proto_err Documentation Release 1

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PROTO_ERR - MAIN PACKAGE

1.1 proto_err.simulation - Simulating Error Reads

```
\textbf{class} \ \texttt{proto\_err.simulation.complexError} \ (\textit{record}, \textit{opt}, \textit{id})
     Bases: proto_err.simulation.simulateError
     Methods
     error()
          Function to induce and error
class proto_err.simulation.simulateError(record, opt, id)
     Class of objects to simulate errors in a SeqRecord
     Methods
     deletion (pos, dlen)
          function to induce a deletion
     indel(pos)
          function to induce an INDEL
     ins (pos, rl)
          function to induce a insertion
     qscore None
     record None
          Return a Bio.SeqRecord
     snp(pos, rl)
          function to induce a SNP
class proto_err.simulation.singleSNP (record, opt, id)
     Bases: proto_err.simulation.simulateError
     Methods
     error()
          Function to induce and error
```

```
proto\_err.simulation.subsample (ref, opt, errorSimulator = < class proto\_err.simulation.complexError at 0x10544c1f0 > )
```

Function to take a fasta file subsample reads and generate a list of subsampled reads

1.2 proto_err.errorCount - Error Counting

```
class proto_err.errorCount.counter(ref, errorList=None, samfile=None, opt=None)
    Takes a list of errors and does some kmer counting
```

Methods

```
countAlignedBases (read)
```

```
countErrorKmer (maxKmerLength=None)
```

Count all kmers in the list of errors of length kmerLen or below before and after and error.

Parameters maxKmerLength: int

This is a type. Maximum kmer length

Returns emmissionDic,beforeAfterCount:

dict,dict emmissionDic counts the number of times a transition occurs

```
e.g. {'A':{'T':123,'C':123,...,},'T':{'A':123,...},...}
```

emmissionDic[trueBase][emmitedBase] = count of trueBase -> emmitedBase transition

beforeAfterCount counts the number of times a kmer appears before or after an error

beforeAfterCount['before'][trueBase][emmitedBase][kmer] = count of kmer occurance before trueBase -> emmitedBase transition

beforeAfterCount['after'][trueBase][emmitedBase][kmer] = count of kmer occurance after trueBase -> emmitedBase transition

These dictonaries are also stored in the counter object in counter.res['errorMode'],counter.res['kmerCounts']

See also:

countRefKmer

Examples

```
>>> from errorCount import counter
>>> errorCounter = counter(ref, samfile)
>>> errorCounter.countErrorKmer(maxKmerLength = 3)
>>> ## counts all possible kmers of length 1,2,3 before and after an error.
>>> ({'A': {'C': 113, 'T': 105, 'G': 84}, ...}, {'after':{'A': {'C': {'CTT': 2, 'GCA': 1,...}}}
```

countRefKmer (maxKmerLength=None)

Count all kmers in the reference of length kmerLen or below

i.e. counter.countRefKmer(maxKmerLength = 3) counts all possible kmers of length 1,2,3

returns a dictonary of counts in the form

```
{'AAT':123,'AA':123,...}
```

```
This dictonary is also stored in the counter object in counter.res['RefCounts']
     getCount (truth=None, emission=None, kmer='', after=False)
           Gets the count for a given {truth,emmision,kmer}
     kmerFreq(seq, kmer)
           Calculate the number of times a kmer appears in a sequence seq: SeqRecord Object kmer: kmer string
     readDiff(read, ref)
     setup(opt)
           Setup output
class proto_err.errorCount.error(true, emission, read, readPos)
     Information about the errors in a read
     Methods
     after(i)
           Return the following j bases, return N when bases missing e.g. error after (2) returns the 2 bases after the
           error
     before (i)
           Return the preceding j bases, return N when bases missing e.g. error.before(2) returns the 2 bases before
           the error "
     errorType None
           The type of read error SNP, Insertion or Deletion
     isDeletion None
           Is the error a deletion
     isIndel None
           Is the error an INDEL
     isInsertion None
           Is the error an insertion
     isSnp None
           Is the error a SNP
     qscore (i)
           Return the quality score at a base +i i from the error start position error.qscore(0) is equivalent to error.qual
     qual None
           Quality score of the base where the error occured. equivalent to error.qscore(0)
class proto_err.errorCount.errorReader(samfile, ref)
     Iterable over errors in aligned reads
     Methods
     checkDeletion(N)
           Checks Deletionread segment for errors. called when cigarstring = D:N
```

1.2. proto_err.errorCount - Error Counting

Checks HardClipped read segment for errors. called when cigarstring = H:N

Checks Insertion read segment for errors. called when cigarstring = I:N

checkHardClipped(N)

checkInsertion(N)

${\tt checkPadding}\,(N)$

Checks Padding read segment for errors. called when cigarstring = P:N

checkRead()

Checks current read for errors

${\tt checkSNPs}\,(N)$

Checks read segment for SNP errors. called when cigarstring = M:N

${\tt checkSeqMismatch}\,(N)$

Checks SeqMismatch read segment for errors. called when cigarstring = =:N

${\tt checkSkipped}\,(N)$

Checks Skipped read segment for errors. called when cigarstring = X:N

${\tt checkSoftClipped}\,(N)$

Checks SoftClipped read segment for errors. called when cigarstring = S:N

next()

Returns the next error in the samfile aligned read

readNext()

Iterates to the next read in samfile

refRead None

Get the reference sequence the read is aligned to

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