# Pylogeny

## API Documentation

## December 16, 2014

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## 1 Package pylogeny

Pylogeny is a Python library and code framework for phylogenetic tree reconstruction and scoring.

Allows one to perform the following tasks: (1) Generate and manage phylogenetic tree landscapes. (2) Build and rearrange phylogenetic trees using preset operators such as NNI, SPR, and TBR. (3) Score phylogenetic trees by Log-likelihood and Parsimony.

Dependencies: Pandas, P4 Phylogenetic Library. Suggested: FastTree, RAxML, PytBEAGLEhon.

#### 1.1 Modules

- **JSONWriter**: Serialize a phylogenetic landscape into a JSON object. (Section 2, p. 3)
- \_\_\_version\_\_\_ (Section 3, p. 5)
- alignment: Handle input biological sequence alignment files for the purposes of phylogenetic inference. (Section 4, p. 6)
- base: Definitions for generalized containers and objects used by other structures in this framework. (Section 5, p. 11)
- database: Connect, access, + manipulate external tree data from a remote SQL server or from a sqlite file.

(Section 6, p. 20)

- executable: Defines an interface to manage interfacing with the system for respective application calls and implements multiple of these for executables such as FastTree and RAxML. (Section 7, p. 31)
- heuristic: Define the interface for a heuristic in order to implement any manner of heuristic for a combinatorial problem that can be abstracted into a state graph.

  (Section 8, p. 38)
- landscape: Encapsulate a phylogenetic tree space. (Section 9, p. 46)
- landscapeWriter: Serialize a phylogenetic landscape into an SQLlite database file made up of three components: all tree IDs and respective scores, the alignment file as a set of sequences, and a representation of the graph as an edge list.

(Section 10, p. 57)

• model: Phylogenetic tree scoring models; intended to be coupled with the use of pytheaglehon (BEA-GLE) high-performance library.

(Section 11, p. 59)

- newick: Newick string parsing and object interaction. (Section 12, p. 62)
- parsimony: Toolkit for performance of Parsimonious Criterion (Parsimony) methods of optimization of a phylogenetic topology with a particular set of data.

  (Section 13, p. 67)
- pll: C Extension to wrap libpl library. (Section 14, p. 69)
- rearrangement: Phylogenetic tree structure encapsulation; allow rearrangement of said structure. (Section 15, p. 71)
- scoring: Phylogenetic tree scoring. (Section 16, p. 78)
- tree: Container definition for (phylogenetic) bifurcating or multifurcating trees defined using Newick strings, collections of them, and for splits of these trees.

  (Section 17, p. 80)

## 2 Module pylogeny.JSONWriter

Serialize a phylogenetic landscape into a JSON object.

#### 2.1 Variables

Name	Description
package	Value: 'pylogeny'

## 2.2 Class JSONWriter

object —	
${\it pylogeny.} landscape Writer. landscape Writer$	
	pylogeny.JSONWriter.JSONWriter

#### 2.2.1 Methods

init(self, ls, name)		
xinit() initializes x; see help(type(x)) for signature		
Overrides: objectinit extit(inherited documentation)		
nodeToJSON(self, node)		
$\boxed{ \mathbf{getOnlyImprovements}(\mathit{self}, \mathit{groups} = \mathtt{None}) }$		
${\bf getCompleteLandscape}(self)$		
$\mathbf{getJSON}(self)$		

 $\label{linear} \textit{Inherited from pylogeny.landscapeWriter.landscapeWriter}(Section~10.2)$  writeFile()

## Inherited from object

#### 2.2.2 Properties

Name	Description
Inherited from object	
class	

# 3 Module pylogeny.\_\_\_version\_\_\_

## 3.1 Variables

Name	Description
VERSION	Value: '0.3.6.2'
package	Value: None

## 4 Module pylogeny.alignment

Handle input biological sequence alignment files for the purposes of phylogenetic inference. Will read all types of alignment files by utilizing the P4 python phylogenetic library.

#### 4.1 Variables

Name	Description
package	Value: 'pylogeny'

## 4.2 Class alignment

object — pylogeny.alignment.alignment

Known Subclasses: pylogeny.alignment.phylipFriendlyAlignment

Wrap a biological sequence alignment to enable functionality necessary for phylogenetic inference. Makes use of temporary files; requires to be closed once no longer needed.

#### 4.2.1 Methods

\_\_\_\_init\_\_\_(self, inal=None)
Instantiate an object intended to wrap an alignment for the purposes of running phylogenetic inference.
:param inal: An alignment file path (most formats are accepted).
Overrides: object.\_\_\_init\_\_\_

\_\_\_getitem\_\_\_(self, i)

\_\_\_str\_\_\_(self)
str(x)
Overrides: object.\_\_\_str\_\_\_ extit(inherited documentation)

\_\_\_len\_\_\_(self)

 $\_$ iter $\_\_$ (self)

#### close(self)

Delete all temporary files and clear data.

#### toStrList(self)

Get all sequences as a list of strings.

#### getStateModel(self)

#### $\mathbf{getSize}(self)$

Return the size of the alignment, or how many characters there are in each respective item in the alignment.

#### getNumSeqs(self)

Return the number of sequences that are present in the sequence alignment.

#### $\mathbf{getDim}(self)$

Return the dimensionality of the sequence alignment (how many different types of characters).

#### getSequence(self, i)

Acquire the ith sequence.

#### getFASTA(self)

Get (and create if not already) a path to a temporary FASTA file. This will be deleted upon closure of the alignment instance.

#### getApproxMLNewick(self)

Get a tree in newick format via use of FastTree that serves as an approximation of the maximum likelihood tree for this data.

#### getApproxMLTree(self)

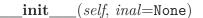
Get a tree object for an approximation of the maximum likelihood tree for this data using FastTree.

$\mathbf{getTaxa}(\mathit{self})$		
	Return taxa names.	
	$\underline{\mathbf{getAlignment}(\mathit{self})}$	
	Acquire the alignment data s	tructure (P4 module).
[	bootstrap(self)	
	Perform bootstrapping on the	e alignment data.
$nh\epsilon$	therited from object	
	delattr(),format reduce(),reduceex subclasshook()	_(),getattribute(),hash(),new(),x(),repr(),setattr(),sizeof()
.2.2	2.2 Properties	
	Name	Description
	Inherited from object	
	class	

## 4.3 Class phylipFriendlyAlignment

An alignment object that renames all comprising taxa in order to be able to be written as a Phylip file.

#### 4.3.1 Methods



Instantiate an object intended to wrap an alignment for the purposes of running phylogenetic inference.

:param inal: An alignment file path (most formats are accepted).

Overrides: object. init extit(inherited documentation)

#### getPhylip(self)

Get a path to a temporary Phylip file. This will be deleted upon closure of the alignment instance.

#### writeProperNexus(self, wri)

Write a Nexus file with proper names.

#### reassignFromReinterpretedNewick(self, tr)

Replace all proper names with reassigned names in a Newick tree.

## reinterpretNewick(self, tr)

Replaces all reassigned names to proper names in a Newick tree.

#### getProperName(self, n)

Return the actual name for an integer-based sequence name that was reassigned at initialization.

#### getTaxa(self)

Return current taxa names in the alignment.

Overrides: pylogeny.alignment.alignment.getTaxa

#### recreateObject(self)

Reintializes the object.

## Inherited from pylogeny.alignment.alignment(Section 4.2)

\_\_getitem\_\_(), \_\_iter\_\_(), \_\_len\_\_(), \_\_str\_\_(), bootstrap(), close(), getAlignment(), getApproxMLNewick(), getApproxMLTree(), getDim(), getFASTA(), getNumSeqs(), getSequence(), getSize(), getStateModel(), toStrList()

Inherited	from	object
-----------	------	--------

delattr(),	$\_{ m format}$	(),	_getattrib	$ute_{\underline{}}()$	$, \underline{\hspace{0.2cm}}$ hash	n(), _	new_	():
reduce(),	$_{ m reduce}$	_ex()	,repr_	(),	$_{ m setattr}\_$	_(),	_sizeof	_(),
subclasshook_	_()							

## 4.3.2 Properties

Name	Description
Inherited from object	
class	

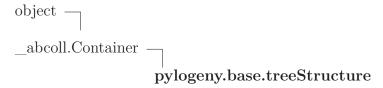
## 5 Module pylogeny.base

Definitions for generalized containers and objects used by other structures in this framework.

#### 5.1 Variables

Name	Description
package	Value: 'pylogeny'

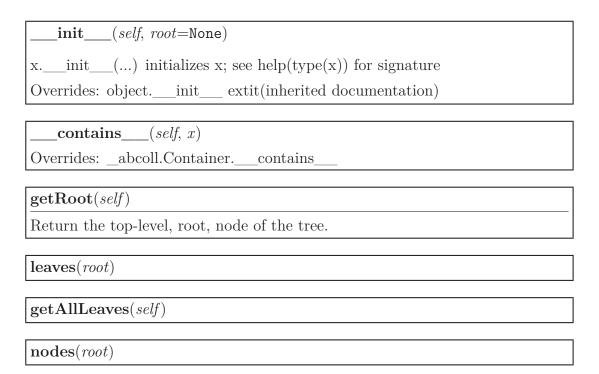
#### 5.2 Class treeStructure



Known Subclasses: pylogeny.base.trie, pylogeny.rearrangement.topology

Defines a base collection of treeNodes and treeBranches in a hierarchical tree structure.

#### 5.2.1 Methods



$\boxed{\mathbf{getAllNodes}(\mathit{self})}$
${\bf postOrderTraversal}(root)$
$\boxed{\mathbf{getPostOrderTraversal}(\mathit{self})}$
$\underline{}$ str $\underline{}$ $(self)$
Returns a string representation of the tree.
Overrides: objectstr
erited from _abcoll.Container _subclasshook()
erited from object
delattr(),format(),getattribute(),hash(),new reduce(),reduceex(),repr(),setattr(),sizeof
2 Properties
Name Description
Inherited from object
class

#### 5.2.3 Class Variables

Name	Description
root	Value: None
abstractmethods	Value: frozenset([])

## 5.3 Class treeNode

object		
	p	$_{ m by}$ logeny. $_{ m base.tree}$ Node

Known Subclasses: pylogeny.base.trieNode, pylogeny.newick.node

A node in a tree.

### 5.3.1 Methods

init(self, lbl=None, children=None, parent=None)		
xinit() initializes x; see help(type(x)) for signature		
Overrides: objectinit extit(inherited documentation)		
$\mathbf{getLabel}(\mathit{self})$		
$\boxed{\mathbf{getParent}(\mathit{self})}$		
${\bf addChild}(\textit{self}, \textit{item})$		
$\boxed{\mathbf{getChildByIndex}(\mathit{self},\ i)}$		
$\mathbf{getChildren}(self)$		
$\mathbf{isLeaf}(\mathit{self})$		
${\bf is Internal Node}(self)$		
nerited from object		

## Inh

delattr(),f	$iormat_{\underline{\hspace{1cm}}}(), \underline{\hspace{1cm}}_{\underline{\hspace{1cm}}}$	getattribute(	),hash( $)$ , .	new()
reduce(),r	educe_ex(), _	repr(),	$_{\text{setattr}}(),$	$\_sizeof\_\_\_(),$
str(),subc	classhook()			

## 5.3.2 Properties

Name	Description
Inherited from object	
class	

### 5.3.3 Class Variables

Name	Description
label	Value: None
parent	Value: None
children	Value: None

### 5.4 Class treeBranch

object	$\neg$
	pylogeny.base.treeBranch

Known Subclasses: pylogeny.newick.branch

A branch in a tree.

#### 5.4.1 Methods

init(self, parent=None, child=None, label=',')	
xinit() initializes $x$ ; see $help(type(x))$ for signature	
Overrides: objectinit extit(inherited documentation)	

|--|

$\boxed{\mathbf{getParent}(\mathit{self})}$
---

$$\mathbf{getChild}(\mathit{self})$$

## $Inherited\ from\ object$

$\_\delattr\_$	_(), _	$\_\_ format_$	(), _	g	etattribu	$ite_{\_\_}$	$(), \underline{\hspace{1cm}}$ has	h(),	new_	():
$\_\_$ reduce $\_$	_(), _	_reduce_	_ex	$(), _{-}$	repr	_(), _	$\_\_$ setattr $\_$	(),	_sizeof	_(),
str(),	su	bclasshoo	ok(	)						

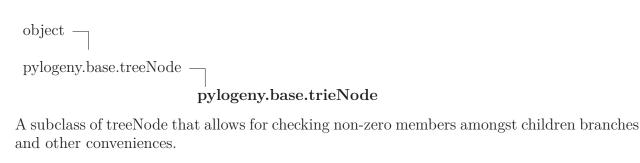
## 5.4.2 Properties

Name	Description
Inherited from object	
class	

#### 5.4.3 Class Variables

Name	Description
label	Value: ''
parent	Value: None
child	Value: None

### 5.5 Class trieNode



### 5.5.1 Methods

	$\mathbf{getParentNode}(\mathit{self})$
	setChildNode(self, child, newchild)
	${\bf iter Non Empty Children Nodes} (self)$
	Iterate over all children that are not empty.
	${\bf getNonEmptyChildrenNodes}(self)$
	Acquire a list of all non-empty children.
	${\bf get Non Empty Children Branches}(self)$
	Acquire a list of all non-empty children.
	${\bf getNonEmptyChildrenBranchLabels} (self)$
	${\bf numEmptyChildrenNodes}(self)$
	Acquire the number of children nodes that are marked 0 or nonexistent.
$\epsilon$	$erited\ from\ pylogeny.base.treeNode(Section\ 5.3)$
	init(), addChild(), getChildByIndex(), getChildren(), getLabel(), getIent(), isInternalNode(), isLeaf()

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

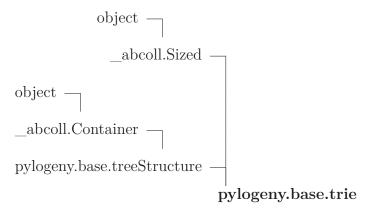
#### 5.5.2 Properties

Name	Description
Inherited from object	
class	

#### 5.5.3 Class Variables

Name	Description		
Inherited from pylogeny.base	treeNode (Section 5.3)		
children, label, parent			

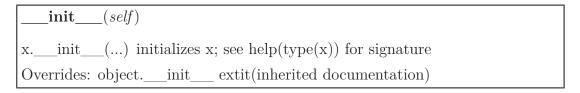
#### 5.6 Class trie



 ${\bf Known~Subclasses:}~{\rm pylogeny.base.patriciaTree}$ 

Defines a trie across a range of strings.

#### 5.6.1 Methods



Γ	$\underline{\text{len}}_{}(self)$
	Implementing for interface (Sized).
	Overrides: _abcoll.Sized len
_	
8	$\mathbf{getAlphabet}(\mathit{self})$
[8	$\mathbf{get}\mathbf{Root}(self)$
]	Return the top-level, root, node of the tree.
	Overrides: pylogeny.base.treeStructure.getRoot extit(inherited documentation)
_	
5	$\mathbf{search}(\mathit{self}, \mathit{seq})$
5	Search for a sequence in the trie. Returns true if it exists.
Γ.	
-	$\operatorname{insert}(\mathit{self}, \mathit{seq})$
	Dynamically insert a sequence into the trie.
[	$\mathbf{delete}(\mathit{self}, \mathit{seq})$
	Remove a sequence from the trie. Will not remove added characters to alphabet.
e	$rited\ from\ \_abcoll.Sized$
_	subclasshook()
e	$rited\ from\ pylogeny.base.tree Structure (Section\ 5.2)$
- I	str(), getAllLeaves(), getAllNodes(), getPostOrderTraversal(), leaves(), nodes postOrderTraversal()
ie	rited from object
_	delattr(),format(),getattribute(),hash(),new(),reduceex()

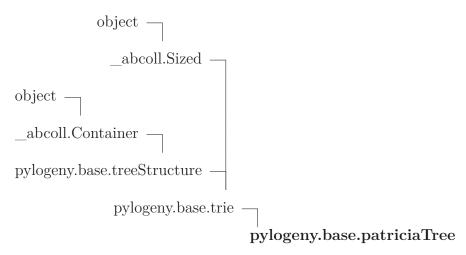
## 5.6.2 Properties

Name	Description
Inherited from object	
class	

#### 5.6.3 Class Variables

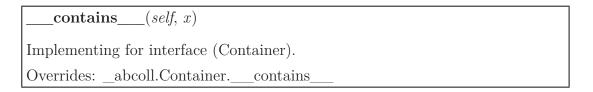
Name	Description
alphabet	Value: None
root	Value: None
count	Value: 0
nextLabel	Value: 1
abstractmethods	Value: frozenset([])

#### 5.7 Class patriciaTree



Defines a PATRICIA tree (condensed trie) across a range of strings.

#### 5.7.1 Methods



#### **search**(*self*, *seq*)

Search for a sequence in the PATRICIA tree. Returns its position in addition sequence if it exists. Else, returns 0.

Overrides: pylogeny.base.trie.search

insert	(self,	seq
	(	0091

Dynamically insert a sequence into the PATRICIA tree. Returns the unique index in the tree for that string.

Overrides: pylogeny.base.trie.insert

## **delete**(self, seq)

Remove a sequence from the PATRICIA tree. Will not remove added characters to alphabet.

Overrides: pylogeny.base.trie.delete

## Inherited from pylogeny.base.trie(Section 5.6)

\_\_init\_\_\_(), \_\_\_len\_\_\_(), getAlphabet(), getRoot()

## $Inherited\ from\ \_abcoll.Sized$

\_\_subclasshook\_\_\_()

## $Inherited\ from\ pylogeny.base.treeStructure(Section\ 5.2)$

 $\underline{\underline{\phantom{a}}}str\underline{\underline{\phantom{a}}}(), getAllLeaves(), getAllNodes(), getPostOrderTraversal(), leaves(), nodes(), postOrderTraversal()$ 

## $Inherited\ from\ object$

$\_\_delattr\_$	(),	$\_$ format $\_$	(),	ge	tattribu	ıte	(),has	h(),	new_	()
reduce	().	reduce	ex	().	repr	().	setattr	().	sizeof	()

#### 5.7.2 Properties

Name	Description
Inherited from object	
class	

#### 5.7.3 Class Variables

Name	Description
Inherited from pylogeny.base	trie (Section 5.6)
abstractmethods, alpl	nabet, count, nextLabel, root

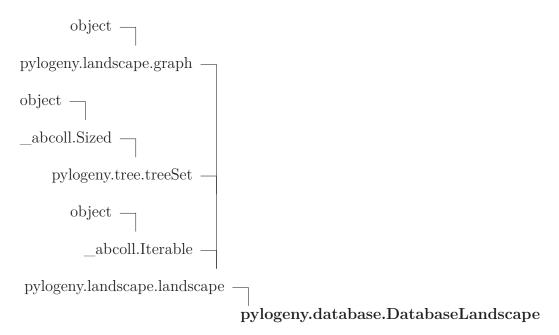
## 6 Module pylogeny.database

Connect, access, + manipulate external tree data from a remote SQL server or from a sqlite file.

#### 6.1 Variables

Name	Description	
package	Value: 'pylogeny'	

## 6.2 Class DatabaseLandscape



 ${\bf Known~Subclasses:}~{\rm pylogeny.database.SQLExhaustive Landscape}$ 

Abstract the landscape to one comprising a landscape.

#### 6.2.1 Methods

 $Inherited\ from\ pylogeny.landscape.landscape(Section\ 9.3)$ 

getitem(),init(),iter(),str(), addTree(), exploreRan-
domTree(), exploreTree(), findTree(), findTreeTopology(), findTreeTopologyByStruc-
$ture(),\ getAlignment(),\ getAllPathsOfBestImprovement(),\ getBestImprovement(),$
getBipartitionFoundInTreeByIndex(), getGlobalOptimum(), getLocalOptima(), get-
Locks(), getNumberTaxa(), getPathOfBestImprovement(), getPossibleNumberRoot-
edTrees(), getPossibleNumberUnrootedTrees(), getRootTree(), getTree(), getVer-
tex(), indexOf(), isLocalOptimum(), isViolating(), iterAllPathsOfBestImprovement()
iterTrees(), lockBranchFoundInTree(), lockBranchFoundInTreeByIndex(), remove-
$Tree(),\ setAlignment(),\ toProperNewickTreeSet(),\ toTreeSet(),\ toggleLock()$
$Inherited\ from\ pylogeny. landscape. graph (Section\ 9.2)$
len(), clearEdgeWeights(), getCenter(), getCliqueNumber(), getCliques(),
getCliquesOfNode(), getComponentOfNode(), getComponents(), getDegreeFor(),
getDiameter(), getEdge(), getEdges(), getEdgesFor(), getMST(), getNeighbors-

For(), getNetworkXObject(), getNodeNames(), getNodes(), getNumCliques(), getNumComponents(), getShortestPath(), getShortestPathLength(), getSize(), has-

## Inherited from pylogeny.tree.treeSet(Section 17.4)

addTreeByNewick(), toTreeFile()

Path(), iterNodes(), setDefaultWeight()

## $Inherited\ from\ \_abcoll.Sized$

\_\_subclasshook\_\_\_()

### Inherited from object

delattr	_(),	$\_{ m format}\_\_$	_(),	_getattrib	${ m ute}$	$(), \underline{\hspace{1cm}}$ hash	(), _	new	_()	),
reduce	_(),	_reduce_e	x()	),repr_	(), _	$\_\_$ setattr $\_\_$	_(), _	_sizeof	_()	)

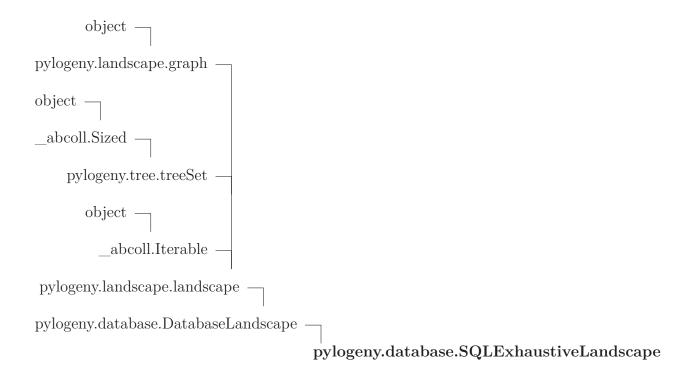
#### 6.2.2 Properties

Name	Description
Inherited from object	
class	

#### 6.2.3 Class Variables

$\mathbf{Name}$	Description	
$\_\_$ abstractmethods $\_\_$	Value:	
	<pre>frozenset(['_fetchRearrangementsFromDatab</pre>	ase',
	'_fetchTre	

## 6.3 Class SQLExhaustiveLandscape



#### 6.3.1 Methods

\_\_\_init\_\_\_(self, dbobj, aliname)
Initialize the landscape.

:param ali: An :class:'alignment.alignment' object. :param starting\_tree: An optional tree object to start the landscape with. :param root: Whether or not to acquire an approximate maximum likelihood tree (FastTree) or start the landscape with a given starting tree. :param operator: A string that describes what operator the landscape is mostly comprised of.

Overrides: object. init extit(inherited documentation)

#### exploreRandomTree(self, i)

Acquire a single neighbor to a tree in the landscape by performing a random rearrangement of type SPR (by default), NNI, or TBR. Rearrangement type is provided as a rearrangement module type definition of form, for example, TYPE SPR, TYPE NNI, etc.

 $Overrides:\ pylogeny.landscape.landscape.exploreRandomTree\ extit(inherited\ documentation)$ 

# getDatabaseNode(self, i) exploreTree(self, i)Get all neighbors to a tree named i in the landscape using a respective rearrangement operator as defined in the rearrangement module. Rearrangement type is provided as a rearrangement module type definition of form, for example, TYPE SPR, TYPE NNI, etc. By default, this is TYPE SPR. Overrides: pylogeny.landscape.landscape.exploreTree extit(inherited documentation) Inherited from pylogeny.database.DatabaseLandscape(Section 6.2) getNode() $Inherited\ from\ pylogeny.landscape.landscape(Section\ 9.3)$ getitem\_\_\_(), \_\_\_iter\_\_\_(), \_\_\_str\_\_\_(), addTree(), findTree(), findTreeTopology(), findTreeTopologyByStructure(), getAlignment(), getAllPathsOfBestImprovement(), getBestImprovement(), getBipartitionFoundInTreeByIndex(), getGlobalOptimum(), getLocalOptima(), getLocks(), getNumberTaxa(), getPathOfBestImprovement(), getPossibleNumberRootedTrees(), getPossibleNumberUnrootedTrees(), get-RootTree(), getTree(), getVertex(), indexOf(), isLocalOptimum(), isViolating(), iterAllPathsOfBestImprovement(), iterTrees(), lockBranchFoundInTree(), lockBranch-FoundInTreeByIndex(), removeTree(), setAlignment(), toProperNewickTreeSet(), toTreeSet(), toggleLock() Inherited from pylogeny.landscape.graph(Section 9.2) len\_\_\_(), clearEdgeWeights(), getCenter(), getCliqueNumber(), getCliques(), getCliquesOfNode(), getComponentOfNode(), getComponents(), getDegreeFor(), getDiameter(), getEdge(), getEdges(), getEdgesFor(), getMST(), getNeighbors-For(), getNetworkXObject(), getNodeNames(), getNodes(), getNumCliques(), get-NumComponents(), getShortestPath(), getShortestPathLength(), getSize(), has-Path(), iterNodes(), setDefaultWeight() Inherited from pylogeny.tree.treeSet(Section 17.4) addTreeByNewick(), toTreeFile() Inherited from abcoll.Sized \_subclasshook\_ () Inherited from object

\_\_\_delattr\_\_(), \_\_format\_\_(), \_\_getattribute\_\_(), \_\_hash\_\_(), \_\_new\_\_(),

```
\underline{\hspace{1cm}} \operatorname{reduce} \underline{\hspace{1cm}} (), \, \underline{\hspace{1cm}} \operatorname{reduce} \underline{\hspace{1cm}} \operatorname{ex} \underline{\hspace{1cm}} (), \, \underline{\hspace{1cm}} \operatorname{repr} \underline{\hspace{1cm}} (), \, \underline{\hspace{1cm}} \operatorname{sizeof} \underline{\hspace{1cm}} ()
```

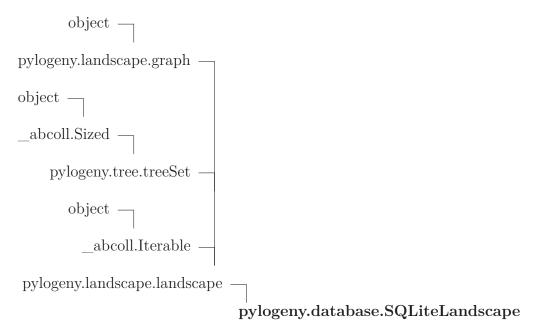
#### 6.3.2 Properties

Name	Description
Inherited from object	
class	

#### 6.3.3 Class Variables

Name	Description
abstractmethods	Value: frozenset([])

### 6.4 Class SQLiteLandscape



Allow random access of all landscape data from an sqlite file found on the hard disk.

## 6.4.1 Methods

init(self, dbobj)
Initialize the landscape.
:param ali: An :class:'alignment.alignment' object. :param starting_tree: An optional tree object to start the landscape with. :param root: Whether or not to acquire an approximate maximum likelihood tree (FastTree) or start the landscape with a given starting tree. :param operator: A string that describes what operator the landscape is mostly comprised of.
Overrides: objectinit extit(inherited documentation)
$Inherited\ from\ pylogeny. landscape. landscape (Section\ 9.3)$
getitem(),iter(),str(), addTree(), exploreRandomTree(), exploreTree(), findTree(), findTreeTopology(), findTreeTopologyByStructure(), getAleignment(), getAllPathsOfBestImprovement(), getBestImprovement(), getBipartitionFoundInTreeByIndex(), getGlobalOptimum(), getLocalOptima(), getLocks(), getNumberTaxa(), getPathOfBestImprovement(), getPossibleNumberRootedTrees(getPossibleNumberUnrootedTrees(), getRootTree(), getTree(), getVertex(), indexOisLocalOptimum(), isViolating(), iterAllPathsOfBestImprovement(), iterTrees(), lockBranchFoundInTree(), lockBranchFoundInTreeByIndex(), removeTree(), setAleignment(), toProperNewickTreeSet(), toTreeSet(), toggleLock()
$Inherited\ from\ pylogeny. landscape. graph (Section\ 9.2)$
(), clearEdgeWeights(), getCenter(), getCliqueNumber(), getCliques(), getCliquesOfNode(), getComponentOfNode(), getComponents(), getDegreeFor(), getDiameter(), getEdge(), getEdges(), getEdgesFor(), getMST(), getNeighborsFor(), getNetworkXObject(), getNode(), getNodeNames(), getNodes(), getNumCliques(), getNumComponents(), getShortestPath(), getShortestPathLength(), getSize(), hasPath(), iterNodes(), setDefaultWeight()
$Inherited\ from\ pylogeny.tree.treeSet(Section\ 17.4)$
addTreeByNewick(), toTreeFile()
$Inherited\ from\ \_abcoll.Sized$
$\_\_subclasshook\_\_()$
Inherited from object
delattr(),format(),getattribute(),hash(),new(), reduceex() repr() setattr() sizeof()

#### 6.4.2 Properties

Name	Description
Inherited from object	
class	

#### 6.4.3 Class Variables

Name	Description
Inherited from pylogeny.tree.	treeSet (Section 17.4)
abstractmethods	

#### 6.5 Class database

object — pylogeny.database.database

**Known Subclasses:** pylogeny.database.SQLDatabase, pylogeny.database.SQLiteDatabase Allow interfacing with a SQL/sqlite database.

#### 6.5.1 Methods

isEmpty(self)
Determine if the database is empty.

getTables(self)
Get the list of tables from the database

getColumns(self, table)
Return column information for a given table.

getHeaders(self, table)

Get only header names for a given table's columns.

getRecordsColumn(self, table, col)

Get all data for a single colmun from records for a table.

getRecords(self, table)

Get all records from a given table in the database.

iterRecords(self, table)

Get a record, one at a time, from a table in the database.

filterRecords(self, table, condn)

Get all records from a given table following a condition.

getRecordsAsDict(self, table)

Acquires records using getRecords() and then leverages access using a dictionary data structure.

newTable(self, tablename, \*args)

insertRecords(self, tablename, items)

insertRecord(self, tablename, record)

query(self, q)

querymany(self, q, i)

 $\mathbf{close}(self)$ 

Inherited from object

delattr(),	$\_\_format\_\_$	$_{-}(),$ $_{}$ $_{\mathrm{getattr}}$	$ribute\_\_(),$	hash	$_{-}(),$ init	_(),
new(),	_reduce()	,reduce_e	ex(),	_repr(), .	setattr	_(),
sizeof(), _	str(), _	subclasshoo	ok()			

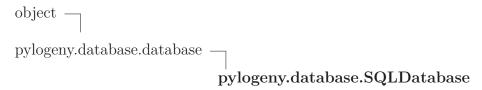
#### 6.5.2 Properties

Name	Description
Inherited from object	
class	

#### 6.5.3 Class Variables

Name	Description
cursor	Value: None
abstractmethods	Value: frozenset(['close', 'query',
	'querymany'])

#### 6.6 Class SQLDatabase



Database object to allow reading from a MySQL database.

#### 6.6.1 Methods

init(self, host, user, pw, db)	
xinit() initializes x; see help(type(x)) for signature	
Overrides: objectinit extit(inherited documentation)	

1 ( 10)	
connect(self)	
( , , )	

```
\begin{array}{l} \textbf{querymany}(\textit{self}, \textit{q}, \textit{i}) \\ \textbf{Overrides: pylogeny.database.database.querymany} \end{array}
```

```
      close(self)

      Overrides: pylogeny.database.database.close
```

#### Inherited from pylogeny.database.database(Section 6.5)

filterRecords(), getColumns(), getHeaders(), getRecords(), getRecordsAsDict(), getRecordsColumn(), getTables(), insertRecord(), insertRecords(), isEmpty(), iter-Records(), newTable()

### Inherited from object

$\_$ _delattr $\_$	_(), _	$\_$ format $\_$	(), _	ge	tattribı	ıte	(),	hash	$\underline{\hspace{1cm}}(),$	new_	()
reduce	_(),	_reduce_	ex(	),	_repr_	_(), _	seta	ttr	_(),	_sizeof	_(),
str(),	su	bclasshool	k()								

#### 6.6.2 Properties

Name	Description
Inherited from object	
class	

#### 6.6.3 Class Variables

Name	Description
abstractmethods	Value: frozenset([])
Inherited from pylogeny.data	base.database (Section 6.5)
cursor	

## 6.7 Class SQLiteDatabase

object —

pylogeny.database.database —

pylogeny.database.SQLiteDatabase

#### 6.7.1 Methods

init(self, filepath)	
xinit() initializes $x$ ; see $help(type(x))$ for signature	
Overrides: objectinit extit(inherited documentation)	

getColumns(self, table)
Return column information for a given table.
Overrides: pylogeny.database.database.getColumns

$\mathbf{querymany}(self, q, i)$
Overrides: pylogeny.database.database.querymany
$\mathbf{close}(\mathit{self})$
Overrides: pylogeny.database.database.close

## $Inherited\ from\ pylogeny.database.database(Section\ 6.5)$

filterRecords(), getHeaders(), getRecords(), getRecordsAsDict(), getRecordsColumn(), getTables(), insertRecord(), insertRecords(), isEmpty(), iterRecords(), newTable()

## $Inherited\ from\ object$

delattr(),fo	$\operatorname{prmat}_{}(), \operatorname{g}\epsilon$	$etattribute\_\_()$	,hash(), _	new()
reduce(),re	$educe_ex_(),$	$\_\operatorname{repr}\_\_(), \_\_$	_setattr(),	$\_sizeof\_\_\_(),$
str(),subcl	asshook()			

## 6.7.2 Properties

Name	Description
Inherited from object	
class	

#### 6.7.3 Class Variables

Name	Description					
abstractmethods	Value: frozenset([])					
Inherited from pylogeny database database (Section 6.5)						
cursor						

#### Module pylogeny.executable 7

Defines an interface to manage interfacing with the system for respective application calls and implements multiple of these for executables such as FastTree and RAxML. Requires a UNIX environment.

#### 7.1 **Functions**

exeExists(cmd)
Determines whether a function exists in a UNIX environment.

#### 7.2Variables

Name	Description
E_FASTTREE	Value: 'fasttree'
E_RAXML	Value: 'raxmlHPC'
E_TREEPUZZ	Value: 'puzzle'
package	Value: 'pylogeny'

#### 7.3 Class a Temporary Directory

A class intended to be used as a context manager that allows Python to run in a temporary directory for a finite period of time.

#### 7.3.1 Methods

exit

Inherited	from	object
-----------	------	--------

$\_\_delattr\_\_$	(), format(	),g	getattrib	ute	(),hash	(), _	new_	()
reduce	_(),reduceex_	(), _	repr_	(), _	setattr	_(),	_sizeof	(),
str (),	subclasshook	()						

#### 7.3.2 Properties

Name	Description
Inherited from object	
class	

#### 7.4 Class executable

object — pylogeny.executable.executable

Known Subclasses: pylogeny.executable.consel, pylogeny.executable.fasttree, pylogeny.executable.raxml, pylogeny.executable.treepuzzle

An interface for the instantation and running of a single instance for a given application.

#### 7.4.1 Methods

## Inherited from object

$\_$ delattr $\_$	(), _	forn	nat	_(), _	getat	tribu	te()	),ha	ish	_(),	$\_$ init $\_$	()
_new(	(),	_reduce	e(	),	_reduce_	_ex	(),	_repr_	(),	se	etattr_	(),
_sizeof	_(), _	str	_(), _	su	bclassh	ook_	_()					

#### 7.4.2 Properties

Name	Description
Inherited from object	
class	

#### 7.4.3 Class Variables

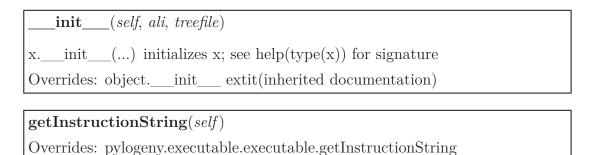
Name	Description
exeName	Value: None
abstractmethods	Value:
	<pre>frozenset(['getInstructionString'])</pre>

# 7.5 Class treepuzzle

object —	
pylogeny.executable.executable	
	pylogeny.executable.treepuzzle

Wrap TREE-PUZZLE in order to create an intermediate file for CONSEL to read and assign confidence to a set of trees. Requires TREE-PUZZLE to be installed.

### 7.5.1 Methods



${\bf getSiteLikelihoodFile}(\mathit{self})$	

 $Inherited\ from\ pylogeny. executable. executable (Section\ 7.4)$ 

run()

Inherited from object

```
___delattr__(), __format__(), __getattribute__(), __hash__(), __new__(), __reduce__(), __reduce__ex__(), __repr__(), __setattr__(), __sizeof__(), __str__(), __subclasshook__()
```

### 7.5.2 Properties

Name	Description
Inherited from object	
class	

#### 7.5.3 Class Variables

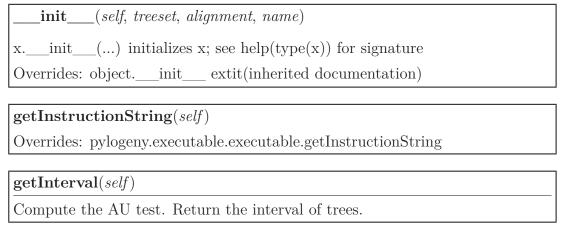
Name	Description
exeName	Value: 'puzzle'
abstractmethods	Value: frozenset([])

### 7.6 Class consel

object —	
pylogeny.executable.executable	
	pylogeny.executable.consel

Denotes a single run of the CONSEL workflow in order to acquire a confidence interval and perform an AU test on a set of trees. Requires CONSEL to be installed.

### 7.6.1 Methods



 $Inherited\ from\ pylogeny. executable. executable (Section\ 7.4)$ 

run()

### Inherited from object

 $\underline{\hspace{1cm}} delattr\underline{\hspace{1cm}}(), \underline{\hspace{1cm}} format\underline{\hspace{1cm}}(), \underline{\hspace{1cm}} getattribute\underline{\hspace{1cm}}(), \underline{\hspace{1cm}} hash\underline{\hspace{1cm}}(), \underline{\hspace{1cm}} new\underline{\hspace{1cm}}(),$ 

reduce(),reduce_ex_	(), _	repr_	_(), _	$\_$ setattr $\_$	(),	_sizeof_	(),
str(),subclasshook	_()						

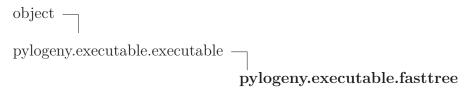
### 7.6.2 Properties

Name	Description
Inherited from object	
class	

#### 7.6.3 Class Variables

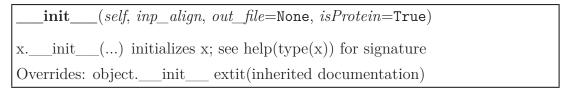
Name Description		
abstractmethods	Value: frozenset([])	
Inherited from pylogeny.executable.executable (Section 7.4)		
exeName		

### 7.7 Class fasttree



Denotes a single run of the FastTree executable in order to acquire an approximate maximum likelihood tree for the input alignment. See http://www.microbesonline.org/fasttree/ for more information on FastTree. Requires FastTree to be installed.

#### 7.7.1 Methods



Inherited from pylogeny.executable.executable(Section 7.4)

run()

Inherited	from	object
-----------	------	--------

$\_$ _delattr $\_$ _	(), format(	),g	getattrib	ute	$(), \underline{\hspace{1cm}}$ hash	n(), .	new_	()
reduce	_(),reduceex_	(), _	repr_	(), _	setattr_	_(),	_sizeof	(),
str (),	subclasshook	()						

#### 7.7.2 Properties

Name	Description
Inherited from object	
class	

### 7.7.3 Class Variables

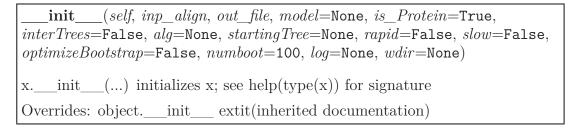
Name	Description
exeName	Value: 'fasttree'
abstractmethods	Value: frozenset([])

#### 7.8 Class raxml

object — pylogeny.executable.executable — pylogeny.executable.raxml

Denotes a single run of the RAxML executable. See http://sco.h-its.org/exelixis/software.html for more information on RAxML. Requires RAxML to be installed.

#### 7.8.1 Methods



 ${\bf getInstructionString}(\mathit{self})$ 

Overrides: pylogeny.executable.executable.getInstructionString

runFunction(self, alg)	
( 0)	

# Inherited from pylogeny.executable.executable(Section 7.4)

run()

# Inherited from object

```
___delattr__(), __format__(), __getattribute__(), __hash__(), __new__(), __reduce__(), __reduce__ex__(), __repr__(), __setattr__(), __sizeof__(), __str__(), __subclasshook__()
```

### 7.8.2 Properties

Name	Description
Inherited from object	
class	

#### 7.8.3 Class Variables

Name	Description
exeName	Value: 'raxmlHPC'
abstractmethods	Value: frozenset([])

# 8 Module pylogeny.heuristic

Define the interface for a heuristic in order to implement any manner of heuristic for a combinatorial problem that can be abstracted into a state graph. In this case, a phylogenetic tree space.

#### 8.1 Variables

Name	Description	
SMGR_MIN_NUM_LIK-	Value: 32	
ELIHOOD		
package	Value: 'pylogeny'	

### 8.2 Class heuristic

object — pylogeny.heuristic.heuristic

Known Subclasses: pylogeny.heuristic.phylogeneticLinearHeuristic

A base interface for a heuristic that explores a state graph.

#### 8.2.1 Methods

### Inherited from object

### 8.2.2 Properties

Name	Description
Inherited from object	
class	

### 8.3 Class phylogeneticLinearHeuristic

object —	
pylogeny.heuristic.heuristic	
	pylogeny.heuristic.phylogeneticLinearHeuristic

**Known Subclasses:** pylogeny.heuristic.RAxMLIdentify, pylogeny.heuristic.likelihoodGreedy, pylogeny.heuristic.parsimonyGreedy, pylogeny.heuristic.smoothGreedy

A base class for a heuristic that works on a phylogenetic landscape and only possesses a single path (of search).

#### 8.3.1 Methods

init(self, ls, startTree)		
xinit() initializes $x$ ; see $help(type(x))$ for signature		
Overrides: objectinit extit(inherited documentation)		
$\mathbf{getPath}(self)$		
getBestTree(self)		

# Inherited from pylogeny.heuristic.heuristic(Section 8.2)

```
explore(), \ getStartState(), \ getStateGraph()
```

# Inherited from object

#### 8.3.2 Properties

Name	Description
Inherited from object	
class	

#### 8.3.3 Class Variables

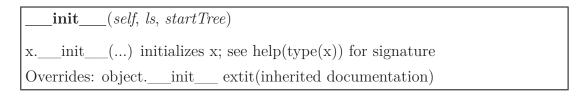
Name	Description
bestTree	Value: None
path	Value: []

# 8.4 Class parsimonyGreedy

object —	
pylogeny.heuristic.heuristic —	
${\it pylogeny.} heuristic. phylogenetic Linear Heuristic$	
	pylogeny.heuristic.parsimonyGreedy

Greedy (hill-climbing) landscape exploration by comparsion of parsimony.

#### 8.4.1 Methods



## explore(self)

Perform greedy search of the landscape using a method of greed via parsimonious criterion.

Overrides: pylogeny.heuristic.heuristic.explore

 $Inherited\ from\ pylogeny.heuristic.phylogeneticLinearHeuristic(Section\ 8.3)$ 

```
getBestTree(), getPath()
```

Inherited from pylogeny.heuristic.heuristic(Section 8.2)

getStartState(), getStateGraph()

Inherited	from	object

$_{}$ delattr $_{}$ (),	$\underline{}$ format $\underline{}$ (	),ge	etattrib	ute	$(), \underline{\hspace{1cm}}$ hash	ı(),	new_	(),
reduce(), _	reduceex_	(), _	repr_	(), _	$\_$ setattr $\_$	_(),	_sizeof	_(),
str(),s	subclasshook	_()						

### 8.4.2 Properties

Name	Description
Inherited from object	
class	

### 8.4.3 Class Variables

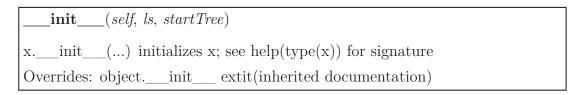
Name	Description
Inherited from pylogeny.heuristic.phylogeneticLinearHeuristic (Section 8.3)	
bestTree, path	

# 8.5 Class likelihoodGreedy

object —	
pylogeny.heuristic.heuristic —	
py logeny. heuristic. phy logenetic Linear Heuristic	pylogeny.heuristic.likelihoodGreedy

Greedy (hill-climbing) landscape exploration by comparsion of likelihood.

### 8.5.1 Methods



# explore(self)

Perform greedy search of the landscape using a method of greed via likelihood. Overrides: pylogeny.heuristic.heuristic.explore

$Inherited\ from\ pylogeny. heuristic. phylogenetic Linear Heuristic (Section\ 8.3)$
getBestTree(), getPath()
$Inherited\ from\ pylogeny. heuristic. heuristic (Section\ 8.2)$
getStartState(), getStateGraph()
Inherited from object
delattr(),format(),getattribute(),hash(),new()reduce(),reduceex(),repr(),setattr(),sizeof(),str(),subclasshook()
8.5.2 Properties
Name Description  Inherited from objectclass
8.5.3 Class Variables
Name Description  Inherited from pylogeny.heuristic.phylogeneticLinearHeuristic (Section 8.3) bestTree, path
8.6 Class smoothGreedy
object —
pylogeny.heuristic.heuristic —
pylogeny.heuristic.phylogeneticLinearHeuristic —
Parsimony-driven greedy landscape exploration by comparsion of likelihoods.

#### 8.6.1 Methods

init(self, ls, startTree)
xinit() initializes $x$ ; see $help(type(x))$ for signature
Overrides: objectinit extit(inherited documentation)

# explore(self)

Perform greedy search of the landscape using a method of greed via parsimonious criterion and then performing final smoothing via likelihood on top 10% of 1-SPR neighbors ranked on basis of parsimony.

Overrides: pylogeny.heuristic.heuristic.explore

# $Inherited\ from\ pylogeny. heuristic. phylogenetic Linear Heuristic (Section\ 8.3)$

getBestTree(), getPath()

# $Inherited\ from\ pylogeny. heuristic. heuristic (Section\ 8.2)$

getStartState(), getStateGraph()

# Inherited from object

$\_\{delattr}$	_(), _	$\_$ format $\_$	(),	_getattri	bute	(), hash	n(), _	new_	()
reduce	_(), _	_reduce_	ex()	,repr	(), _	$\_\_$ setattr $\_$	(),	_sizeof	_(),
str(),	su	bclasshoo	k()						

### 8.6.2 Properties

Name	Description
Inherited from object	
class	

### 8.6.3 Class Variables

Name	Description
Inherited from pylogeny.heur	istic.phylogeneticLinearHeuristic (Section 8.3)
bestTree, path	

# 8.7 Class RAxMLIdentify

object —
pylogeny.heuristic.heuristic —
pylogeny.heuristic.phylogeneticLinearHeuristic —
pylogeny.heuristic.RAxMLIdentify
$RAxML-driven\ landscape\ evaluation\ of\ intermediate\ checkpoint\ trees\ output\ from\ the\ RAxML\ executable.$
8.7.1 Methods
init(self, ls, startNode, workdir='.rxml')
xinit() initializes x; see help(type(x)) for signature
Overrides: objectinit extit(inherited documentation)
$\boxed{\_\_setupWorkDir}\_\_(\mathit{self})$
$\boxed{ \underline{} \mathbf{setupExecutable}\underline{} (\mathit{self})}$
$\boxed{ \_\_readLogFile}\_\_(\mathit{self})$
readIterTrees(self, iters)
$\mathbf{explore}(\mathit{self})$
Overrides: pylogeny.heuristic.heuristic.explore
$Inherited\ from\ pylogeny. heuristic. phylogenetic Linear Heuristic (Section\ 8.3)$
getBestTree(), getPath()
$Inherited\ from\ pylogeny. heuristic. heuristic (Section\ 8.2)$
$getStartState(), \ getStateGraph()$
Inherited from object
delattr(),format(),getattribute(),hash(),new(),reduce(),repr(),setattr(),sizeof(),str(),subclasshook()

# 8.7.2 Properties

Name	Description
Inherited from object	
class	

# 8.7.3 Class Variables

Name	Description
Inherited from pylogeny.heur	ristic.phylogeneticLinearHeuristic (Section 8.3)
bestTree, path	

# 9 Module pylogeny.landscape

Encapsulate a phylogenetic tree space. A phylogenetic landscape or tree space refers to the entire combinatorial space comprising all possible phylogenetic tree topologies for a set of n taxa. The landscape of n taxa can be defined as consisting of a finite set T of tree topologies. Tree topologies can be associated with a fitness function  $f(t_i)$  describing their fit. This forms a discrete solution search space and finite graph (T, E) = G. E(G) refers to the neighborhood relation on E(G). Edges in this graph are bidirectional and represent transformation from one tree topology to another by a tree rearrangement operator. An edge between E(G) would be notated as E(G).

### 9.1 Variables

Name	Description
LS_NOT_DEFINED	Value: -1
package	Value: 'pylogeny'

### 9.2 Class graph

object — pylogeny.landscape.graph

Known Subclasses: pylogeny.landscape.landscape

Define an empty graph object.

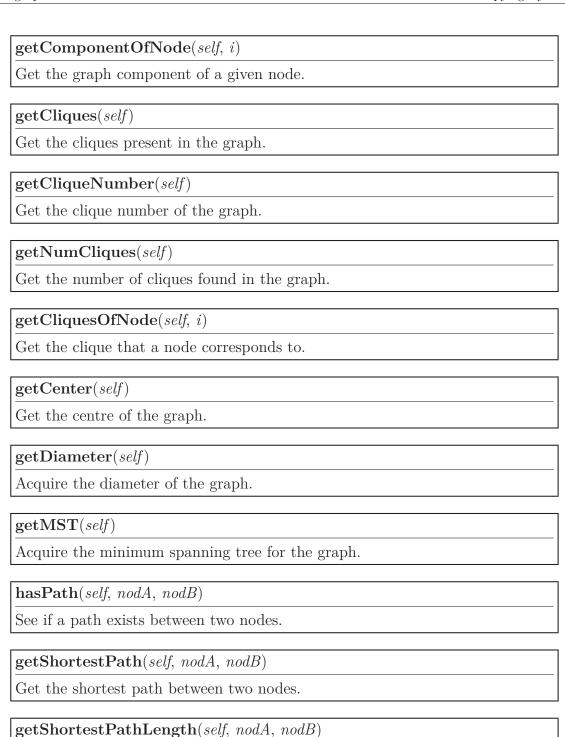
#### 9.2.1 Methods

\_\_\_\_init\_\_\_\_(self, gr=None)
Instantiate a graph.
:param gr: A networkx graph object, if already exists.
Overrides: object.\_\_\_init\_\_\_

Return the internal networkx graph object.

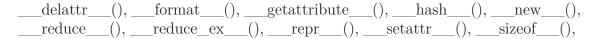
\_\_\_len\_\_\_(self)

 $_{
m iter}_{
m }$ (self)getSize(self)Return the number of nodes in the graph. getNodeNames(self)Return the names of nodes in the graph. iterNodes(self) Iterate over all node keys. getNodes(self)getEdges(self)getEdgesFor(self, i)getNode(self, i)getEdge(self, i, j)getNeighborsFor(self, i)getDegreeFor(self, i)Return in- and out-degree for node named i. setDefaultWeight(self, w)clearEdgeWeights(self) getNumComponents(self) Get the number of components of the graph. getComponents(self) Get the connected components in the graph.



# $Inherited\ from\ object$

Get the shortest path length between two nodes.

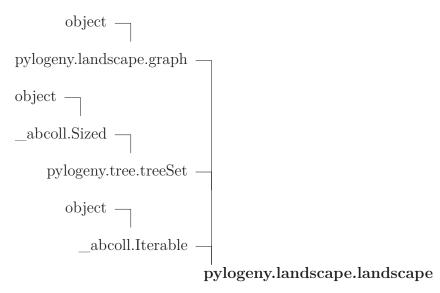


```
___str___(), ___subclasshook___()
```

### 9.2.2 Properties

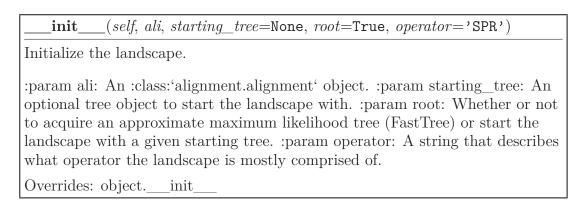
Name	Description
Inherited from object	
class	

# 9.3 Class landscape



**Known Subclasses:** pylogeny.database.DatabaseLandscape, pylogeny.database.SQLiteLandscape Defines an entire phylogenetic tree space.

### 9.3.1 Methods



# getAlignment(self)

Acquire the alignment object associated with this space.

# $\mathbf{getNumberTaxa}(self)$

Return the number of different taxa present in any respective tree in the landscape.

### getPossibleNumberRootedTrees(self)

Assuming all of the trees in the space are rooted, return the maximum possible number of unrooted trees that can possibly be generated for the number of taxa of trees in the landscape.

### getPossibleNumberUnrootedTrees(self)

Assuming all of the trees in the space are unrooted, return the maximum possible number of unrooted trees that can possibly be generated for the number of taxa of trees in the landscape.

### getRootTree(self)

Acquire the first tree that was placed in this space.

# setAlignment(self, ali)

Set the alignment present in this landscape. WARNING; will not modify existing scores.

### getTree(self, i)

Get the tree object for a tree by its ID or name i.

### iterTrees(self)

Iterate over all trees found in this landscape.

\_\_\_iter\_\_\_(self)

Overrides: abcoll.Iterable. iter

### getVertex(self, i)

Acquire a vertex object from the landscape; this is a high-level representation of a tree in the landscape with additional functionality. Object created upon invocation of this function.

### removeTree(self, tree)

Remove a tree from the landscape by object.

Overrides: pylogeny.tree.treeSet.removeTree

### addTree(self, tree)

Add a tree to the landscape. Will return its index.

Overrides: pylogeny.tree.treeSet.addTree

### exploreRandomTree(self, i, type=1)

Acquire a single neighbor to a tree in the landscape by performing a random rearrangement of type SPR (by default), NNI, or TBR. Rearrangement type is provided as a rearrangement module type definition of form, for example, TYPE\_SPR, TYPE\_NNI, etc.

## exploreTree(self, i, type=1)

Get all neighbors to a tree named i in the landscape using a respective rearrangement operator as defined in the rearrangement module. Rearrangement type is provided as a rearrangement module type definition of form, for example, TYPE\_SPR, TYPE\_NNI, etc. By default, this is TYPE\_SPR.

### getLocks(self)

### $\mathbf{toggleLock}(self, lock)$

Add a biparition to the list of locked bipartitions if not present; otherwise, remove it. Return status of lock.

### lockBranchFoundInTree(self, tr, br)

Given a tree node and a branch object, add a given bipartition to the bipartition lock list. Returns true if locked.

### getBipartitionFoundInTreeByIndex(self, tr, brind, topol=None)

Given a tree node and a branch index, return the associated bipartition.

### lockBranchFoundInTreeByIndex(self, tr, brind)

Given a tree node and a branch index, add a given bipartition to the bipartition lock list. Returns true if locked.

### isViolating(self, i)

Determine if a tree is violating any locks intrinsic to the landscape.

 $\underline{\underline{\phantom{a}}}$ getitem $\underline{\underline{\phantom{a}}}$ (self, i)

Overrides: pylogeny.tree.treeSet. getitem

### indexOf(self, tr)

Acquire the index/name in this landscape of a tree object. Returns -1 if not found.

Overrides: pylogeny.tree.treeSet.indexOf

### findTree(self, newick)

Find a tree by Newick string, taking into account branch lengths. Returns the name of this tree in the landscape.

## findTreeTopology(self, newick)

Find a tree by topology, not taking into account branch lengths.

# findTreeTopologyByStructure(self, struct)

Find a tree by topology, not taking into account branch lengths, given the topology.

### getBestImprovement(self, i)

For a tree in the landscape, investigate neighbors to find a tree that leads to the best improvement of fitness function score on the basis of likelihood.

### getPathOfBestImprovement(self, i)

For a tree in the landscape, investigate neighbors iteratively until a best path of score improvement is found on basis of likelihood.

### getAllPathsOfBestImprovement(self)

Return all paths of best improvement as a dictionary.

### iterAllPathsOfBestImprovement(self)

Return an iterator for all paths of best improvement.

# isLocalOptimum(self, i)

Determine if a tree is, without any doubt, a local optimum.

# getLocalOptima(self)

Get all trees in the landscape that can be labelled as a local optimum.

# getGlobalOptimum(self)

Get the global optimum of the current space.

```
__str___(self)
str(x)
Overrides: object.__str__ extit(inherited documentation)
```

# toProperNewickTreeSet(self)

Convert this landscape into an unorganized set of trees where taxa names are transformed to their original form ( i.e. not transformed to a state friendly for the Phylip format).

# toTreeSet(self)

Convert this landscape into an unorganized set of trees.

# $Inherited\ from\ pylogeny. landscape. graph (Section\ 9.2)$

\_\_len\_\_(), clearEdgeWeights(), getCenter(), getCliqueNumber(), getCliques(), getCliquesOfNode(), getComponentOfNode(), getComponents(), getDegreeFor(), getDiameter(), getEdge(), getEdges(), getEdgesFor(), getMST(), getNeighbors-For(), getNetworkXObject(), getNode(), getNodeNames(), getNodes(), getNum-Cliques(), getNumComponents(), getShortestPath(), getShortestPathLength(), getSize(), hasPath(), iterNodes(), setDefaultWeight()

# Inherited from pylogeny.tree.treeSet(Section 17.4)

addTreeByNewick(), toTreeFile()

### $Inherited\ from\ \_abcoll.Sized$

 $_{\text{subclasshook}}$  ()

### Inherited from object

$\underline{\hspace{1cm}}$ delattr $\underline{\hspace{1cm}}$	_(), _	$\_$ format $\_$	(),	ge	etattribu	ite	$(), \underline{\hspace{1cm}} hash$	(), _	new	()
reduce	Ö,	reduce	ex	(),	repr	(),	setattr	(),	sizeof	()

### 9.3.2 Properties

Name	Description
Inherited from object	
class	

### 9.3.3 Class Variables

Name	Description
Inherited from pylogeny.tree.	treeSet (Section 17.4)
abstractmethods	

## 9.4 Class vertex

Encapsulate a single vertex in the landscape and add convenient functionality to alias parent landscape functions.

### 9.4.1 Methods

$\_\_$ init $\_\_$ (self, i, obj, ls)
xinit() initializes x; see help(type(x)) for signature
Overrides: objectinit extit(inherited documentation)
$\mathbf{getIndex}(\mathit{self})$
$\mathbf{getDict}(self)$
$\mathbf{getObject}(self)$
$\mathbf{getTree}(self)$
$\mathbf{getNewick}(\mathit{self})$
$\mathbf{getScore}(self)$

getOrigin(self)

getNeighbors(self)

getDegree(self)

isLocalOptimum(self)

isExplored(self)

isFailed(self)

setExplored(self, exp)

Sets the "explored" flag of this node in the landscape.

# approximatePossibleNumNeighbors(self)

Approximate the possible number of neighbors to this vertex by considering the type of tree rearrangement operator.

# scoreLikelihood(self)

Acquire the log-likelihood for this vertex.

### getBestImprovement(self)

Alias function for function of same name in parent landscape.

### getPathOfBestImprovement(self)

Alias function for function of same name in parent landscape.

### isBestImprovement(self)

Check to see if this vertex is a best move for another node.

### isViolating(self)

Alias function for function of same name in parent landscape.

### getProperNewick(self)

Get the proper Newick string for a tree. :returns: A string.

${f getBipartitions}(self)$	
Get all bipartitions for this vertex.	

# ${\bf getBipartitionScores}(self)$

Get all corresponding bipartition vectors of SPR scores.

# ${\bf getNeighborsOfBipartition}(\mathit{self},\ \mathit{bi})$

Get corresponding neighbors of a bipartition in this vertex's tree.

# getNeighborsOfBranch(self, br)

Get corresponding neighbors of a branch in this vertex's tree.

# Inherited from object

delattr(),	$\_$ format $\_$ ()	),ge	etattribi	ute(	(),hash	(), _	new_	()
reduce(),	_reduce_ex_	(), _	repr	(),	_setattr	_(),	_sizeof	_(),
str(),su	bclasshook	_()						

### 9.4.2 Properties

Name	Description
Inherited from object	
class	

# 10 Module pylogeny.landscapeWriter

Serialize a phylogenetic landscape into an SQLlite database file made up of three components: all tree IDs and respective scores, the alignment file as a set of sequences, and a representation of the graph as an edge list.

#### 10.1 Variables

Name	Description
package	Value: 'pylogeny'

## 10.2 Class landscapeWriter

 $\begin{array}{c} \text{object} \ \ \, \\ \text{pylogeny.landscapeWriter.landscapeWriter} \end{array}$ 

Known Subclasses: pylogeny.JSONWriter.JSONWriter

Encapsulate the writing of a landscape to a file format.

#### 10.2.1 Methods

init(self, landscape, name)
xinit() initializes $x$ ; see $help(type(x))$ for signature
Overrides: objectinit extit(inherited documentation)

writeFile(self, path='.')
Write the landscape serialized file to given path.

## Inherited from object

delattr(), _	format(),	,ge	tattribu	ıte(	(),hash	(), _	new_	()
reduce(),	_reduce_ex_	_(),	_repr	_(), _	_setattr	_(),	_sizeof	_(),
str(),su	ıbclasshook	_()						

### 10.2.2 Properties

Name	Description
Inherited from object	
class	

# 10.3 Class landscapeParser

object — pylogeny.landscapeWriter.landscapeParser

Encapsulates the construction of a landscape object from a pickle file.

### 10.3.1 Methods

init(	self, path)
xinit(	() initializes x; see help(type(x)) for signature
Overrides: ob	bjectinit extit(inherited documentation)

 $\frac{\mathbf{getName}(\mathit{self})}{\mathbf{Acquire the name of the parsed landscape}}.$ 

parse(self)	
Parse the file.	

# $Inherited\ from\ object$

delattr(	$(), \underline{\hspace{1cm}} format \underline{\hspace{1cm}} ()$	,getattrik	$\mathrm{oute}\_\_(), \_$	$_{\text{hash}}(),$	new()
reduce(	),reduce_ex_	$\underline{\hspace{1cm}}(), \underline{\hspace{1cm}} repr_{\underline{\hspace{1cm}}}$	(),set	attr(),	$_{\text{sizeof}}$ (),
str(),	$\_$ subclasshook $\_$	_()			

### 10.3.2 Properties

Name	Description
Inherited from object	
class	

# 11 Module pylogeny.model

Phylogenetic tree scoring models; intended to be coupled with the use of pytbeaglehon (BEAGLE) high-performance library.

### 11.1 Variables

Name	Description
pytbeaglehonEnabled	Value: True
package	Value: 'pylogeny'

## 11.2 Class PhyloModelError

object —	
exceptions.BaseException —	
exceptions.Exception	
	pylogeny.model. PhyloModel Error

### 11.2.1 Methods

init	(self, v)
xinit	() initializes x; see help(type(x)) for signature
Overrides:	objectinit extit(inherited documentation)
$\lfloor$ str	(self)
str(x)	
Overrides:	object. str extit(inherited documentation)

Inherited from exceptions. Exception

 $Inherited\ from\ exceptions. Base Exception$ 

```
\underline{\hspace{0.5cm}} \begin{array}{lll} \underline{\hspace{0.5cm}} & \underline{\hspace{0.5cm
```

# $Inherited\ from\ object$

$\_\_format\_\_$	$(), \_$	_hash_	_(), _	$\_$ reduce $\_$ ex $\_$	(), _	$\_$ sizeof $\_$	_(), _	subclasshook	()

### 11.2.2 Properties

Name	Description	
Inherited from exceptions.Ba	aseException	
args, message		
Inherited from object		
class		

## 11.3 Class DiscreteStateModel

object — pylogeny.model.DiscreteStateModel

Initialize a discrete state model for phylogenetic data. State frequencies and character time are determined from the given alignment object.

### 11.3.1 Methods

init(self, alignment)
xinit() initializes $x$ ; see $help(type(x))$ for signature
Overrides: objectinit extit(inherited documentation)
$\mathbf{getAlignment}(self)$
${\bf getAlignmentAsStateList}(self)$
${f getSequenceMatrix}(self)$
$\mathbf{getCharType}(\mathit{self})$
$\mathbf{getStateFreqs}(self)$
getRawStateFreqs(self)

	${\bf getRawStateFreqsAsList}(self)$
	${\bf getRawStateFreqsAsDict}(self)$
	$\boxed{ \mathbf{getFrequencyOfState}(\mathit{self},  i) }$
	${\bf getRawFrequencyOfState}(\textit{self}, i)$
nh	nerited from object
	delattr(),format(),getattribute(),hash(),new()reduce(),reduce_ex(),repr(),setattr(),sizeof()str(),subclasshook()

# 11.3.2 Properties

Name	Description
Inherited from object	
class	

# 12 Module pylogeny.newick

Newick string parsing and object interaction. A Newick string can represent a phylogenetic tree.

### 12.1 Functions

## assignParents(top)

Should be a one-time use function. Goes through and assigns parents to the parsed newick tree structure nodes and branches to allow for up-traversal.

# removeBranchLengths(top)

Goes through and removes any stored branch lengths.

### removeUnaryInternalNodes(top)

Goes through and ensures any degree-2 internal nodes are smoothed into a single degree-3 internal node.

# invertAlongPathToNode(target, top)

DANGEROUS: Reverses all directionality to a given node from a top-level node. Intended as a low-level function for rerooting a tree.

### shuffleLeaves(top)

DANGEROUS: Given a top-level node, shuffle all leaves in this tree.

### getAllBranches(br)

Given a branch, traverse subtree and return comprising branches as a list.

### **isSibling**(br, other)

Given a branch, determine if that branch is adjacent to another branch.

### getBalancingBracket(newick, i)

Given a position of an opening bracket in a newick string, i, output the closing bracket's position that corresponds to this opening bracket.

## getBranchLength(newick, i)

Given a position of a colon symbol (indicating a branch length), return the branch length.

### getLeafName(newick, i)

Given the position of a leaf, find its complete name.

## parseNewick(newick, i, j, top)

Parse a newick string into a topological newick structure given a top-level node.

### 12.2 Variables

Name	Description
package	Value: 'pylogeny'

### 12.3 Class ParsingError

```
object —
exceptions.BaseException —
exceptions.Exception —
pylogeny.newick.ParsingError
```

### 12.3.1 Methods

init(	(self, val)
xinit(	() initializes x; see help(type(x)) for signature
Overrides: ol	bjectinit extit(inherited documentation)

```
str___(self)
str(x)
Overrides: object.___str___ extit(inherited documentation)
```

# Inherited from exceptions. Exception

new() Inherited from exceptions.BaseException
delattr(),getattribute(),getitem(),getslice(),reduce(),repr(),setattr(),setstate(),unicode()
$Inherited\ from\ object$
format(),hash(),reduce_ex(),sizeof(),subclasshook(
12.3.2 Properties
Name Description
Inherited from exceptions.BaseException
args, message Inherited from object
class
object — pylogeny.base.treeNode — pylogeny.newick.node  Newick node.  12.4.1 Methods
init(self, lbl=',', children=None, parent=None)
xinit() initializes x; see help(type(x)) for signature
Overrides: objectinit extit(inherited documentation)
$\_\_str\_\_(self)$
str(x)
Overrides: objectstr extit(inherited documentation)

 $Inherited\ from\ pylogeny. base. treeNode (Section\ 5.3)$ 

addChild(), getChildByIndex(), getChildren(), getLabel(), getParent(), isInternalNode(), isLeaf()

# $Inherited\ from\ object$

```
___delattr__(), ___format__(), __getattribute__(), __hash__(), __new__(), __reduce__(), __reduce_ex__(), __repr__(), __setattr__(), __sizeof__(), __subclasshook__()
```

### 12.4.2 Properties

Name	Description
Inherited from object	
class	

#### 12.4.3 Class Variables

Name	Description	
Inherited from pylogeny.base.treeNode (Section 5.3)		
children, label, parent		

### 12.5 Class branch

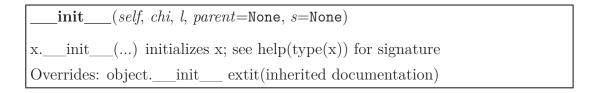
object —

pylogeny.base.treeBranch —

pylogeny.newick.branch

Newick branch.

### 12.5.1 Methods



$\_\_str\_\_(self)$
str(x)
Overrides: objectstr extit(inherited documentation)

# Inherited from pylogeny.base.treeBranch(Section 5.4)

```
getChild(), getLabel(), getParent()
```

# Inherited from object

$\underline{}$ delattr $\underline{}$ (), $\underline{}$	$\{ m format}$	(), _	getatt	ribute	(),hash	(), _	new_	(),
reduce(),	_reduce_	_ex(	),re	pr(), _	setattr	_(),	_sizeof	_(),
subclasshook_	_()							

## 12.5.2 Properties

Name	Description
Inherited from object	
class	

### 12.5.3 Class Variables

Name	Description		
Inherited from pylogeny.base.treeBranch (Section 5.4)			
child, label, parent			

# 12.6 Class parser

Parsing object for Newick strings.

### 12.6.1 Methods

init(self, newick)
$\mathbf{parse}(\mathit{self})$
Parse the stored newick string into a topological structure.
$\underline{}$ str $\underline{}$ (self)

# 13 Module pylogeny.parsimony

Toolkit for performance of Parsimonious Criterion (Parsimony) methods of optimization of a phylogenetic topology with a particular set of data.

### 13.1 Functions

## fitch\_cost(topology, profiles)

Calculate the cost using Fitch algorithm on profile set and alignment. Deprecated: Python implementation of the Fitch algorithm; see fitch C++ module for a C++ implementation that is roughly four times faster.

# fitch(topology, alignment)

Perform the Fitch algorithm on a given tree topology and associated alignment. Deprecated: Python implementation of the Fitch algorithm; see fitch C++ module for a C++ implementation that is roughly four times faster.

### 13.2 Variables

Name	Description
package	Value: 'pylogeny'

# 13.3 Class profile\_set

Hold a set of site\_profile profiles for an entire alignment.

### 13.3.1 Methods

init(self, alignment)	
1 ( 76)	
len(self)	
$\mathbf{weight}(self, val)$	
$\mathbf{get}(\mathit{self}, \mathit{val})$	

getForTaxa(self, val, tax)

# 13.4 Class site\_profile

Consolidate the single-column alignment at a region into a set of components on the basis of similarity alone.

### 13.4.1 Methods

init(self, alignment, site)
$\underline{}$ eq $\underline{}$ (self, o)
$\underline{}$ ne $\underline{}$ (self, o)
str(self)

Class dataModel Module pylogeny.pll

## 14 Module pylogeny.pll

C Extension to wrap libpll library.

#### 14.1 Variables

Name	Description
package	Value: 'pylogeny'

#### 14.2 Class dataModel

Encapsulating a phylogenetic tree (as topology) + corresponding alignment into a libpll-associated data structure. Allows for log-likelihood scoring of this model. MUST BE CLOSED AFTER USE.

#### 14.2.1 Methods

init(self, topo, alignm, model=None)
Initialize all structures.

${\bf getLogLikelihood}(\mathit{self})$	
Calculates log-likelihood using libp	11.

$\mathbf{close}(\mathit{self})$	
If done with this particular problem.	

## 14.3 Class partitionModel

A partition model intended for libpll.

#### 14.3.1 Methods

init(self, ali)	
-----------------	--

$\boxed{\mathbf{getFileName}(\mathit{self})}$	
Get the file name of the model file.	

${\bf createSimpleModel}(\textit{self}, \textit{protein})$
Establish a simple model (e.g., one type).
createModel(self, models, partnames, ranges)
Establish a more complex model.
$\mathbf{close}(\mathit{self})$
Delete file.

## 15 Module pylogeny.rearrangement

Phylogenetic tree structure encapsulation; allow rearrangement of said structure. Tree rearrangements inducing other topologies include Nearest Neighbor Interchange (NNI), Subtree Pruning and Regrafting (SPR), and Tree Bisection and Reconstruction (TBR). Each of these describe a transfer of one node in phylogenetic trees from one parent of a tree to a new parent. Respectively, these operators describe transformations that are subsets of those possible by the successive operator. For example, an NNI operator can perform transformations that are a subset of the transformations possible by the SPR operator.

#### 15.1 Functions

dup(topo, where=None)	
-----------------------	--

#### 15.2 Variables

Name	Description
TYPE_NNI	Value: 2
TYPE_SPR	Value: 1
TYPE_TBR	Value: 3
package	Value: 'pylogeny'

#### 15.3 Class RearrangementError

```
exceptions.BaseException —

exceptions.Exception —

pylogeny.rearrangement.RearrangementError
```

#### 15.3.1 Methods

```
___init___(self, val)
x.___init___(...) initializes x; see help(type(x)) for signature
Overrides: object.___init___ extit(inherited documentation)
```

$\_\_str\_\_(self)$	
$\operatorname{str}(x)$	
Overrides: objectstr extit(inherited document	ntation)
$nherited\ from\ exceptions. Exception$	,
new()	
$herited\ from\ exceptions. Base Exception$	
delattr(),getattribute(),getitem_ duce(),repr(),setattr(),setstat	(),getslice(),re- e(),unicode()
nherited from object	
$\_\_format\_\_(), \_\_hash\_\_(), \_\_reduce\_ex\_\_(), \_$	sizeof(),subclasshook_
2.2 Dramonting	
5.3.2 Properties	
	cription
Inherited from exceptions.BaseException args, message	
Inherited from object	
class	
5.4 Class rearrangement  ncapsulates a single rearrangement move of type SPR,  5.4.1 Methods	NNI,
init(self, struct, type, targ, dest)	
Initialize by providing a pointer to a base topology, moved, and its destination.	a target branch to be
$\mathbf{getType}(\mathit{self})$	
Get the type of movement.	
$\mathbf{isNNI}(self)$	

is SPR(self)
$isTBR(\mathit{self})$
to Topology(self)
Commit the actual move and return the topology.
toNewick(self)
Commit the move but do not create a new structure. Only retrieve resultant Newick string; will be more efficient.
toTree(self)
Commit the move and transform to tree object.
doMove(self)
str(self)

## 15.5 Class topology

```
object —
_abcoll.Container —
pylogeny.base.treeStructure —
pylogeny.rearrangement.topology
```

Encapsulate a tree topology, wrapping the newick tree structure. Is immutable.

#### 15.5.1 Methods

$\underline{\hspace{1cm}} \texttt{init}\underline{\hspace{1cm}} (\textit{self}, \textit{t} = \texttt{None}, \textit{rerootToLeaf} = \texttt{True}, \textit{toLeaf} = \texttt{None})$
Initialize structure with a top-level internal node OR nothing.
Overrides: objectinit

#### rerootToLeaf(self, toleaf=None)

PRIVATE: Reroots the given tree structure such that it is rooted nearest the lowest-order leaf.

### getBranches(self)

#### getLeaves(self)

#### getBipartitions(self)

Get all bipartitions.

### getStrBipartitionFromBranch(self, br)

Given a branch, return corresponding bipartition.

#### getBranchFromStrBipartition(self, bip)

Given a bipartition of taxa, return a branch that creates that partition of tree taxa.

#### getBranchFromBipartition(self, bip)

Given a bipartition object, return a branch that creates that partition of taxa.

#### lockBranch(self, branch)

Given a branch, lock it such that no transitions can ever occur across it.

### **move**(self, branch, destination, returnStruct=True)

Move a branch and attach to a destination branch. Return new structure, or return merely the resultant Newick string.

#### SPR(self, branch, destination)

Perform an SPR move of a branch to a destination branch, creating a new node there. Returns a rearrangement structure (not the actual new structure) that can then be polled for the actual move; this is in order to save memory.

#### **NNI**(self, branch, destination)

Perform an NNI move of a branch to a destination, only if that destination branch is a parent's parent or a parent's sibling. Returns a rearrangement structure (not the actual new structure) that can then be polled for the actual move; this is in order to save memory.

#### iterSPRForBranch(self, br, flip=True)

Consider all valid SPR moves for a given branch in the topology and yield all possible rearrangements as a generator.

#### allSPRForBranch(self, br, flip=True)

Consider all valid SPR moves for a given branch in the topology and return all possible rearrangements.

### $\mathbf{allSPR}(self)$

Consider all valid SPR moves for a given topology and return all possible rearrangements.

### iterNNIForBranch(self, br, flip=True)

Consider all valid NNI moves for a given branch in the topology and and yield all possible rearrangements as a generator.

### allNNIForBranch(self, br, flip=True)

Consider all valid NNI moves for a given branch in the topology and return all possible rearrangements.

### $\mathbf{allNNI}(self)$

Consider all valid NNI moves for a given topology and return all possible rearrangements.

#### allType(self, type=1)

Consider all valid moves of a given rearrangement operator for a given topology. Uses a given rearrangement operator type defined in this module. For example, calling this function by providing TYPE\_NNI as the type will iterate over all NNI operations. By default, the type is TYPE\_SPR.

### iterTypeForBranch(self, br, type=1, flip=True)

Iterate over all possible rearrangements for a branch using a given rearrangement operator type defined in this module. For example, calling this function by providing TYPE\_NNI as the type will iterate over all NNI operations. By default, the type is TYPE\_SPR.

#### fromNewick(self, newickstr)

Alias for parse().

parse	(self,	newicks	str

Parse a newick string and assign the tree to this object. Cannot already be initialized with a tree.

### toNewick(self)

Return the newick string of the tree.

#### toUnrootedNewick(self)

Return the newick string of the tree as an unrooted topology with a multifurcating top-level node.

### toTree(self)

Return the tree object for this topology.

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

Return the tree object of the unrooted version of this topology.

(000] )	str(	(self)
---------	------	--------

Return the newick string of the tree.

Overrides: object.\_\_\_str\_\_\_

## Inherited from pylogeny.base.treeStructure(Section 5.2)

\_\_contains\_\_(), getAllLeaves(), getAllNodes(), getPostOrderTraversal(), getRoot(), leaves(), nodes(), postOrderTraversal()

## $Inherited\ from\ \_abcoll. Container$

\_\_subclasshook\_\_\_()

## Inherited from object

delattr(),	$\_\_format$	(),	getattribu	ite(	),hash_	(), _	new_	()
reduce(),	reduce_	_ex(),	repr_	_(), _	_setattr_	_(),	_sizeof_	()

#### 15.5.2 Properties

Name	Description
Inherited from object	
class	

## 15.5.3 Class Variables

Name Description	
Inherited from pylogeny.base.treeStructure (Section 5.2)	
abstractmethods, root	

## 16 Module pylogeny.scoring

Phylogenetic tree scoring.

#### 16.1 Functions

#### beaglegetLogLikelihood(tree, alignment)

Acquire log-likelihood via C++ library BEAGLE via use of pybeaglethon wrapper library. Parameters: newick.tree object and alignment object. Currently uses HKY85 model.

### getLogLikelihoodForTopology(topo, alignment)

Acquire log-likelihood via C library libpll. Parameters: rearrangement.topology object and alignment object.

### getLogLikelihood(tree, alignment)

Acquire log-likelihood via C library libpll. Parameters: newick.tree object and alignment object.

## getParsimony(newick, alignment)

Acquire parsimony via a C++ implementation. Parameters: newick string and alignment object.

#### getParsimonyForTopology(topology, alignment)

Acquire parsimony via a C++ implementation. Parameters: rearrangement.topology and alignment object.

### getParsimonyFromProfiles(newick, profiles)

Acquire parsimony via a C++ implementation. Parameters: newick string and parsimony.profile set object.

## ${f getParsimonyFromProfilesForTopology}(topology, profiles)$

Acquire parsimony via a C++ implementation. Parameters: rearrangement.topology and parsimony.profile set object.

#### 16.2 Variables

Name	Description
package	Value: 'pylogeny'

## 17 Module pylogeny.tree

Container definition for (phylogenetic) bifurcating or multifurcating trees defined using Newick strings, collections of them, and for splits of these trees.

#### 17.1 Functions



#### 17.2 Variables

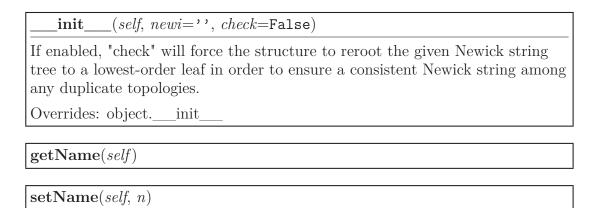
Name	Description
package	Value: 'pylogeny'

#### 17.3 Class tree

object — pylogeny.tree.tree

Defines a single (phylogenetic) tree by newick string; can possess other metadata.

#### 17.3.1 Methods



setScore(self, s)

getOrigin(self)

### **setOrigin**(self, o)

Set the "origin" or specification of where this tree was acquired or constructed from; a string.

getNewick(self)

toNewick(self)

### setNewick(self, n)

Set Newick string to n; also reacquires corresponding "structure" or Newick string without branch lengths.

### getStructure(self)

Returns "structure", a Newick string without branch lengths.

### getRerootedNoBranchLengthNewick(self)

See getStructure().

## getSimpleNewick(self)

Return a Newick string with all taxa name replaced with successive integers.

#### toTopology(self)

Return a rearrangement.topology instance for this tree to allow for rearrangement of the actual structure of the tree.

 $\underline{\phantom{a}}$ eq $\underline{\phantom{a}}$ (self, o)

 $\underline{\phantom{a}}$   $\mathbf{ne}\underline{\phantom{a}}$  (self, o)

 $\_\_str\_\_(self)$ 

str(x)

Overrides: object.\_\_str\_\_ extit(inherited documentation)

## Inherited from object

```
___delattr__(), ___format__(), __getattribute__(), __hash__(), __new__(), __reduce__(), __reduce__ex__(), __repr__(), __setattr__(), __sizeof__(), subclasshook ()
```

#### 17.3.2 Properties

Name	Description
Inherited from object	
class	

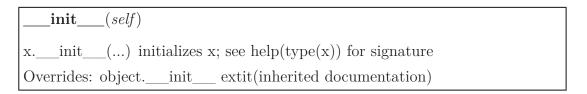
#### 17.4 Class treeSet

```
object —
_abcoll.Sized —
pylogeny.tree.treeSet
```

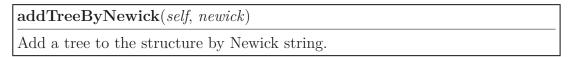
Known Subclasses: pylogeny.landscape.landscape

Represents an ordered, unorganized collection of trees that do not necessarily comprise a combinatorial space.

#### 17.4.1 Methods







```
\frac{\mathbf{removeTree}(\mathit{self}, \mathit{tr})}{\mathbf{Remove a tree object from the collection if present.}}
```

$indexOf(\mathit{self}, \mathit{tr})$	
Acquire the index in this collection of a tree object. Returns -1 if not found	
getitem(self, i)	
len(self)	
Overrides: _abcoll.Sizedlen	
$\mathbf{toTreeFile}(self, fout)$	
Output this landscape as a series of trees, separated by newlines, as a text f saved at the given path.	ile
$\_\{ ext{str}} (self)$	
$\operatorname{str}(\mathtt{x})$	
Overrides: objectstr extit(inherited documentation)	

## Inh

\_\_subclasshook\_\_\_()

## $Inherited\ from\ object$

delattr	_(), _	$\_$ format $\_$	(),	ge	etattribu	ıte	$(), \underline{\hspace{1cm}}$ hash	(), _	new_	()
reduce	(),	reduce	ex	(),	repr	(),	setattr	(),	sizeof	()

## 17.4.2 Properties

Name	Description
Inherited from object	
class	

### 17.4.3 Class Variables

Name	Description
abstractmethods	Value: frozenset([])

### 17.5 Class bipartition



A tree bipartition. Requires a tree topology. Using the term borrowed from nomenclature of a bipartite graph, a bipartition for a phylogenetic tree coincides with the definition of two disjoint sets U and V . A branch in a phylogenetic tree defines a single bipartition that divides the tree into two disjoint sets U and V . The set U comprises all of the children leaf of the subtree associated with that branch. The set V contains the rest of the leaves or taxa in the tree.

#### 17.5.1 Methods

(self, topol, bra=None) init Construct a bipartition from a branch in a topology. :param topol: A topology. :type topol: :class: 'rearrangement.topology' :param bra: An optional argument; can still acquire a bipartition from a string. :type bra: :class: 'newick.branch' Overrides: object. hash (self)hash(x)Overrides: object. hash extit(inherited documentation) (self, o)eq (self, o) $\mathbf{n}\mathbf{e}$ fromStringRepresentation(self, st) Acquire all component elements from a string representation of a bipartition. :param st: A string representation from a :class:'bipartition' object. getBranch(self)

Get branch corresponding to this bipartition.

:returns: :class:'newick.branch'

### getBranchIndex(self)

Return an index of the branch with respect to a post order traversal of the topology.

### getStringRepresentation(self)

Get the string representation corresponding to this bipartition.

### getShortStringRepresentation(self)

Get the shorter string representation corresponding to this bipartition.

## getShortStringMappings(self)

Get the mapping of symbols from taxa names for the shorter string representation.

### getBranchListRepresentation(self)

Get the tuple of lists of branches that represent this bipartition.

### getSPRRearrangements(self)

Return the set of all scores related to this bipartition.

## $\mathbf{getSPRScores}(\mathit{self}, \mathit{ls}, \mathit{node} \texttt{=} \mathtt{None})$

Given a landscape, return all possible scores, not actively performing scoring if not done.

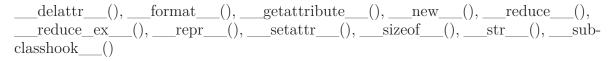
## ${\bf getMedianSPRScore}(\mathit{self}, \mathit{ls}, \mathit{node}{=} \mathtt{None})$

Given a landscape, return the median SPR score.

## ${\tt getBestSPRScore}(\mathit{self}, \mathit{ls}, \mathit{node} \texttt{=} \texttt{None})$

Given a landscape, return the best SPR score.

## $Inherited\ from\ object$



#### 17.5.2 Properties

Name	Description
Inherited from object	
class	

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