



Construct a `PhyloSim` object:

```
> sim <- PhyloSim()
```

Set the phylo object:

```
> sim$phylo <- tree
```

Set the root sequence:

```
> sim$rootSeq <- root.seq
```

Run the simulation:

```
> Simulate(sim)
```

```
Simulating edge 1 of 4  
Simulating edge 2 of 4  
Simulating edge 3 of 4  
Simulating edge 4 of 4
```

Display the resulting alignment matrix:

