# Guided Assember API

## API Documentation

## December 7, 2013

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Variables Package src

## 1 Package src

## 1.1 Modules

- aligner (Section 2, p. 3)
- assembler (Section 3, p. 5)
- bwt (Section 4, p. 6)
- csc\_matrix2 (Section 5, p. 9)
- dynamic\_bwt (Section 6, p. 12)
- lil\_matrix2 (Section 7, p. 16)
- reference (Section 8, p. 18)
- runtests (Section 9, p. 21)
- target\_reads (Section 10, p. 22)
- utils (Section 11, p. 25)

Name	Description
package	Value: None

Class Aligner Module src.aligner

## 2 Module src.aligner

#### 2.1 Functions

## partition(read, k)

Partition the read into k parts

#### **Parameters**

read: Is the read to partition

k: Number of parts for the partition

## $\mathbf{kEdit}(p, t, k)$

Find an approximate match of p in t with up to k edits

## Parameters

p: query string

 ${\tt t:} \ \ {\rm reference} \ {\rm string}$ 

k: max number of edits

test()

## 2.2 Variables

Name	Description
package	Value: 'src'

## 2.3 Class Aligner

#### 2.3.1 Methods

\_\_init\_\_(self, ref\_str, target)

Object used for alignment of a target object that can generate multiple reads related to target string. i.e. reads to be aligned

#### **Parameters**

ref\_str: the reference string
target: the target string

## $\mathbf{align}(\mathit{self})$

Find an approximate match of the read in the reference. Pulls reads from the target\_reads class.

Class Aligner Module src.aligner

## $alter\_bwt(self, no\_opt)$

Alters the BWT dynamically based on the updates pending in the queue created in the align() method.

## Parameters

no\_opt: boolean if true do no optimizations i.e use a static bwt & no dbwt

Variables Module src.assembler

## 3 Module src.assembler

#### 3.1 Functions

**assemble**(reference, target, threshold, min\_consensus, no\_opt)

Execute method that runs the Guided Assembler on a given reference and target string

**Parameters** 

reference: an object of class Reference – representing the reference string

target: an object of class Target - representing the target string

threshold: the minimum value per index required for the addition of index

to a contig

min\_consensus: the minimum total fraction of indexes that have come to

concesus

eval\_acc(target\_seq, contigs)

Evaluate the accuracy of the assembly of target reads

**Parameters** 

target\_seq: The target the sequence

contigs: The contiguous sequences that are found

randStrings(n, corrupt)

Generate a random reference string and a related target string

**Parameters** 

n: length of toy strings

corrupt: Percentage of corrupted nt

main()

Name	Description
_package	Value: 'src'

Class BWT Module src.bwt

## 4 Module src.bwt

## 4.1 Functions

$\mathbf{test}(s)$		
main()		

## 4.2 Variables

Name	Description
_package	Value: 'src'

## 4.3 Class BWT

object — src.bwt.BWT

Known Subclasses: src.dynamic\_bwt.dBWT

#### 4.3.1 Methods

\_\_init\_\_(self, seq)

A bwt class with a few auxilliary data structures

Parameters

seq: The seq in question

Overrides: object.\_\_init\_\_

 $\mathbf{new}(\mathit{self}, \mathit{seq})$ 

Create a new bwt, F, L and Tally arrays (All necessary attributes for FM index)

**Parameters** 

seq: the insertion seq

 $rank_bwt(self)$ 

Given BWT string bw, return parallel list of B-ranks. Also returns tots: map from character to # times it appears. Adapted from Prof. Ben Langmend's example code

Class BWT Module src.bwt

#### first\_col(self, tots)

Return map from character to the range of rows prefixed by the character. Adapted from Prof. Ben Langmend's example code

#### Parameters

tots: a list with the a mapping of each character to the number of times it appears in F

#### Return Value

the character and total list

#### $\mathbf{get\_seq}(self)$

Make T from BWT(T) Adapted from Prof. Ben Langmend's example code

#### Return Value

the original sequence given the bwt

#### $\mathbf{suffixArray}(\mathit{self}, s)$

Create a suffix array from a string s Adapted from Prof. Ben Langmend's example code

#### **Parameters**

s: the sequence we will use to create the suffix array

#### Return Value

the actual suffix array

## $\mathbf{bwtViaSa}(\mathit{self}, \mathit{seq})$

Given T, returns BWT(T) by way of the suffix array Adapted from Prof. Ben Langmend's example code

#### **Parameters**

seq: the sequence we want to build the bwt from

#### Return Value

the BWT as a list

#### $\mathbf{get\_lcp}(self)$

TODO: DM

#### $\mathbf{get\_bwt}(self)$

TODO: DM

## $\mathbf{build\_lcp}(\mathit{self}, \mathit{seq})$

#### **Parameters**

seq: the sequence we will get lcp values for

## Inherited from object

```
__delattr__(), __format__(), __getattribute__(), __hash__(), __new__(), __reduce__(), __reduce_ex__(), __repr__(), __setattr__(), __sizeof__(), __str__(), __subclasshook__()
```

Class BWT Module src.bwt

## 4.3.2 Properties

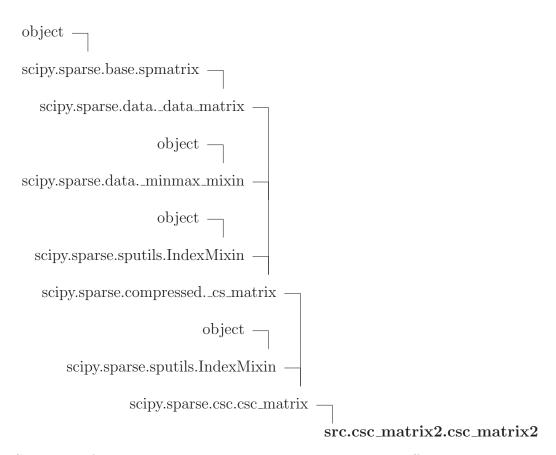
Name	Description
Inherited from object	
_class	

## 5 Module src.csc\_matrix2

## 5.1 Variables

Name	Description
_package_	Value: 'src'

## 5.2 Class csc\_matrix2



Sub-class of lil\_matrix that allows permits popping rows off

#### 5.2.1 Methods

( 16)	
<b>pop_row</b> (self)	
P - P · · · ( • • • • ) /	

Class csc\_matrix2 Module src.csc\_matrix2

## append\_col(self, sp\_mat=None, init=True)

Add a column to the sparse matrix given another sp\_mat to append. Used when adding a new letter to the alphabet.

#### **Parameters**

sp\_mat: the sparse matrix to be appended to the self object

### $append\_row(self)$

Append a row to the bottom of a lil\_matrix2 object

## $Inherited\ from\ scipy.sparse.csc.csc\_matrix$

```
__getitem__(), __iter__(), getcol(), getrow(), nonzero(), tocsc(), tocsr(), transpose()
```

## $Inherited\ from\ scipy.sparse.compressed.\_cs\_matrix$

## $Inherited\ from\ scipy.sparse.data\_data\_matrix$

```
_abs__(), _imul__(), _itruediv__(), _neg__(), arcsin(), arcsinh(), arctan(), arctanh(), astype(), ceil(), conj(), copy(), deg2rad(), expm1(), floor(), log1p(), rad2deg(), rint(), sign(), sin(), sinh(), sqrt(), tan(), tanh(), trunc()
```

## Inherited from scipy.sparse.base.spmatrix

## $Inherited\ from\ scipy.sparse.data.\_minmax\_mixin$

```
\max(), \min()
```

## Inherited from object

```
__delattr__(), __format__(), __getattribute__(), __hash__(), __new__(), __reduce__(), __reduce_ex__(), __setattr__(), __sizeof__(), __subclasshook__()
```

#### 5.2.2 Properties

Name	Description
Inherited from scipy.sparse.compressedcs_matrix	

 $continued\ on\ next\ page$ 

Name	Description	
has_sorted_indices, nnz		
Inherited from scipy.sparse.a	Inherited from scipy.sparse.datadata_matrix	
dtype		
Inherited from scipy.sparse.base.spmatrix		
shape		
Inherited from object		
class		

## 5.2.3 Class Variables

Name	Description
Inherited from scipy.sparse.base.spmatrix	
_array_priority, ndim	

## 6 Module src.dynamic\_bwt

### 6.1 Functions

, ,		
I toat(a)		
Lest(s)		
1000(0)		

#### 6.2 Variables

Name	Description
package	Value: 'src'

#### 6.3 Class dBWT

object —
src.bwt.BWT —
src.dynamic\_bwt.dBWT

#### 6.3.1 Methods

 $\_$ **init** $\_$ (self, seq)

A dynamic Burrows Wheeler Transform class that supports on the fly changes to the seq that defined the BWT

**Parameters** 

seq: str - the sequence you want to use to form the bwt

Overrides: object.\_\_init\_\_

build\_psums(self)

Build the partial sums sparse matrix given a new seq

 $delete\_one(self, pos)$ 

Delete a char at some positin in the bwt

**Parameters** 

pos: the position that should be deleted

## replace\_one(self, char, pos)

Replace a char at some position in the bwt

### **Parameters**

char: the char that will replace the one at pos

pos: the position that where the replacement is to occur

## **insert\_one**(self, char, pos)

Insert a character at a certain position 'pos' of the original sequence

#### **Parameters**

char: the character to insert

pos: the index of the original string where the character is to be

inserted

## updateSA\_naive(self)

Update the suffix array to an alteration in the sequence defining the bwt

## updateSA\_dynamic(self)

## reorder(self, i, Lp, Fp, j, jp, psumsp)

Move a row from row j to row jp

#### **Parameters**

i: the index (row) in the bwt where the change occurred

Lp: the L' (prime) new L after the change

Fp: the F' (prime) new F after the change

j: the j actual position of j

jp: the j' (prime) expected position of j

psumsp: the partial sums' (prime)

## moverow(self, F, L, j, jp, psums)

Take F and L and move row jp to j and moving others as necessary

#### **Parameters**

F: a list that corresponds to the first column of the bwm

L: a list that corresponds to the last column of the bwm

j: a row index i.e in range len(F/L)

jp: a row index i.e in range len(F/L)

#### Return Value

the new F and L with rows j & p switched

## $\mathbf{LF}(self, F, L, i, psums)$

LF computes a mapping from a char in F to a char in L in the BWM

#### **Parameters**

F: a list that corresponds to the first column of the bwm

L: a list that corresponds to the last column of the bwm

i: a row of the bwt

psums: a partial sums matrix

## $\mathbf{match}(\mathit{self}, \mathit{seq})$

#### **Parameters**

seq: the sequence we are looking for

#### Return Value

an array of all perfect matches

## get\_rank(self, row, char, psums, get\_tot=True)

" Get the rank of a letter at a particular row in the BWT.

#### **Parameters**

row: what row of the bwt to look at

char: the character whose rank we see

psums: the partial sums matrix corresponding to the state of the

bwt we are concerned with

get\_tot: boolean whether or not to get the total count for that

character

#### Return Value

a rank and totals list of 2-item tuples

### rank\_bwt(self, psums)

Given BWT string bw, return parallel list of B-ranks. Also returns tots: map from character to # times it appears. Adapted from Prof. Ben Langmend's example code

#### **Parameters**

psums: the partial sums matrix corresponding to the state of the bwt we are concerned with

Overrides: src.bwt.BWT.rank\_bwt

## get\_seq(self, psums)

Make T (The original sequence) from BWT(T) (The Burrows Wheeler Transform string)

#### **Parameters**

psums: the partial sums matrix corresponding to the state of the bwt we are concerned with

## Return Value

the original sequence given the bwt

Overrides: src.bwt.BWT.get\_seq

## Inherited from src.bwt.BWT(Section 4.3)

build\_lcp(), bwtViaSa(), first\_col(), get\_bwt(), get\_lcp(), new(), suffixArray()

## Inherited from object

```
__delattr__(), __format__(), __getattribute__(), __hash__(), __new__(), __reduce__(), __reduce_ex__(), __repr__(), __setattr__(), __sizeof__(), __str__(), __subclasshook__()
```

#### 6.3.2 Properties

Name	Description
Inherited from object	
class	

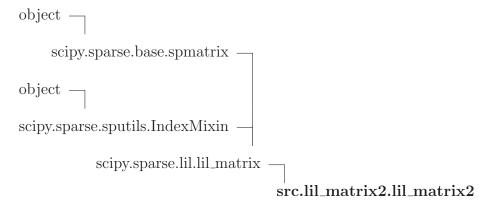
Class lil\_matrix2 Module src.lil\_matrix2

## 7 Module src.lil\_matrix2

#### 7.1 Variables

Name	Description
_package_	Value: 'src'

#### 7.2 Class lil\_matrix2



Sub-class of lil\_matrix that allows permits popping rows off

#### 7.2.1 Methods

```
\mathbf{pop\_row}(self)
```

append\_col(self, sp\_mat=None, init=True)

Add a column to the sparse matrix sp\_mat1 Used when adding a new letter to the alphabet

**Parameters** 

sp\_mat: the sparse matrix to be appended to the self object

```
\mathbf{append\_row}(\mathit{self})
```

Append a row to the bottom of a lil\_matrix2 object

## $Inherited\ from\ scipy.sparse.lil.lil\_matrix$

```
__getitem__(), __iadd__(), __imul__(), __init__(), __isub__(), __itruediv__(), __setitem__(), __str__(), __truediv__(), copy(), getnnz(), getrow(), getrowview(), reshape(), set_shape(), toarray(), tocsc(), tocsr(), tolil(), transpose()
```

Class lil\_matrix2 Module src.lil\_matrix2

## Inherited from scipy.sparse.base.spmatrix

## Inherited from object

#### 7.2.2 Properties

Name	Description
Inherited from scipy.sparse.lil.lil_matrix	
nnz, shape	
Inherited from object	
class	

#### 7.2.3 Class Variables

Name	Description
Inherited from scipy.sparse.base.spmatrix	
array_priority, ndim	

Class Reference Module src.reference

## 8 Module src.reference

## 8.1 Functions

```
\mathbf{test}(show = \mathsf{True})
```

## 8.2 Variables

Name	Description
package	Value: 'src'

#### 8.3 Class Reference

object — src.reference.Reference

#### 8.3.1 Methods

 $\_$ init $\_$ (self, R, data\_counts=9)

Object to hold a reference string and accompanying metadata associated with keeping track of how many matches/mismatches occur at each position

**Parameters** 

R: Is the reference string

data\_counts: the counts related to which letter landed at a

particular index

Overrides: object.\_\_init\_\_

Class Reference Module src.reference

### match(self, idx, char, cnt=1, thresh=10)

If there is a match in the reference at some position

#### **Parameters**

idx: the index in R where char matched

char: the char that matched

cnt: the number of times we should record char matched.

Default=1

thresh: threshold to indicate a change in the reference should be

made

#### Return Value

True or False on (....something... TODO: SL)

# build\_hist(self, coverage, show=False, save=False, save\_fn='max\_hist\_plot')

Build a histogram to determine what the maxes look & visualize match\_count Might be used to determine a resonable threshold

### **Parameters**

coverage: the average coverage for an single nt

show: Show visualization with match maxes

save\_fn: Save to disk with this file name or else it will be the

default

#### Return Value

the histogram array

#### get\_contigs(self, thresh)

Use thresholding to determine what is a contiguousing the match\_count

#### Parameters

thresh: anything under this value will not be included in the

#### Return Value

the contigs found in the string

#### $plot_{maxes}(self, show = False)$

Plot maxes to try to visualize where contigs will lie

## **Parameters**

show: boolean on if you want to show the image on the screen

Class Reference Module src.reference

## get\_consensus(self, thresh)

Get the fraction of positions in the reference that have come to consus on the nt at that position.

#### **Parameters**

thresh: the number that defines what nt count is sufficient to be confident about the result at a single position

#### Return Value

number that gives the fraction of positions that have come to consensus

## $\mathbf{del}_{-i}\mathbf{dx}(self, idx)$

Delete an index within the count array

#### **Parameters**

idx: the index we want deleted

### $insert_idx(self, idx)$

Insert an index.

#### **Parameters**

idx: the index where we want to insert the charactere

## $zero_idx(self, idx)$

Zero out an index within the count array

#### **Parameters**

idx: the index we want zeroed

## Inherited from object

#### 8.3.2 Properties

Name	Description
Inherited from object	
class	

Variables Module src.runtests

## 9 Module src.runtests

## 9.1 Functions

runtests(num\_tests, scriptname, out\_fn)

Run a series of tests to obtain benchmarks for guided assembler

**Parameters** 

num\_tests: the number of tests to run

scriptname: the name of the script containing the \_main\_ that we

want to run

out\_fn: the name of the output file that we want to generate

Name	Description
package	Value: 'src'

## 10 Module src.target\_reads

## 10.1 Functions

pp(var)

Used in mapping operation for lists to ++ an index in the list

Parameters

var: some integer

Return Value

plus one to value of var

 $\mathbf{test}()$ 

main()

## 10.2 Variables

Name	Description
_package_	Value: 'src'

## 10.3 Class Target

object — src.target\_reads.Target

#### 10.3.1 Methods

## \_\_init\_\_(self, p, read\_length, T, seed=None, coverage=5)

An Object that enables the partitioning &generation of synthetically mutated data given a full Target sequence read

#### **Parameters**

p: the probability of having a polymorphism at any

single letter within the read

read\_length: read lengths that we will produce

T: the target string which we are trying to assemble

using R, the ref

seed: seed for random

coverage: max redundancy at any single nt position

Overrides: object.\_init\_\_

## get\_read(self, \*\*kwargs)

Get a single read from the Target sequence for a streaming read model

#### **Parameters**

p: the probability of SNP occurring

read\_length: the read length

max\_trials: the maximum number of times to rand redraw the

idx if we keep finding over-covered idxs

### Return Value

a string with with a read obtained at a random position

#### mutate(self, read)

Use p to determine how to add SNPs to the returned string

#### **Parameters**

read: the read we want mutated

## Return Value

a string with some SNPs added

## get\_read\_list(self, \*\*kwargs)

Return a list of even-coverage randomly sampled strings with possible SNPs given T. For the non-streaming version of the read splitting.

### **Parameters**

p: the probability of SNP occurring

read\_length: the read length

save: boolean save or don't to disk

save\_fn: the filename you want to use to write to disk

## Inherited from object

```
__delattr__(), __format__(), __getattribute__(), __hash__(), __new__(), __reduce__(), __reduce_ex__(), __repr__(), __setattr__(), __sizeof__(), __str__(), __subclasshook__()
```

## 10.3.2 Properties

Name	Description
Inherited from object	
class	

Variables Module src.utils

## 11 Module src.utils

## 11.1 Functions

## $\mathbf{Override}(\mathit{interface\_class})$

Method decorator for overriding class method name checking. Adapted from http://stackoverflow.com/questions/1167617/in-python-how-do-i-indicate-im-overriding-a-method

## $\mathbf{edta}(X, Y)$

Compute the Edit distance between two sequences

## **Parameters**

X: any arbritrary string

Y: any arbritrary string

Name	Description
package	Value: None

Variables Package tests

# 12 Package tests

## 12.1 Modules

• tdynamic\_bwt (Section 13, p. 27)

Name	Description
package	Value: None

# $13 \quad Module \ tests.tdynamic\_bwt$

## 13.1 Functions

test_move_row()	
Test the functionality of dbwt moverow	

Name	Description
_package_	Value: 'tests'

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