

## Kepler - Bug #2249

### Need to support a useful subset of PHYLIP (PHYlogeny Inference Package)

11/06/2005 05:59 PM - Timothy McPhillips

<b>Status:</b>	In Progress	<b>Start date:</b>	11/06/2005
<b>Priority:</b>	Normal	<b>Due date:</b>	
<b>Assignee:</b>	Timothy McPhillips	<b>% Done:</b>	0%
<b>Category:</b>	actors	<b>Estimated time:</b>	0.00 hour
<b>Target version:</b>	3.X.Y	<b>Spent time:</b>	0.00 hour
<b>Bugzilla-Id:</b>	2249		

#### Description

At present, actors wrap the following PHYLIP programs (but do not yet support all features of these programs):

```
consense, dnaml, dnamlk, dnapars, dnapenny,  
drawgram, pars, penny, proml, promlk, protpars
```

At the very least, the following programs need to be wrapped by new actors and their basic capabilities supported:

```
dnadist, protdist, seqboot, fitch, kitsch, neighbor, factor, drawtree
```

#### History

#1 - 03/27/2013 02:19 PM - Redmine Admin

Original Bugzilla ID was 2249