
InSilicoSeq Documentation

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InSilicoSeq is a sequencing simulator producing realistic Illumina reads. Primarily intended for simulating metagenomic samples, it can also be used to produce sequencing data from a single genome.

InSilicoSeq is written in python, and use kernel density estimators to model the read quality of real sequencing data.

InSilicoSeq supports substitution, insertion, deletion errors, and models gc bias and insert size distribution.

CHAPTER 1

Details

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- **License:** MIT

2.1 Installing InSilicoSeq

2.1.1 Using pip

To install InSilicoSeq, type the following in your terminal:

```
pip3 install InSilicoSeq
```

It will install InSilicoSeq as well as the following dependencies:

- biopython
- joblib
- numpy
- pysam
- scipy

Other installation options

- If you can't / don't want to use python3:

```
pip install InSilicoSeq
```

- Upgrading InSilicoSeq to the latest version:

```
pip3 install --upgrade InSilicoSeq
```

- If you don't have administration rights on your machine:

```
pip3 install --user InSilicoSeq
```

- if you wish to install InSilicoSeq at a custom location (i.e with a module system):

```
prefix="/path/to/install/prefix"
pip3 install --install-option="--prefix=$prefix" InSilicoSeq
```

then add `$prefix/bin` to your `PATH`, and `$prefix/lib/pythonX.X/site-packages` to your `PYTHONPATH` (replacing `pythonX.X` with your python version)

2.1.2 Using docker

If you wish to use InSilicoSeq using docker

```
docker pull hadrieng/insilicoseq:1.2.0
```

To use InSilicoSeq with docker, you need to provide a *volume* to the `docker run` command. Given with the `-v` option, the volume is your way of exchanging data (in this case, your input and output files) with the docker container.

```
docker run -v /Users/hadrien/data:/mnt/data -it --rm \
  hadrieng/insilicoseq:1.2.0 iss generate \
  --genomes /mnt/data/genomes.fasta -m miseq \
  -o /mnt/data/reads
```

The above command will mount the local folder `/Users/hadrien/data` onto `/mnt/data` on the docker side. The output reads will be located in `/Users/hadrien/data` when InSilicoSeq has finished running.

2.2 Generating reads

InSilicoSeq comes with a set of pre-computed error models to allow the user to easily generate reads from the most popular Illumina instruments:

- HiSeq
- MiSeq
- NovaSeq

Per example generate 1 million MiSeq reads from a set of input genomes called *genomes.fasta* (not provided):

```
curl -O -J -L https://osf.io/thser/download # download the example data
iss generate --genomes SRS121011.fasta --model miseq --output miseq_reads
```

This will create 2 fastq files, *miseq_reads_R1.fastq* and *miseq_reads_R2.fastq* in your current directory, as well as *miseq_reads_abundance.txt*, a tab-delimited file containing the abundance of each genomes.

InSilicoSeq will use 2 cpus by default. For multithreading, use `--cpus`:

```
curl -O -J -L https://osf.io/thser/download # download the example data
iss generate --cpus 8 --genomes SRS121011.fasta --model hiseq --output hiseq_reads
```

If you have created your custom model, give to `--model` the path of your custom model file:

```
curl -O -J -L https://osf.io/thser/download # download the example data
iss generate --genomes SRS121011.fasta --model model.npz --output model_reads
```

If your multi-fastq file contain more genomes than the number of organisms for which you wish to simulate reads, you can use the `--n_genomes/-u` parameter:

```
curl -O -J -L https://osf.io/thser/download # download the example data
iss generate --genomes SRS121011.fasta --n_genomes 5 --model novaseq --output novaseq_
↳ reads
```

The above command will pick 5 random genomes in your multi-fastq and generate reads from them.

2.2.1 Required input files

By default, InSilicoSeq only requires 1 file in order to start generating reads: 1 (multi-)fastq files containing your input genome(s).

If you don't want to use a multi-fastq file or don't have one at hand but are equipped with an Internet connection, you can download random genomes from the ncbi with the `--ncbi/-k` parameter:

```
iss generate --ncbi bacteria -u 10 --model miseq --output miseq_ncbi
```

The above command will generate reads from 10 random bacterial genomes from the NCBI

Additionally, you can supply tab separated kingdoms if you wish to have mixed datasets:

```
iss generate -k bacteria viruses -u 10 4 --model miseq --output miseq_ncbi
```

The above command will generate reads from 10 random bacteria and 4 random viruses. `--ncbi/-k` accepts the following values: `bacteria`, `viruses` and `archaea`.

In addition the the 2 fastq files and the abundance file, the downloaded genomes will be saved in `miseq_ncbi_genomes.fasta` in your current directory.

Note: If possible, I recommend using InSilicoSeq with a fastq file as input. The eutils utilities from the ncbi can be slow and quirky.

2.2.2 Abundance distribution

With default settings, the abundance of the input genomes is drawn from a log-normal distribution.

Alternatively, you can use other distributions with the `--abundance` parameter: *uniform*, *halfnormal*, *exponential* or *zero-inflated-lognormal*

If you wish to fine-tune the distribution of your genomes, InSilicoSeq also accepts an abundance file:

```
curl -O -J -L https://osf.io/thser/download # download the example data
iss generate -g SRS121011.fasta --abundance_file abundance.txt -m HiSeq -o HiSeq_reads
```

Example abundance file for a multi-fastq containing 2 genomes: `genome_A` and `genome_B`.

```
genome_A    0.2
genome_B    0.8
```

For the abundance to make sense, the total abundance in your abundance file must equal 1.

2.2.3 GC bias

InSilicoSeq can also model gc bias:

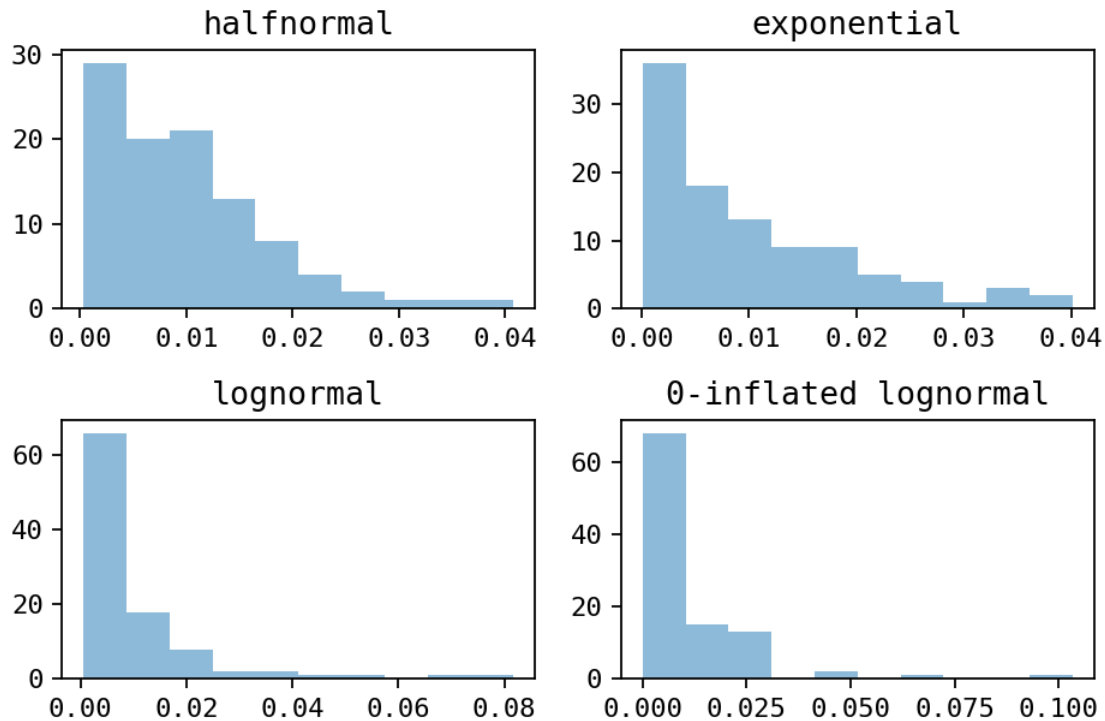


Fig. 1: Histograms of the different distribution (drawn with 100 samples)

```
curl -O -J -L https://osf.io/thser/download # download the example data
iss generate -g SRS121011.fasta --model miseq --gc_bias --output reads
```

2.2.4 Basic error model

By default InSilicoSeq uses Kernel Density Estimators for generating reads. Both the pre-built models (miseq, hiseq and novaseq), as well as the model files you build yourselves are that way.

If you wish to use a much simpler model (because you don't have the need for insertions and deletion errors per example), you can use `--mode basic`

```
curl -O -J -L https://osf.io/thser/download # download the example data
iss generate -g SRS121011.fasta --mode basic --output basic_reads
```

2.2.5 Full list of options

`--genomes`

Input genome(s) from where the reads will originate

`--ncbi`

Download input genomes from RefSeq instead of using `--genomes`. Requires `-n_genomes` option. Can be bacteria, viruses, archaea or a combination of the three (space-separated)

-n_genomes

How many genomes will be downloaded from the ncbi. Required if -ncbi is set. If more than one kingdom is set with -ncbi, multiple values are necessary (space-separated).

-abundance

Abundance distribution (default: lognormal). Can be uniform, halfnormal, exponential, lognormal or zero_inflated_lognormal.

-abundance_file

Abundance file for coverage calculations (default: None).

-n_reads

Number of reads to generate (default: 1000000). Allows suffixes k, K, m, M, g and G (ex 0.5M for 500000).

-mode

Error model. If not specified, using kernel density estimation (default: kde). Can be 'kde' or 'basic'

-model

Error model file. (default: None). Use HiSeq, NovaSeq or MiSeq for a pre-computed error model provided with the software, or a file generated with iss model. If you do not wish to use a model, use -mode basic. The name of the built-in models is case insensitive.

-gc_bias

If set, may fail to sequence reads with abnormal GC content. Does not guarantee -n_reads (default: False)

-cpus

Number of cpus to use. (default: 2).

-quiet

Disable info logging

-debug

Enable debug logging

-output

Output file prefix (Required)

2.3 Error models

2.3.1 Pre-built models

Available models

Model name	Read length
MiSeq HiSeq NovaSeq	300 bp 125 bp 150 bp

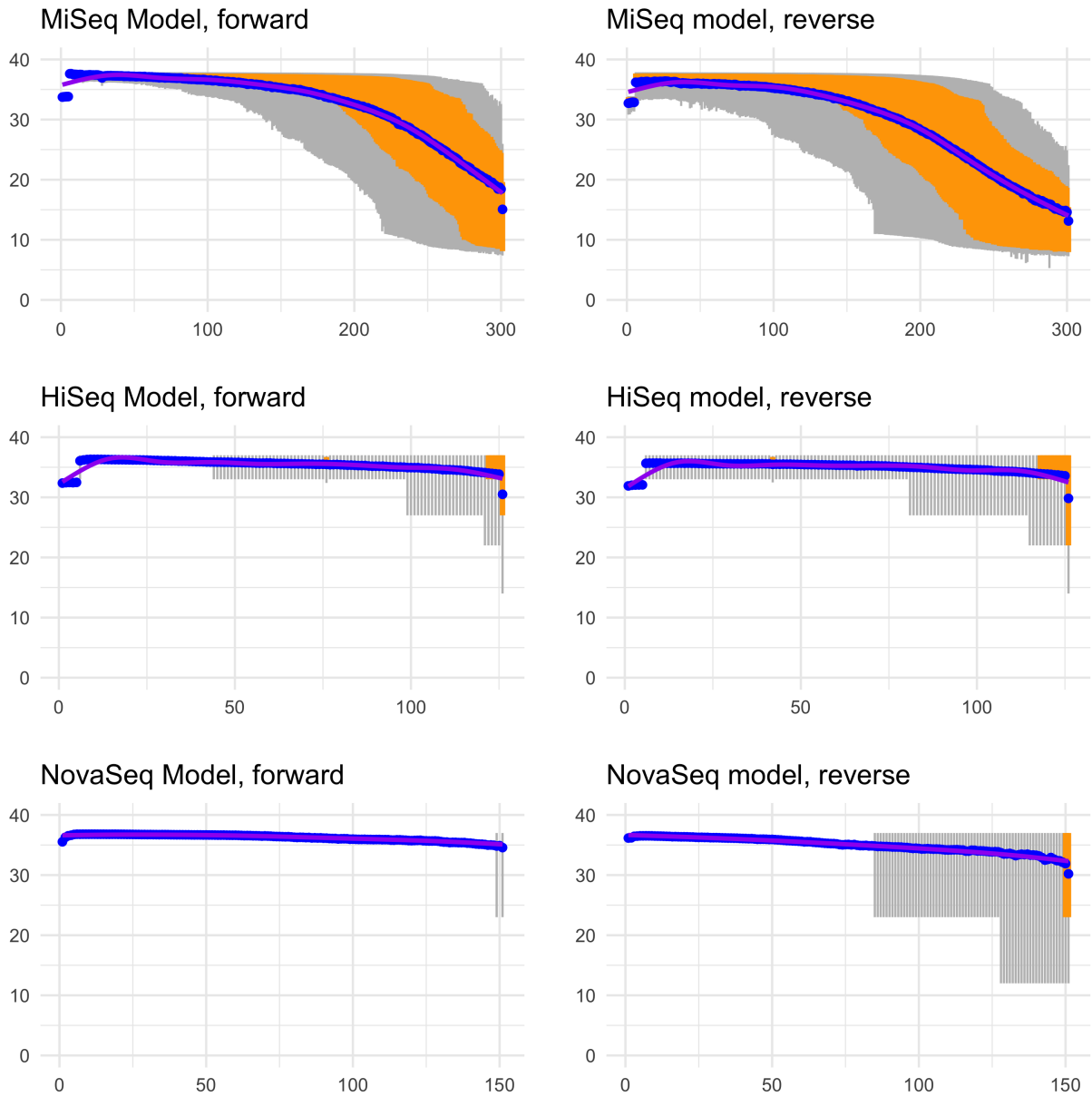


Fig. 2: Average per base quality profiles for the prebuilt error models

Qualities

The prebuilt models were built with the following commands:

```
megahit -1 reads_R1.fastq -2 reads_R2.fastq -o asm
bowtie2-build asm/final.contigs.fa miseq_asm/final.contigs
bowtie2 -x asm/final.contigs -1 reads_R1.fastq \
-2 reads_R2.fastq | samtools view -bS | samtools sort -o mapping.bam
samtools index mapping.bam
iss model -b mapping.bam -o name_of_model
```

The MiSeq model was built from an ocean metagenomics project in Kenya (sample accession number ERR1912174).

The HiSeq and NovaSeq models were built from human run obtained via basespace.

2.3.2 Creating an Error Model

If you do not wish to use the pre-computed error models provided with InSilicoSeq, it is possible to create your own.

InSilicoSeq creates error models from .bam files. The input bam file should be a set of reads aligned against a reference genome or metagenome.

Given you have two read files, *reads_R1.fastq.gz* and *reads_R2.fastq.gz*, and a reference metagenome *ref.fasta*:

Align you reads against the reference

```
bowtie2-build ref.fasta ref
bowtie2 -x ref -1 reads_R1.fastq.gz \
-2 reads_R2.fastq.gz | samtools view -bS | samtools sort -o ref.bam
samtools index ref.bam
```

Build the model

```
iss model -b ref.bam -o my_model
```

which will create a *my_model.npz* file containing your newly built model

2.3.3 Full list of options

–bam

aligned reads from which the model will be inferred (Required)

–model

Error model to build. If not specified, using kernel density estimation (default: kde). Can be ‘kde’ or ‘cdf’

–output

Output file prefix (Required)

-quiet

Disable info logging

-debug

Enable debug logging

2.4 iss package

2.4.1 Subpackages

iss.error_models package

Submodules

iss.error_models.basic module

class `iss.error_models.basic.BasicErrorModel`

Bases: `iss.error_models.ErrorModel`

Basic Error Model class

Basic error model. The phred scores are based on a normal distribution. Only substitutions errors occur. The substitution rate is assumed equal between all nucleotides.

gen_phred_scores (*mean_quality, orientation*)

Generate a normal distribution, transform to phred scores

Generate a list of phred score according to a normal distribution centered around the ErrorModel quality

Parameters `mean_quality` (*int*) – mean phred score

Returns list of phred scores following a normal distribution

Return type list

random_insert_size ()

Fake random function returning the default insert size of the basic error model

Returns insert size

Return type int

iss.error_models.cdf module

iss.error_models.kde module

class `iss.error_models.kde.KDEErrorModel` (*npz_path*)

Bases: `iss.error_models.ErrorModel`

KDEErrorModel class.

Error model based on an .npz files derived from read alignments. the npz file must contain:

- the length of the reads

- the mean insert size
- the size of mean sequence quality bins (for R1 and R2)
- **a cumulative distribution function of quality scores for each position** (for R1 and R2)
- the substitution for each nucleotide at each position (for R1 and R2)
- the insertion and deletion rates for each position (for R1 and R2)

gen_phred_scores (*cdfs, orientation*)

Generate a list of phred scores based on cdfs and mean bins

For each position, draw a phred score from the cdf and append to the phred score list

Parameters

- **cdfs** (*ndarray*) – array containing the cdfs
- **orientation** (*string*) – orientation of the read. Can be ‘forward’ or ‘reverse’

Returns a list of phred scores

Return type list

random_insert_size ()

Draw a random insert size from the insert size cdf

Parameters **i_size_cdf** – cumulative distribution function of the insert size

Returns an insert size

Return type int

Module contents

class `iss.error_models.ErrorModel`

Bases: `object`

Main ErrorModel Class

This class is used to create inheriting classes and contains all the functions that are shared by all ErrorModel classes

adjust_seq_length (*mut_seq, orientation, full_sequence, bounds*)

Truncate or Extend reads to make them fit the read length

When insertions or deletions are introduced to the reads, their length will change. This function takes a (mutable) read and a reference sequence, and extend or truncate the read if it has had an insertion or a deletion

Parameters

- **mut_seq** (*MutableSeq*) – a mutable sequence
- **orientation** (*string*) – orientation of the read. Can be ‘forward’ or ‘reverse’
- **full_sequence** (*Seq*) – the reference sequence from which mut_seq comes from
- **bounds** (*tuple*) – the position of the read in the full_sequence

Returns a sequence fitting the ErrorModel

Return type Seq

introduce_error_scores (*record, orientation*)

Add phred scores to a SeqRecord according to the error_model

Parameters

- **record** (*SeqRecord*) – a read record
- **orientation** (*string*) – orientation of the read. Can be ‘forward’ or ‘reverse’

Returns a read record with error scores

Return type SeqRecord

introduce_indels (*record, orientation, full_seq, bounds*)

Introduce insertions or deletions in a sequence

Introduce insertion and deletion errors according to the probabilities present in the indel choices list

Parameters

- **record** (*SeqRecord*) – a sequence record
- **orientation** (*string*) – orientation of the read. Can be ‘forward’ or ‘reverse’
- **full_seq** (*Seq*) – the reference sequence from which mut_seq comes from
- **bounds** (*tuple*) – the position of the read in the full_sequence

Returns a sequence with (eventually) indels

Return type Seq

load_npz (*npz_path, model*)

load the error profile .npz file

Parameters

- **npz_path** (*string*) – path to the npz file
- **model** (*string*) – type of model. Could be ‘cdf’ or ‘kde’. ‘cdf’ has been deprecated and is no longer available

Returns

numpy object containg variables necessary for error model construction

Return type ndarray

logger

mut_sequence (*record, orientation*)

Introduce substitution errors to a sequence

If a random probability is higher than the probability of the basecall being correct, introduce a substitution error

Parameters

- **record** (*SeqRecord*) – a read record with error scores
- **orientation** (*string*) – orientation of the read. Can be ‘forward’ or ‘reverse’

Returns a sequence

Return type Seq

2.4.2 Submodules

2.4.3 iss.abundance module

`iss.abundance.exponential(record_list)`

Generate scaled exponential abundance distribution from a number of records

Parameters `record_list` (*list*) – a list of record.id

Returns a dictionary with records as keys, abundance as values

Return type dict

`iss.abundance.halfnormal(record_list)`

Generate scaled halfnormal abundance distribution from a number of records

Parameters `record_list` (*list*) – a list of record.id

Returns a dictionary with records as keys, abundance as values

Return type dict

`iss.abundance.lognormal(record_list)`

Generate scaled lognormal abundance distribution from a number of records

Parameters `record_list` (*list*) – a list of record.id

Returns a dictionary with records as keys, abundance as values

Return type dict

`iss.abundance.parse_abundance_file(abundance_file)`

Parse an abundance or coverage file

The abundance/coverage file is a flat file of the format “genome_id<TAB>abundance” or “genome_id<TAB>coverage”

Parameters `abundance_file` (*string*) – the path to the abundance file

Returns genome_id as keys, abundance as values

Return type dict

`iss.abundance.to_coverage(total_n_reads, species_abundance, read_length, genome_size)`

Calculate the coverage of a genome in a metagenome given its size and abundance

Parameters

- **total_n_reads** (*int*) – total amount of reads in the dataset
- **species_abundance** (*float*) – abundance of the species, between 0 and 1
- **read_length** (*int*) – length of the reads in the dataset
- **genome_size** (*int*) – size of the genome

Returns coverage of the genome

Return type float

`iss.abundance.to_file(abundance_dic, output)`

Write the abundance dictionary to a file

Parameters

- **abundance_dic** (*dict*) – the abundance dictionary
- **output** (*str*) – the output file name

`iss.abundance.uniform(record_list)`

Generate uniform abundance distribution from a number of records

Parameters **record_list** (*list*) – a list of record.id

Returns a dictionary with records as keys, abundance as values

Return type dict

`iss.abundance.zero_inflated_lognormal(record_list)`

Generate scaled zero-inflated lognormal abundance distribution from a number of records

Parameters **record_list** (*list*) – a list of record.id

Returns a dictionary with records as keys, abundance as values

Return type dict

2.4.4 iss.app module

`iss.app.generate_reads(args)`

Main function for the *iss generate* submodule

This submodule generates reads from an ErrorModel and write them to `args.output + _R(1/2).fastq`

Parameters **args** (*object*) – the command-line arguments from argparse

`iss.app.main()`

`iss.app.model_from_bam(args)`

Main function for the *iss model* submodule

This submodule write all variables necessary for building an ErrorModel to `args.output + .npz`

Parameters **args** (*object*) – the command-line arguments from argparse

2.4.5 iss.bam module

`iss.bam.random()` → *x* in the interval [0, 1).

`iss.bam.read_bam(bam_file, n_reads=1000000)`

Bam file reader. Select random mapped reads from a bam file

Parameters **bam_file** (*string*) – path to a bam file

Yields *read* – a pysam read object

`iss.bam.to_model(bam_path, output)`

from a bam file, write all variables needed for modelling reads in a .npz model file

For a brief description of the variables that will be written to the `output` file, see the `bam.write_to_file` function

Parameters

- **bam_path** (*string*) – path to a bam file
- **output** (*string*) – prefix of the output file

`iss.bam.write_to_file(model, read_length, mean_f, mean_r, hist_f, hist_r, sub_f, sub_r, ins_f, ins_r, del_f, del_r, i_size, output)`

Write variables to a .npz file

Parameters

- **model** (*string*) – the type of error model
- **read_length** (*int*) – read length of the dataset
- **mean_f** (*list*) – list of mean bin sizes
- **mean_r** (*list*) – list of mean bin sizes
- **hist_f** (*list*) – list of cumulative distribution functions for the forward read quality
- **hist_r** (*list*) – list of cumulative distribution functions for the reverse read quality
- **sub_f** (*list*) – list of dictionaries representing the substitution probabilities for the forward reads
- **sub_r** (*list*) – list of dictionaries representing the substitution probabilities for the reverse reads
- **ins_f** (*list*) – list of dictionaries representing the insertion probabilities for the forward reads
- **ins_r** (*list*) – list of dictionaries representing the insertion probabilities for the reverse reads
- **del_f** (*list*) – list of dictionaries representing the deletion probabilities for the forward reads
- **del_r** (*list*) – list of dictionaries representing the deletion probabilities for the reverse reads
- **i_size** (*int*) – distribution of insert size for the aligned reads
- **output** (*string*) – prefix of the output file

2.4.6 iss.generator module

`iss.generator.cleanup(file_list)`

remove temporary files

Parameters **file_list** (*list*) – a list of files to be removed

`iss.generator.concatenate(file_list, output)`

Concatenate fastq files together

Outputs two files: output_R1.fastq and output_R2.fastq

Parameters

- **file_list** (*list*) – the list of input files prefix
- **output** (*string*) – the output files prefix

`iss.generator.reads(record, ErrorModel, n_pairs, cpu_number, output, gc_bias=False)`

Simulate reads from one genome (or sequence) according to an ErrorModel

This function makes use of the `simulate_read` function to simulate reads and save them in a fastq file

Parameters

- **record** (*SeqRecord*) – sequence or genome of reference
- **ErrorModel** (*ErrorModel*) – an ErrorModel
- **n_pairs** (*int*) – the number of reads to generate
- **cpu_number** (*int*) – an int identifying the cpu that is used by the function. Is used for naming the output file
- **output** (*str*) – the output file prefix
- **gc_bias** (*bool*) – if set, the function may skip a read due to abnormal GC content

Returns the name of the output file

Return type *str*

`iss.generator.simulate_read(record, ErrorModel, i)`

From a read pair from one genome (or sequence) according to an ErrorModel

Each read is a SeqRecord object returns a tuple containing the forward and reverse read.

Parameters

- **record** (*SeqRecord*) – sequence or genome of reference
- **ErrorModel** (*ErrorModel*) – an ErrorModel class
- **i** (*int*) – a number identifying the read

Returns tuple containing a forward read and a reverse read

Return type *tuple*

`iss.generator.to_fastq(generator, output)`

Write reads to a fastq file

Take a generator or a list containing read pairs (tuples) and write them in two fastq files: `output_R1.fastq` and `output_R2.fastq`

Parameters

- **generator** (*generator*) – a read generator (or list)
- **output** (*string*) – the output files prefix

2.4.7 iss.modeller module

`iss.modeller.dispatch_indels(read)`

Return the x and y position of a insertion or deletion to be inserted in the indel matrix.

The substitution matrix is a 2D array of size 301 * 9 The x axis (301) corresponds to the position in the read, while the y axis (9) represents the match or indel (see the dispatch dict in the function). Positions 0 is match or substitution, other positions in 'N1' are insertions, 'N2 are deletions'

The size of x axis is 301 because we haven't calculated the read length yet

Parameters **read** (*read*) – an aligned read object

Yields *tuple* – a tuple with the x, y position for dispatching the indel in the indel matrix

`iss.modeller.dispatch_subst(base, read, read_has_indels)`

Return the x and y position of a substitution to be inserted in the substitution matrix.

The substitution matrix is a 2D array of size 301 * 16 The x axis (301) corresponds to the position in the read, while the y axis (16) represents the match or substitution (see the dispatch dict in the function). Positions 0, 4, 8 and 12 are matches, other positions are substitutions

The size of x axis is 301 because we haven't calculated the read length yet

Parameters

- **base** (*tuple*) – one base from an alignment object. According to the pysam documentation: an alignment is a list of tuples: aligned read (query) and reference positions. the parameter `with_seq` adds the ref sequence as the 3rd element of the tuples. substitutions are lower-case.
- **read** (*read*) – a read object, from which the alignment comes from
- **read_has_indels** (*bool*) – a boolean flag to keep track if the read has an indel or not

Returns x and y position for incrementing the substitution matrix and a third element: True if an indel has been detected, False otherwise

Return type *tuple*

`iss.modeller.divide_qualities_into_bins(qualities, n_bins=4)`

Divides the raw quality scores in bins according to the mean phred quality of the sequence they come from

Parameters

- **qualities** (*list*) – raw count of all the phred scores and mean sequence quality
- **n_bins** (*int*) – number of bins to create (default: 4)

Returns a list of lists containing the binned quality scores

Return type *list*

`iss.modeller.indel_matrix_to_choices(indel_matrix, read_length)`

Transform an indel matrix into probabilities of indels for at every position

From the raw indel count at one position, returns a dictionary with probabilities of indel

Parameters

- **indel_matrix** (*np.array*) – the substitution matrix is a 2D array of size `read_length * 16`. the x axis (`read_length`) corresponds to the position in the read, while the y axis (9) represents the match or indel. Positions 0 is match or substitution, other positions in 'N1' are insertions, 'N2' are deletions
- **read_length** (*int*) – read length

Returns tuple containing two lists of dictionaries representing the insertion or deletion probabilities for a collection of reads

Return type *tuple*

`iss.modeller.insert_size(insert_size_distribution)`

Calculate cumulative distribution function from the raw insert size distributin. Uses 1D kernel density estimation.

Parameters

- **insert_size_distribution** (*list*) – list of insert sizes from aligned

- **pairs**(*read*) –

Returns a cumulative density function

Return type 1darray

`iss.modeller.quality_bins_to_histogram(bin_lists)`

Wrapper function to generate cdfs for each quality bins

Generate cumulative distribution functions for a number of mean quality bins

Parameters

- **bins_lists**(*list*) – list of list containing raw count of all phred
- **scores** –

Returns a list of lists containg cumulative density functions

Return type list

`iss.modeller.raw_qualities_to_histogram(qualities)`

Approximate the distribution of base quality at each position in a read using a pseudo 2d kernel density estimation

Generate cumulative distribution functions

Parameters **qualities**(*list*) – raw count of all phred scores

Returns

list of cumulative distribution functions. One cdf per base. The list has the size of the read length

Return type list

`iss.modeller.subst_matrix_to_choices(substitution_matrix, read_length)`

Transform a substitution matrix into probabilties of substitutions for each base and at every position

From the raw mismatches at one position, returns a dictionary with probabilties of substitutions

Parameters

- **substitution_matrix**(*np.array*) – the substitution matrix is a 2D array of size `read_length * 16`. the x axis (`read_length`) corresponds to the position in the read, while the y axis (16) represents the match or substitution. Positions 0, 4, 8 and 12 are matches, other positions are substitutions
- **read_length**(*int*) – read length

Returns

list of dictionaries representing the substitution probabilities for a collection of reads

Return type list

2.4.8 iss.util module

`iss.util.convert_n_reads(unit)`

For strings representing a number of bases and ending with k, K, m, M, g, and G converts to a plain old number

Parameters **n**(*str*) – a string representing a number ending with a suffix

Returns a number of reads

Return type float

`iss.util.count_records(fasta_file)`
 Count the number of records in a fasta file and return a list of records id

Parameters `fasta_file` (*string*) – the path to a fasta file

Returns a list of record ids

Return type list

`iss.util.genome_file_exists(filename)`
 Checks if the output file from the `-ncbi` option already exists

Parameters `filename` (*str*) – a file name

`iss.util.nplog(type, flag)`

`iss.util.phred_to_prob(q)`
 Convert a phred score (Sanger or modern Illumina) in probability

Given a phred score `q`, return the probability `p` of the call being right

Parameters `q` (*int*) – phred score

Returns probability of basecall being right

Return type float

`iss.util.prob_to_phred(p)`
 Convert a probability into a phred score (Sanger or modern Illumina)

Given a probability `p` of the basecall being right, return the phred score `q`

Parameters `p` (*int*) – probability of basecall being right

Returns phred score

Return type int

`iss.util.reservoir(records, record_list, n=None)`
 yield a number of records from a fasta file using reservoir sampling

Parameters `records` (*obj*) – fasta records from SeqIO.parse

Yields `record` (*obj*) – a fasta record

`iss.util.rev_comp(s)`
 A simple reverse complement implementation working on strings

Parameters `s` (*string*) – a DNA sequence (IUPAC, can be ambiguous)

Returns reverse complement of the input sequence

Return type list

`iss.util.split_list(l, n_parts=1)`
 Split a list in a number of parts

Parameters

- `l` (*list*) – a list
- `n_parts` (*in*) – the number of parts to split the list in

Returns a list of `n_parts` lists

Return type list

2.4.9 Module contents

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