - example with previously used SNP example:

```
>SNP_higher_path_3 high left_contig_length_86 right_contig_length_52 78 5 rank_0.89839
tctctaccgcgctctgtggaagtgcacttgatcggttttctgtagaaaaaacttaataacagaatgccgatgaaggcactactgtACTAATAGGGCCGGGCTACATGTTAAC TACAAGGCTA
TAACCTATTGATGACCCGGTCCATacataacttgatcggtcatgtagcgttcaaggctatagcaattccgacg >SNP_lower_path_3 high left_contig_length_86
right_contig_length_52 4 91 rank_0.89839
tctctaccgcgctctgtggaagtgcacttgatcggttttctgtagaaaaaacttaataacagaatgccgatgaaggcactactgtACTAATAGGGCCGGGCTACATGTTAAC TACTAGGCTA
TAACCTATTGATGACCCGGTCCATacataacttgatcggtcatgtagcgttcaaggctatagcaattccgacg
```

- **Genotyping the results:** If you wish to genotype your results:
 - `#python output_analyses/discoSnp_to_genotypes.py discoSnp_output.fa threshold_value`
 - will output a file containing on each line the “genotypes” of a SNP. For each input data set it indicates if the SNP is:
 - heterozygous ALT1 path (coverage ALT1 >= threshold and ALT2 < threshold): **1**
 - heterozygous ALT2 path (coverage ALT1 < threshold and ALT2 >= threshold): **-1**
 - homozygous (coverage ALT1 >= threshold and ALT2 >= threshold): **2**
 - absent (coverage ALT1 < threshold and ALT2 < threshold): **0**
 - then it outputs the central sequence of length 2k-1 replacing the central position by ALT1/ALT2
 - example with previously used SNP example and threshold 20:

```
GENOTYPES_SNP_3_THRESHOLD_20 1 -1 TACTAATAGGGCCGGGCTACATGTTAAC TACA/TAGGCTATAACCTATTGATGACCCGGTCCATA
```