

Math 150 Survival Analysis Project

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April 8, 2019

```
knitr::opts_chunk$set(message=FALSE, warning=FALSE, fig.height=4, fig.width=5,  
                        fig.align = "center")  
library(tidyverse)  
library(broom)  
library(survival)  
library(survminer)
```

Outline of “Something New”

For my “something new”, I will do a power analysis of the model. I will perform this analysis via simulation by randomly generating a dataset where the null hypothesis is false - there is a difference between the treatment groups. I think it will be useful to look at the power to distinguish between treatment and control, and between all 4 treatment groups (would we be able to distinguish IDV having an effect on survival in the ZDV + 3TC + IDV group, but not in the d4T + 3TC + IDV group?)

The power analysis of the model is relevant to this survival analysis model because it is useful to know whether our model can reject the null hypothesis when it is warranted. If the model is not very powerful and we fail to reject the null hypothesis, it may be a good idea to continue research with a larger sample size. Or, if the model is powerful and we fail to reject the null hypothesis, we can say that if there were a true difference, our model would probably have detected it, so it may not be worth continuing the research.

I’m going to use the class textbook and *The Analysis of Biological Data* by Whitlock and Schluter (2015) to learn about power and how it relates to sample and effect size. I will also read published articles such as Cohen 1992 and Dorey 2011 (see working bibliography).

This will be challenging because I need to learn how to apply power analysis to an experiment that has already been completed, rather than to determine an ideal sample size. Additionally, I will need to learn how to do power analysis simulations for survival data - how do I generate realistic survival data? What variables do I include? How do I handle effect size? What about censoring?

Working Bibliography

Cohen, Jacob. “Statistical Power Analysis.” *Current Directions in Psychological Science*, vol. 1, no. 3, June 1992, pp. 98–101. SAGE Journals, doi:10.1111/1467-8721.ep10768783.

Dorey, Frederick J. “In Brief: Statistics in Brief: Statistical Power: What Is It and When Should It Be Used?” *Clinical Orthopaedics and Related Research*, vol. 469, no. 2, Feb. 2011, pp. 619–20. PubMed Central, doi:10.1007/s11999-010-1435-0.

Kuiper, Shonda, and Jeffrey Sklar. *Practicing Statistics : Guided Investigations for the Second Course*. Pearson, 2013.

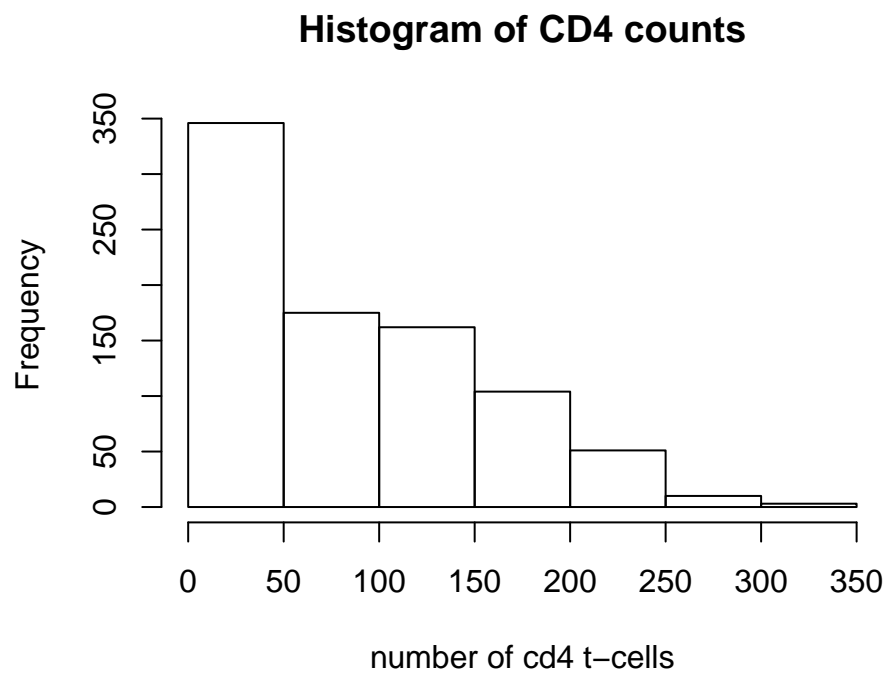
Whitlock, Michael, and Dolph Schluter. *The Analysis of Biological Data*. Second ed., Roberts and Company, 2015.

Importing data:#

```
AD = read.csv("AIDSdata.csv")
```

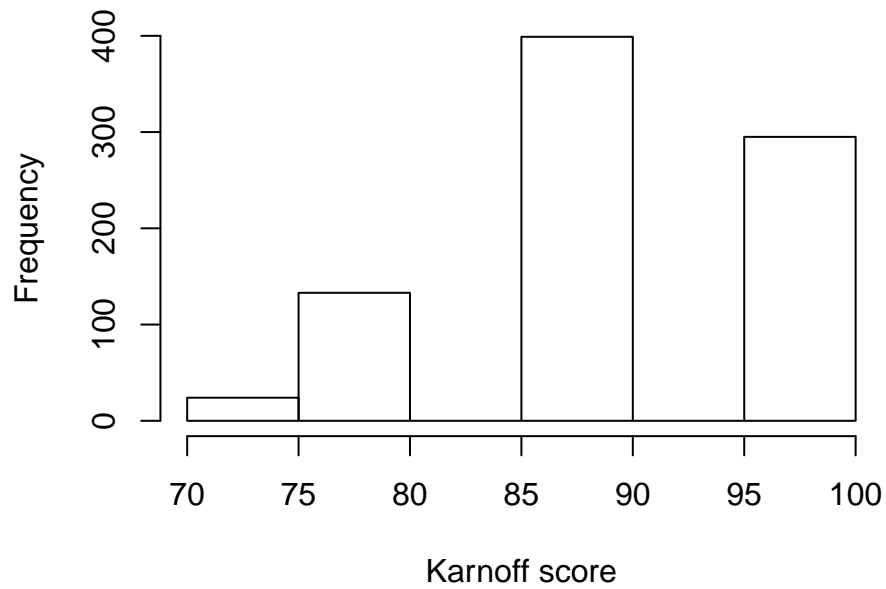
Some exploratory plots:

```
hist(AD$cd4, main = "Histogram of CD4 counts", xlab = "number of cd4 t-cells")
```



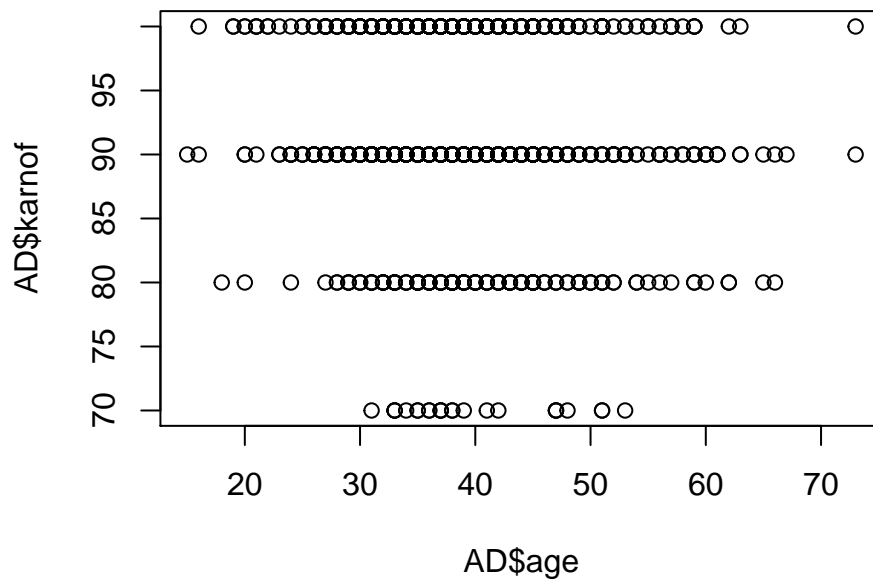
```
hist(AD$karnof, main = "Histogram of Karnof scores", xlab = "Karnoff score", breaks = 5)
```

Histogram of Karnof scores

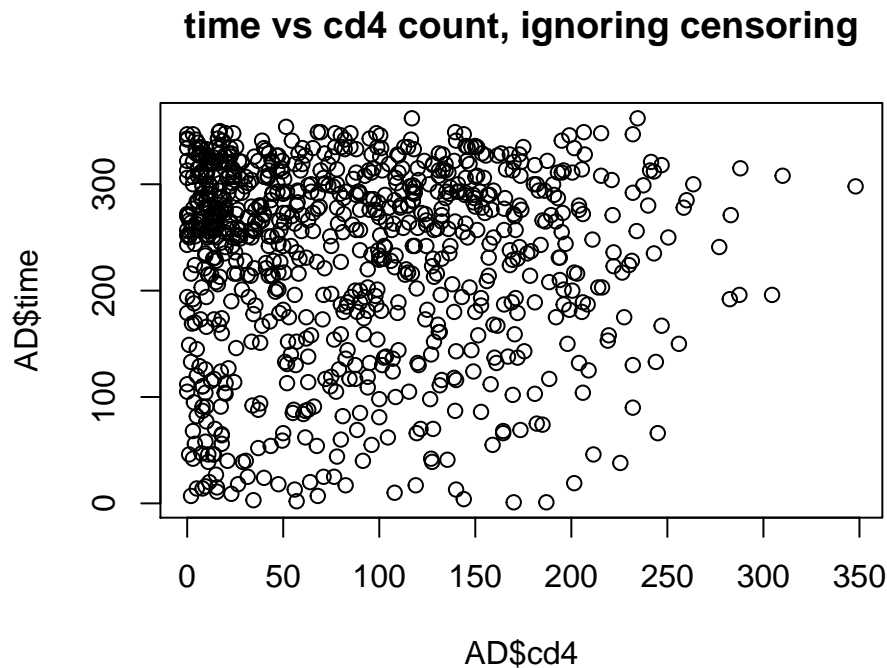


#I'm having a hard time getting the histogram breaks right - karnof scores are multiples of 10 and it
`plot(ADage, ADkarnof, main = "plot of karnof score vs age")`

plot of karnof score vs age



```
plot(AD$cd4, AD$time, main = "time vs cd4 count, ignoring censoring")
```



Working on COX model

Variables: Response: time, censor Not using: time.d, censor.d (because we're using "aids defining event or death", not just death) Explanatory: tx, txgrp, strat2, sex, raceth, ivdrug, hemophil, karnof, cd4, priorzdv, age

Let's check if we need interaction. Likelihood ratio test is $2\ln(\text{Likelihood of full}) - 2\ln(\text{Likelihood of reduced})$

```
full = coxph(Surv(time, censor) ~ (tx+strat2+sex+raceth+ivdrug+hemophil+karnof+cd4+priorzdv+age)^2, data = AD)
full$loglik[2]
```

```
## [1] -380.5977
```

```
red = coxph(Surv(time, censor) ~ tx+strat2+sex+raceth+ivdrug+hemophil+karnof+cd4+priorzdv+age, data = AD)
red$loglik[2]
```

```
## [1] -411.5144
```

```
length(red$coefficients)
```

```
## [1] 10
```

```
1 - pchisq(2 * full$loglik[2] - 2 * red$loglik[2], df = length(full$coefficients) - length(red$coefficients))
```

```
## [1] 0.04845761
```

```
full
```

```
## Call:
```

```
## coxph(formula = Surv(time, censor) ~ (tx + strat2 + sex + raceth +
```

```
##      ivdrug + hemophil + karnof + cd4 + priorzdv + age)^2, data = AD)
##
##              coef exp(coef)   se(coef)      z      p
## tx            -5.501e+00  4.084e-03  4.369e+00 -1.259 0.20807
## strat2        -9.622e-01  3.820e-01  7.284e+00 -0.132 0.89490
## sex            1.137e+01  8.710e+04  5.589e+00  2.035 0.04182
## raceth         7.870e+00  2.617e+03  2.418e+00  3.255 0.00113
## ivdrug        -7.581e+00  5.101e-04  3.252e+00 -2.331 0.01976
## hemophil       1.996e+01  4.646e+08  2.107e+04  0.001 0.99924
## karnof         1.860e-01  1.204e+00  1.246e-01  1.493 0.13539
## cd4           -1.073e-01  8.983e-01  8.413e-02 -1.275 0.20221
## priorzdv       6.378e-02  1.066e+00  8.320e-02  0.767 0.44336
## age           4.436e-01  1.558e+00  2.030e-01  2.185 0.02890
## tx:strat2      1.039e-02  1.010e+00  9.648e-01  0.011 0.99141
## tx:sex         1.969e+00  7.163e+00  7.915e-01  2.487 0.01287
## tx:raceth      -6.084e-02  9.410e-01  3.554e-01 -0.171 0.86408
## tx:ivdrug      9.461e-02  1.099e+00  5.560e-01  0.170 0.86488
## tx:hemophil    -1.611e+01  1.008e-07  4.131e+03 -0.004 0.99689
## tx:karnof      2.166e-02  1.022e+00  3.952e-02  0.548 0.58369
## tx:cd4         5.997e-03  1.006e+00  1.114e-02  0.538 0.59049
## tx:priorzdv    -3.839e-02  9.623e-01  1.685e-02 -2.278 0.02273
## tx:age         3.409e-02  1.035e+00  3.266e-02  1.044 0.29656
## strat2:sex     -2.387e-01  7.876e-01  1.326e+00 -0.180 0.85716
## strat2:raceth  -4.696e-01  6.253e-01  6.182e-01 -0.760 0.44747
## strat2:ivdrug  5.624e-01  1.755e+00  7.919e-01  0.710 0.47756
## strat2:hemophil 1.885e+00  6.585e+00  3.504e+00  0.538 0.59061
## strat2:karnof  -1.333e-02  9.868e-01  5.889e-02 -0.226 0.82091
## strat2:cd4     -2.740e-03  9.973e-01  1.214e-02 -0.226 0.82142
## strat2:priorzdv 4.170e-02  1.043e+00  2.261e-02  1.845 0.06510
## strat2:age     4.497e-02  1.046e+00  4.961e-02  0.906 0.36468
## sex:raceth     -1.886e+00  1.516e-01  6.562e-01 -2.875 0.00404
## sex:ivdrug     4.405e-01  1.553e+00  6.784e-01  0.649 0.51617
## sex:hemophil   -2.067e+01  1.060e-09  2.085e+04 -0.001 0.99921
## sex:karnof     -7.926e-02  9.238e-01  5.430e-02 -1.460 0.14439
## sex:cd4        -8.461e-03  9.916e-01  1.769e-02 -0.478 0.63250
## sex:priorzdv   -3.032e-04  9.997e-01  2.286e-02 -0.013 0.98941
## sex:age        -5.357e-02  9.478e-01  4.356e-02 -1.230 0.21880
## raceth:ivdrug  2.133e-01  1.238e+00  2.426e-01  0.879 0.37933
## raceth:hemophil -1.350e+01  1.373e-06  3.044e+03 -0.004 0.99646
## raceth:karnof  -5.435e-02  9.471e-01  2.404e-02 -2.261 0.02374
## raceth:cd4     7.225e-03  1.007e+00  6.483e-03  1.114 0.26509
## raceth:priorzdv -3.059e-03  9.969e-01  9.559e-03 -0.320 0.74898
## raceth:age     -3.873e-02  9.620e-01  2.056e-02 -1.884 0.05957
## ivdrug:hemophil 2.633e+01  2.712e+11  6.088e+03  0.004 0.99655
## ivdrug:karnof  5.604e-02  1.058e+00  2.796e-02  2.004 0.04506
## ivdrug:cd4     -1.876e-02  9.814e-01  1.333e-02 -1.408 0.15921
## ivdrug:priorzdv 2.655e-02  1.027e+00  1.055e-02  2.517 0.01182
## ivdrug:age     2.986e-02  1.030e+00  3.208e-02  0.931 0.35186
## hemophil:karnof -8.703e-02  9.167e-01  1.461e-01 -0.596 0.55134
## hemophil:cd4   -9.746e-03  9.903e-01  4.981e-02 -0.196 0.84486
## hemophil:priorzdv -4.504e-02  9.560e-01  3.127e-02 -1.440 0.14975
## hemophil:age   -7.388e-02  9.288e-01  1.262e-01 -0.586 0.55820
## karnof:cd4     1.096e-03  1.001e+00  6.856e-04  1.599 0.10983
## karnof:priorzdv -4.181e-04  9.996e-01  7.074e-04 -0.591 0.55454
```

```
## karnof:age      -4.056e-03  9.960e-01  2.148e-03 -1.888 0.05905
## cd4:priorzdv   -2.991e-04  9.997e-01  2.646e-04 -1.130 0.25830
## cd4:age        3.926e-04  1.000e+00  5.166e-04  0.760 0.44732
## priorzdv:age   -1.207e-03  9.988e-01  8.244e-04 -1.464 0.14323
##
## Likelihood ratio test=144.1 on 55 df, p=6.536e-10
## n= 851, number of events= 69
```

This is close enough to 0.05 that I'm not comfortable eliminating interaction.

lets eliminate hemophil entirely

```
full = coxph(Surv(time, censor) ~ (tx+strat2+sex+raceth+ivdrug+hemophil+karnof+cd4+priorzdv+age)^2, data = AD)
full$loglik[2]
```

```
## [1] -380.5977
```

```
red = coxph(Surv(time, censor) ~ (tx+strat2+sex+raceth+ivdrug+karnof+cd4+priorzdv+age)^2, data = AD)
red$loglik[2]
```

```
## [1] -384.3829
```

```
1 - pchisq(2 * full$loglik[2] - 2 * red$loglik[2] , df = length(full$coefficients) - length(red$coefficients))
```

```
## [1] 0.6707304
```

```
#red
```

We can eliminate hemophil entirely. Let's try that with strat 2

```
full = coxph(Surv(time, censor) ~ (tx+strat2+sex+raceth+ivdrug+karnof+cd4+priorzdv+age)^2, data = AD)
full$loglik[2]
```

```
## [1] -384.3829
```

```
red = coxph(Surv(time, censor) ~ (tx+sex+raceth+ivdrug+karnof+cd4+priorzdv+age)^2, data = AD)
red$loglik[2]
```

```
## [1] -387.8855
```

```
1 - pchisq(2 * full$loglik[2] - 2 * red$loglik[2] , df = length(full$coefficients) - length(red$coefficients))
```

```
## [1] 0.6365669
```

```
red
```

```
## Call:
```

```
## coxph(formula = Surv(time, censor) ~ (tx + sex + raceth + ivdrug +
##       karnof + cd4 + priorzdv + age)^2, data = AD)
```

```
##
```

	coef	exp(coef)	se(coef)	z	p
## tx	-6.310e+00	1.818e-03	4.296e+00	-1.469	0.14191
## sex	1.144e+01	9.324e+04	5.571e+00	2.054	0.03999
## raceth	7.255e+00	1.415e+03	2.301e+00	3.153	0.00162
## ivdrug	-6.516e+00	1.480e-03	2.981e+00	-2.186	0.02881
## karnof	1.679e-01	1.183e+00	1.184e-01	1.418	0.15611
## cd4	-7.608e-02	9.267e-01	5.281e-02	-1.441	0.14969
## priorzdv	-3.132e-03	9.969e-01	6.658e-02	-0.047	0.96248
## age	4.069e-01	1.502e+00	1.893e-01	2.150	0.03156
## tx:sex	2.125e+00	8.372e+00	7.668e-01	2.771	0.00558
## tx:raceth	1.504e-01	1.162e+00	3.420e-01	0.440	0.66003

```
## tx:ivdrug      4.191e-02  1.043e+00  5.375e-01  0.078 0.93784
## tx:karnof      2.505e-02  1.025e+00  3.819e-02  0.656 0.51179
## tx:cd4         4.788e-03  1.005e+00  7.088e-03  0.676 0.49930
## tx:priorzdvdv -3.927e-02  9.615e-01  1.679e-02 -2.339 0.01933
## tx:age         3.413e-02  1.035e+00  3.090e-02  1.104 0.26946
## sex:raceth     -1.675e+00  1.874e-01  6.383e-01 -2.624 0.00870
## sex:ivdrug     3.202e-01  1.377e+00  6.562e-01  0.488 0.62555
## sex:karnof     -7.869e-02  9.243e-01  5.442e-02 -1.446 0.14816
## sex:cd4        -1.099e-02  9.891e-01  1.298e-02 -0.847 0.39703
## sex:priorzdvdv -4.393e-03  9.956e-01  2.031e-02 -0.216 0.82876
## sex:age        -6.038e-02  9.414e-01  4.138e-02 -1.459 0.14451
## raceth:ivdrug  1.385e-03  1.001e+00  2.362e-01  0.006 0.99532
## raceth:karnof  -5.064e-02  9.506e-01  2.266e-02 -2.235 0.02543
## raceth:cd4     2.794e-03  1.003e+00  4.207e-03  0.664 0.50658
## raceth:priorzdvdv -1.678e-03  9.983e-01  8.282e-03 -0.203 0.83939
## raceth:age     -3.409e-02  9.665e-01  1.899e-02 -1.795 0.07264
## ivdrug:karnof  5.035e-02  1.052e+00  2.597e-02  1.939 0.05256
## ivdrug:cd4     -9.323e-03  9.907e-01  7.417e-03 -1.257 0.20874
## ivdrug:priorzdvdv 2.362e-02  1.024e+00  9.567e-03  2.469 0.01356
## ivdrug:age     2.753e-02  1.028e+00  3.120e-02  0.883 0.37747
## karnof:cd4     6.475e-04  1.001e+00  4.480e-04  1.445 0.14839
## karnof:priorzdvdv -2.237e-05  1.000e+00  6.636e-04 -0.034 0.97311
## karnof:age     -3.687e-03  9.963e-01  1.942e-03 -1.898 0.05769
## cd4:priorzdvdv -4.921e-05  1.000e+00  1.366e-04 -0.360 0.71869
## cd4:age        4.985e-04  1.000e+00  3.177e-04  1.569 0.11670
## priorzdvdv:age -2.041e-04  9.998e-01  5.395e-04 -0.378 0.70521
##
## Likelihood ratio test=129.5 on 36 df, p=1.777e-12
## n= 851, number of events= 69
```

Okay let's eliminate anything with a p-value of 0.1 or larger.

```
full = coxph(Surv(time, censor) ~ (tx+sex+raceth+ivdrug+karnof+cd4+priorzdvdv+age)^2, data = AD)
full$loglik[2]
```

```
## [1] -387.8855
```

```
red = coxph(Surv(time, censor) ~ tx*(sex + priorzdvdv) + raceth*(sex + karnof + age) + ivdrug*(karnof + priorzdvdv) +
red$loglik[2]
```

```
## [1] -395.5924
```

```
1 - pchisq(2 * full$loglik[2] - 2 * red$loglik[2] , df = length(full$coefficients) - length(red$coefficients))
```

```
## [1] 0.7522683
```

```
red
```

```
## Call:
```

```
## coxph(formula = Surv(time, censor) ~ tx * (sex + priorzdvdv) +
##      raceth * (sex + karnof + age) + ivdrug * (karnof + priorzdvdv) +
##      karnof * age + cd4, data = AD)
```

```
##
```

	coef	exp(coef)	se(coef)	z	p
## tx	-1.773877	0.169674	0.886051	-2.002	0.04528
## sex	2.217867	9.187711	0.876329	2.531	0.01138
## priorzdvdv	-0.013380	0.986709	0.010620	-1.260	0.20770
## raceth	5.731699	308.492931	1.817565	3.154	0.00161

```
## karnof      0.027056  1.027426  0.081709  0.331  0.74055
## age        0.195550  1.215980  0.163624  1.195  0.23204
## ivdrug     -2.935066  0.053127  1.896507 -1.548  0.12171
## cd4        -0.016165  0.983965  0.003300 -4.899 9.63e-07
## tx:sex      1.644482  5.178329  0.681884  2.412  0.01588
## tx:priorzdv -0.035672  0.964957  0.014254 -2.503  0.01233
## sex:raceth  -1.480031  0.227631  0.588021 -2.517  0.01184
## raceth:karnof -0.036726  0.963940  0.019241 -1.909  0.05629
## raceth:age  -0.028096  0.972295  0.017905 -1.569  0.11660
## karnof:ivdrug  0.025423  1.025749  0.021618  1.176  0.23958
## priorzdv:ivdrug  0.016103  1.016233  0.006869  2.344  0.01906
## karnof:age   -0.001477  0.998524  0.001803 -0.819  0.41276
##
## Likelihood ratio test=114.1 on 16 df, p=< 2.2e-16
## n= 851, number of events= 69
```

We can do that, so let's eliminate karnof*age and karnof*ivdrug

```
full = coxph(Surv(time, censor) ~ tx*(sex + priorzdv) + raceth*(sex + karnof + age) + ivdrug*(karnof +
full$loglik[2]
```

```
## [1] -395.5924
```

```
red = coxph(Surv(time, censor) ~ tx*(sex + priorzdv) + raceth*(sex + karnof + age) + ivdrug*priorzdv +
red$loglik[2]
```

```
## [1] -396.5796
```

```
1 - pchisq(2 * full$loglik[2] - 2 * red$loglik[2] , df = length(full$coefficients) - length(red$coeffic
```

```
## [1] 0.3726069
```

```
red
```

```
## Call:
```

```
## coxph(formula = Surv(time, censor) ~ tx * (sex + priorzdv) +
##      raceth * (sex + karnof + age) + ivdrug * priorzdv + cd4,
##      data = AD)
```

```
##
```

```
##              coef exp(coef) se(coef)      z      p
## tx          -1.651633  0.191736  0.877322 -1.883  0.05976
## sex           2.340187 10.383173  0.875181  2.674  0.00750
## priorzdv     -0.013415  0.986674  0.010817 -1.240  0.21490
## raceth        5.275991 195.584220  1.762487  2.993  0.00276
## karnof       -0.006901  0.993123  0.030802 -0.224  0.82274
## age           0.064565  1.066695  0.031193  2.070  0.03847
## ivdrug       -0.804226  0.447434  0.354498 -2.269  0.02329
## cd4          -0.015752  0.984371  0.003258 -4.834 1.34e-06
## tx:sex        1.551639  4.719197  0.674424  2.301  0.02141
## tx:priorzdv   -0.035633  0.964994  0.014349 -2.483  0.01302
## sex:raceth    -1.504677  0.222089  0.586714 -2.565  0.01033
## raceth:karnof -0.031977  0.968528  0.019002 -1.683  0.09240
## raceth:age    -0.025912  0.974421  0.017915 -1.446  0.14806
## priorzdv:ivdrug  0.015861  1.015988  0.007212  2.199  0.02786
##
```

```
## Likelihood ratio test=112.1 on 14 df, p=< 2.2e-16
```

```
## n= 851, number of events= 69
```


Let's try raceth*age

```
full = coxph(Surv(time, censor) ~ tx*(sex + priorzdv) + raceth*sex + raceth*karnof + raceth*age + ivdrug*age, data = AD)
full$loglik[2]
```

```
## [1] -396.5796
```

```
red = coxph(Surv(time, censor) ~ tx*(sex + priorzdv) + raceth*sex + raceth*karnof + ivdrug*priorzdv + cd4, data = AD)
red$loglik[2]
```

```
## [1] -398.9897
```

```
1 - pchisq(2 * full$loglik[2] - 2 * red$loglik[2], df = length(full$coefficients) - length(red$coefficients))
```

```
## [1] 0.08981025
```

```
red
```

```
## Call:
```

```
## coxph(formula = Surv(time, censor) ~ tx * (sex + priorzdv) +  
##       raceth * sex + raceth * karnof + ivdrug * priorzdv + cd4,  
##       data = AD)
```

```
##
```

	coef	exp(coef)	se(coef)	z	p
## tx	-1.555087	0.211171	0.864569	-1.799	0.07207
## sex	2.283299	9.808991	0.877912	2.601	0.00930
## priorzdv	-0.013985	0.986112	0.010731	-1.303	0.19251
## raceth	4.287019	72.749312	1.625738	2.637	0.00837
## karnof	-0.009523	0.990523	0.030620	-0.311	0.75581
## ivdrug	-0.837568	0.432762	0.351801	-2.381	0.01728
## cd4	-0.015009	0.985103	0.003152	-4.762	1.91e-06
## tx:sex	1.473724	4.365463	0.668784	2.204	0.02755
## tx:priorzdv	-0.034477	0.966111	0.014294	-2.412	0.01587
## sex:raceth	-1.480506	0.227523	0.587672	-2.519	0.01176
## raceth:karnof	-0.032507	0.968016	0.018972	-1.713	0.08663
## priorzdv:ivdrug	0.016117	1.016247	0.007143	2.256	0.02405

```
##
```

```
## Likelihood ratio test=107.3 on 12 df, p=< 2.2e-16
```

```
## n= 851, number of events= 69
```

Let's try raceth*karnof

```
full = coxph(Surv(time, censor) ~ tx*(sex + priorzdv) + raceth*sex + raceth*karnof + ivdrug*priorzdv + cd4, data = AD)
full$loglik[2]
```

```
## [1] -398.9897
```

```
red = coxph(Surv(time, censor) ~ tx*(sex + priorzdv) + raceth*sex + karnof + ivdrug*priorzdv + cd4, data = AD)
red$loglik[2]
```

```
## [1] -400.5166
```

```
1 - pchisq(2 * full$loglik[2] - 2 * red$loglik[2], df = length(full$coefficients) - length(red$coefficients))
```

```
## [1] 0.08054651
```

```
red
```

```
## Call:
```

```
## coxph(formula = Surv(time, censor) ~ tx * (sex + priorzdv) +  
##       raceth * sex + karnof + ivdrug * priorzdv + cd4, data = AD)
```

```
##
##               coef exp(coef) se(coef)      z      p
## tx            -1.453900  0.233657  0.862695 -1.685 0.091931
## sex            2.469187 11.812844  0.866826  2.849 0.004392
## priorzdv      -0.015350  0.984767  0.010419 -1.473 0.140691
## raceth         1.670770  5.316262  0.625436  2.671 0.007554
## karnof        -0.056287  0.945268  0.014591 -3.857 0.000115
## ivdrug        -0.855328  0.425144  0.337158 -2.537 0.011185
## cd4           -0.015267  0.984849  0.003145 -4.854 1.21e-06
## tx:sex         1.392238  4.023845  0.666413  2.089 0.036694
## tx:priorzdv    -0.034642  0.965951  0.014195 -2.441 0.014666
## sex:raceth     -1.599834  0.201930  0.578075 -2.768 0.005648
## priorzdv:ivdrug 0.017395  1.017547  0.006697  2.597 0.009395
##
## Likelihood ratio test=104.2 on 11 df, p=< 2.2e-16
## n= 851, number of events= 69
```

Okay all the interaction terms are now below 0.05 and the only p-values above 0.05 are variables that are also in interaction terms. So, I have a model. Let's check against the full model with all interaction just to be sure.

```
full = coxph(Surv(time, censor) ~ (tx+strat2+sex+raceth+ivdrug+hemophil+karnof+cd4+priorzdv+age)^2, data=AD)
red = coxph(Surv(time, censor) ~ tx*(sex + priorzdv) + raceth*sex + ivdrug*priorzdv + karnof + cd4, data=AD)
1 - pchisq(2 * full$loglik[2] - 2 * red$loglik[2], df = length(full$coefficients) - length(red$coefficients))
```

```
## [1] 0.6505501
```

Alright that works then.

The model is:

```
model = coxph(Surv(time, censor) ~ tx*(sex + priorzdv) + raceth*sex + ivdrug*priorzdv + karnof + cd4, data=AD)
model
```

```
## Call:
## coxph(formula = Surv(time, censor) ~ tx * (sex + priorzdv) +
##       raceth * sex + ivdrug * priorzdv + karnof + cd4, data = AD)
##
##               coef exp(coef) se(coef)      z      p
## tx            -1.453900  0.233657  0.862695 -1.685 0.091931
## sex            2.469187 11.812844  0.866826  2.849 0.004392
## priorzdv      -0.015350  0.984767  0.010419 -1.473 0.140691
## raceth         1.670770  5.316262  0.625436  2.671 0.007554
## ivdrug        -0.855328  0.425144  0.337158 -2.537 0.011185
## karnof        -0.056287  0.945268  0.014591 -3.857 0.000115
## cd4           -0.015267  0.984849  0.003145 -4.854 1.21e-06
## tx:sex         1.392238  4.023845  0.666413  2.089 0.036694
## tx:priorzdv    -0.034642  0.965951  0.014195 -2.441 0.014666
## sex:raceth     -1.599834  0.201930  0.578075 -2.768 0.005648
## priorzdv:ivdrug 0.017395  1.017547  0.006697  2.597 0.009395
##
## Likelihood ratio test=104.2 on 11 df, p=< 2.2e-16
## n= 851, number of events= 69
```

Let's test removing tx from the model to see what that does to the p-value so I can talk about it in my results.

```

model = coxph(Surv(time, censor) ~ tx*(sex + priorzdv) + raceth*sex + ivdrug*priorzdv + karnof + cd4, data = AD)
modelNoTx = coxph(Surv(time, censor) ~ raceth*sex + ivdrug*priorzdv + karnof + cd4, data = AD)
1 - pchisq(2 * model$loglik[2] - 2 * modelNoTx$loglik[2] , df = length(model$coefficients) - length(modelNoTx$coefficients))

```

```
## [1] 0.000307816
```

P value of 0.000307816 that model is the same without tx (so model is not the same)