rho<seq(1,30,length=50)
cut90<-rep(-128.162,50)
cut95<-rep(-129.292,50)
cut99<-rep(-132.082,50)
xrange<-range(0,30)
yrange<-range(-133,-125)
rhoa<-seq(0,18,length=50)
rhob<-seq(0,22.5,length=50)
rhoc<-seq(0,30,length=50)
plot(rho,TwoLL,type="l",lwd=3,xlim=xrange,ylim=yrange,xlab="RHO: Relative Potency",ylab="2*Log-Likelihood")
par(new=T)
plot(rhoa,cut90,type="l",lwd=3,xlim=xrange,ylim=yrange,xlab="",ylab="",lty=4)
par(new=T)
plot(rhob,cut95,type="l",lwd=3,xlim=xrange,ylim=yrange,xlab="",ylab="",lty=3)
par(new=T)
plot(rhoc,cut99,type="l",lwd=3,xlim=xrange,ylim=yrange,xlab="",ylab="",lty=2)
legend(locator(1),legend=c("99% CI cut line"))
legend(locator(1),legend=c("95% CI cut line"))
legend(locator(1),legend=c("90% CI cut line"))
pi.for.LL2<-function(x,th2,th3) {
  t<-(x/th2)^th3
  den<-1+t
  t/den
}
dose<-seq(0.005,100,length=1000)
dos<pi.for.LL2(dose,29.4724,0.7234)
pi.n<pi.for.LL2(dose,5.2035,0.7234)
xrange<-range(0.005,100)
yrange<-range(0,1)
n.dose<-c(0.01,0.03,0.1,0.3,1,3,10,30)
n.y<-c(0,1,1,4,4,5,7)
n.n<-c(30,30,10,10,10,10,10,10)
n.pct<-n.y/n.n
s.dose<-c(0.30,1,3,10,30,100)
s.y<-c(0,0,1,4,5,8)
s.n<-c(10,10,10,10,10,10)
s.pct<-s.y/s.n
plot(dose,pi.s,type="l",lwd=3,xlim=xrange,ylim=yrange,xlab="Dose of Peptide",ylab="Percent dead",log="x")
par(new=T)
plot(dose,pi.n,type="l",lwd=3,xlim=xrange,ylim=yrange,xlab="",ylab="",log="x",lty=4)
par(new=T)
plot(s.dose,s.pct,xlim=xrange,ylim=yrange,xlab="",ylab="",cex=2,log="x")
par(new=T)
plot(n.dose,n.pct,xlim=xrange,ylim=yrange,xlab="",ylab="",cex=2,pch=20,log="x")
Full Model (after retaining parallelism):

```r
proc nlmixed;
   parms rho=1 th2N=2 th3=1;
   th2=rho*th2N*S_Peptide+th2N*N_Peptide;
   t=(dose/th2)**th3; p=t/(1+t);
   model y~binomial(n,p);
run;
```

The NLMIXED Procedure
Fit Statistics

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>-2 Log Likelihood</td>
<td>33.4</td>
</tr>
<tr>
<td>AIC (smaller is better)</td>
<td>39.4</td>
</tr>
<tr>
<td>AICC (smaller is better)</td>
<td>41.8</td>
</tr>
<tr>
<td>BIC (smaller is better)</td>
<td>41.4</td>
</tr>
</tbody>
</table>

Parameter Estimates

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Estimate</th>
<th>Error</th>
<th>DF</th>
<th>t Value</th>
<th>Pr &gt;</th>
<th>t</th>
<th>Alpha</th>
<th>Lower</th>
<th>Upper</th>
</tr>
</thead>
<tbody>
<tr>
<td>rho</td>
<td>5.6639</td>
<td>3.5241</td>
<td>14</td>
<td>1.61</td>
<td>0.1303</td>
<td>0.05</td>
<td>-1.8946</td>
<td>13.2224</td>
<td></td>
</tr>
<tr>
<td>th2N</td>
<td>5.2036</td>
<td>2.3301</td>
<td>14</td>
<td>2.23</td>
<td>0.0424</td>
<td>0.05</td>
<td>0.2060</td>
<td>10.2011</td>
<td></td>
</tr>
<tr>
<td>th3</td>
<td>0.7234</td>
<td>0.1177</td>
<td>14</td>
<td>6.15</td>
<td>&lt;.0001</td>
<td>0.05</td>
<td>0.4709</td>
<td>0.9759</td>
<td></td>
</tr>
</tbody>
</table>

Reduced Model (after imposing the Null Hypothesis)

```r
proc nlmixed;
   parms th2N=2 th3=1; rho=1;
   th2=rho*th2N*S_Peptide+th2N*N_Peptide;
   t=(dose/th2)**th3; p=t/(1+t);
   model y~binomial(n,p);
run;
```

The NLMIXED Procedure
Fit Statistics

<p>| | |</p>
<table>
<thead>
<tr>
<th></th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>-2 Log Likelihood</td>
<td>40.2</td>
</tr>
<tr>
<td>AIC (smaller is better)</td>
<td>44.2</td>
</tr>
<tr>
<td>AICC (smaller is better)</td>
<td>45.3</td>
</tr>
<tr>
<td>BIC (smaller is better)</td>
<td>45.5</td>
</tr>
</tbody>
</table>

Parameter Estimates

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Estimate</th>
<th>Error</th>
<th>DF</th>
<th>t Value</th>
<th>Pr &gt;</th>
<th>t</th>
<th>Alpha</th>
<th>Lower</th>
<th>Upper</th>
</tr>
</thead>
<tbody>
<tr>
<td>th2N</td>
<td>14.0797</td>
<td>5.6074</td>
<td>14</td>
<td>2.51</td>
<td>0.0249</td>
<td>0.05</td>
<td>2.0530</td>
<td>26.1065</td>
<td></td>
</tr>
<tr>
<td>th3</td>
<td>0.6138</td>
<td>0.1047</td>
<td>14</td>
<td>5.86</td>
<td>&lt;.0001</td>
<td>0.05</td>
<td>0.3893</td>
<td>0.8384</td>
<td></td>
</tr>
</tbody>
</table>

\[ \chi_1^2 = 40.2 - 33.4 = 6.8, \text{ p-value: (R code) "1-pchisq(6.8,1)" (R result) "0.009115787"} \]

This demonstrates that \( p < 0.01 \), which is what we discerned by looking at the plots on pp.1-2 above and noticing that the vertical line at \( x = 1 \) hits the curve just outside of the 99% PLCI.