RJE Python Appendices

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1. Introduction

1.1. Using this Manual

`written in Courier New`

`written in bold Courier New` **`red`** **`dark`**

`[ ]`

coloured normal text

1.2. Getting Help

`help`

`python program.py` **`help`**

readme.txt

readme.html

1.3. Availability and Local Installation

`help`

2. Fundamentals

2.1. Installation and setup

2.1.1. Directory Structure

- **data/**
- **docs/**
- **extras/**
- **libraries/**
- **settings/**
- **tools/**

2.2. Command-line Options

2.2.1. How to Use this Section

rje.py **`help`**

```
print rje.__doc__
python rje.py help
```

2.2.2. Option Types

`option=X`

`option=FILE`

`option=PATH`

`option=COMMAND`

`option=T/F`

`option=F` **`option=False`**

`option` **`option=T`** **`option=True`**

`option=X,Y` .. **`option=X,Y,..,Z`**

`option=X` **`option=A,B,C,D`** **`option=LIST`**

`LIST`

`option=VALUE`

`option VALUE`

```
python rje.py -v 1 i=0 -newlog
```

2.2.3. Long option values, whitespace and special characters

E.g.

```
python rje.py option="Two words" limits="2,3"
```

2.2.4. INI Files

ini=FILE

haqesac.ini **rje.ini**

rje.ini **2.3 External Programs Used by RJE Programs**

blastpath=PATH

fastapath=PATH

clustalw=COMMAND

muscle=COMMAND

3.3 Replacing Components with Other Programs

win32=T ***.ini**

NB. **PATH** / **path="example path"**

2.2.5. Option Precedence

rje.ini

program.ini

`xxx.py ini=eg.ini i=1` **eg.ini** **i=1**

`xxx.py i=1 ini=eg.ini` **eg.ini** **i=1**

2.2.6. Interactivity and Verbosity settings

i=1

```
python xxx.py commandlist i=1
```

i=X **v=X** **X**

i=-1 **v=-1**

2.2.7. General Command-line Options

2.3. External Components of RJE Programs

ALIGN:

BLAST:

CLUSTALW: **Replacing Components with Other Programs**

MUSCLE:

R: libraries/r/

INI **Setting up the INI File** **3.3 Replacing Components with Other Programs**

2.4. Log Files

gasp.py gasp.log `log=FILE` `newlog` `newlog=T`

Table 1. Common command-line options.

Option	Description	Default*	Module
	General Input/Output Options		
`v=X`			all
`i=X`			all
`log=FILE`			all
`newlog=T/F`	*or*		all
`silent=T/F`			all
`errorlog=FILE`			all
`help`			all
`basefile=FILE`			limited
`outfile=FILE`			limited
`delimit=X`			most
`mysql=T/F`			most
`append=T/F`			most
`force=T/F`			limited
`backups=T/F`			most
`maxbin=X`			limited
	System Info		
`win32=T/F`			all
`memsaver=T/F`			limited
`runpath=PATH`			limited
`rpath=PATH`			limited
	Forking		
`forks=X`			limited
`killforks=X`			limited
`noforks=T/F`			limited

3. Appendices

3.1. Troubleshooting & FAQ

- `win32=T`

3.2. [illegible]

- **GO.**
- **PPI**

3.3. Replacing Components with Other Programs

3.3.1. Alignment programs

`cwcut=X`

`-in INFILE -out OUTFILE` `INFILE` `OUTFILE`

`muscle=PATH`

`INFILE` `INFILE` *.fas *.aln

`clustalw=PATH`

3.3.2. Tree-drawing programs

`maketree=PATH`

`-infile=INFILE -bootstrap=X -seed=X [-kimura]`

`INFILE -bootstrap=X -seed=X [-kimura]` `INFILE`
***.fas** ***.phb**

should ***.nsf**

rje_tree

3.3.3. Wrapper scripts

3.3.4. Incorporating Other Programs into the Python Code

rje_seq.muscleAln() **rje_seq.clustalAln()** **rje_tree.makeTree()**

3.4. References

- Altschul SF, Gish W, Miller W, Myers EW and Lipman DJ (1990). Basic local alignment search tool. *J Mol Biol*, **215**: 403-410.
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- Pearson WR (1994). Using the FASTA program to search protein and DNA sequence databases. *Methods Mol Biol*, **24**: 307-331.
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