**qwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmrtyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmrtyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmrtyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmrtyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmrtyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmrtyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmrtyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnmqwertyuiopasdfghjklzxcvbnm**

|  |
| --- |
| Examination Project  Survival Analysis  15338673  Paul-Willem Janse van Rensburg |

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# Part A

A medical collaborator is interested in how time to re-infection depends on the type of initial infection.

## Question 1

Consider the three types of initial infections and compute a survival curve of the time to re-infection. Plot them on the same graph. What does the graph suggest?

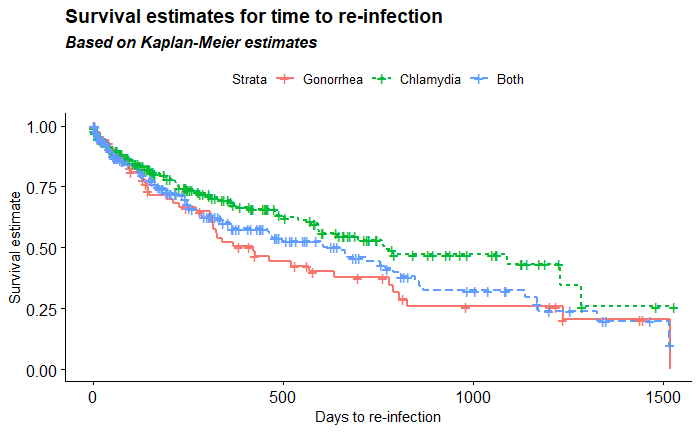


Figure 1 - Kaplan-Meier Estimates

We implement the Kaplan-Meier survival estimate as the majority of the groups have their final observation as an event.

From Figure 1 we can see that Chlamydia has an overall higher survival rate in terms of re-infection than does Gonorrhea. A person who has been infected with both appears to lie in between the two singular infections.

This essentially tells us that your chance of re-infection is lower if you’ve initially been infected with Chlamydia than if you had been infected with both Chlamydia and Gonorrhea or just Gonorrhea. The suspicion is that Gonorrhea pulls down the survival rate for initial infection of both, seeing as it standing alone has the lowest survival rate.

## Question 2

Obtain an appropriate estimator and confidence interval for the 3 quartiles of the survival curves for the three types of initial infections. Interpret the results.

Table 1 - Survival Estimates for Gonorrhea

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| obs | t | nrisk | nevent | ncensored | |  | | σ | | upper | | lower | | strata | |
| 4 | 5 | 73 | 1 | 0 | 0.986301 | | 0.013793 | | 1 | | 0.959994 | | 1 | |
| 5 | 9 | 72 | 1 | 0 | 0.972603 | | 0.019644 | | 1 | | 0.935868 | | 1 | |
| … | … | … | … | … | … | | … | | … | | … | | … | |
| 24 | 126 | 51 | 1 | 0 | 0.779978 | | 0.06458 | | 0.885223 | | 0.687245 | | 1 | |
| 26 | 136 | 49 | 1 | 0 | 0.76406 | | 0.067792 | | 0.872633 | | 0.668995 | | 1 | |
| 28 | 143 | 47 | 1 | 0 | 0.747803 | | 0.071121 | | 0.859658 | | 0.650502 | | 1 | |
| 29 | 144 | 46 | 1 | 0 | 0.731547 | | 0.07444 | | 0.846458 | | 0.632235 | | 1 | |
| 31 | 146 | 44 | 1 | 0 | 0.71492 | | 0.077909 | | 0.832864 | | 0.613679 | | 1 | |
| … | … | … | … | … | … | | … | | … | | … | | … | |
| 44 | 338 | 30 | 1 | 0 | 0.522395 | | 0.123089 | | 0.664925 | | 0.410417 | | 1 | |
| 45 | 367 | 29 | 1 | 0 | 0.504381 | | 0.127994 | | 0.648198 | | 0.392474 | | 1 | |
| 48 | 420 | 26 | 1 | 0 | 0.484982 | | 0.133869 | | 0.630486 | | 0.373058 | | 1 | |
| 49 | 426 | 25 | 1 | 1 | 0.465583 | | 0.139956 | | 0.61253 | | 0.353889 | | 1 | |
| 50 | 464 | 23 | 1 | 0 | 0.44534 | | 0.146846 | | 0.593865 | | 0.333961 | | 1 | |
| … | … | … | … | … | … | | … | | … | | … | | … | |
| 61 | 805 | 11 | 1 | 0 | 0.289529 | | 0.232895 | | 0.457018 | | 0.183422 | | 1 | |
| 63 | 827 | 9 | 1 | 0 | 0.257359 | | 0.261015 | | 0.429256 | | 0.154299 | | 1 | |
| 67 | 1238 | 5 | 1 | 1 | 0.205888 | | 0.343699 | | 0.403819 | | 0.104972 | | 1 | |
| 70 | 1519 | 1 | 1 | 0 | 0 | | Inf | | NA | | NA | | 1 | |

We highlight the largest smaller than 0.75, 0.5 and 0.25 for Gonorrhea. The upper and lower confidence interval for the survival estimates are displayed in Table 1. We then estimate the time to re-infection quartiles as below:

We calculate a 95% confidence interval using the below equation:

**[i]**

Where is the quartile estimate for re-infection, around the aforementioned quartile, with the standard error as retrieved from the table and with a , with the following result (α = 0.05):

Table 2 - Survival Estimates for Chlamydia

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| obs | t | nrisk | nevent | ncensored | |  | | σ | | upper | | lower | | strata | |
| 71 | 1 | 215 | 1 | 1 | 0.995349 | | 0.004662 | | 1 | | 0.986295 | | 2 | |
| 72 | 2 | 213 | 1 | 1 | 0.990676 | | 0.006624 | | 1 | | 0.977897 | | 2 | |
| … | … | … | … | … | … | | … | | … | | … | | … | |
| 153 | 218 | 103 | 1 | 0 | 0.761108 | | 0.043293 | | 0.828509 | | 0.699191 | | 2 | |
| 154 | 221 | 102 | 1 | 0 | 0.753647 | | 0.044399 | | 0.822168 | | 0.690836 | | 2 | |
| 155 | 223 | 101 | 1 | 0 | 0.746185 | | 0.045501 | | 0.815787 | | 0.682521 | | 2 | |
| 160 | 247 | 96 | 1 | 1 | 0.738412 | | 0.04669 | | 0.809173 | | 0.673839 | | 2 | |
| 164 | 264 | 91 | 1 | 0 | 0.730298 | | 0.04798 | | 0.802307 | | 0.664752 | | 2 | |
| … | … | … | … | … | … | | … | | … | | … | | … | |
| 217 | 698 | 34 | 1 | 0 | 0.530748 | | 0.091675 | | 0.635218 | | 0.44346 | | 2 | |
| 224 | 761 | 27 | 1 | 0 | 0.511091 | | 0.099141 | | 0.620707 | | 0.420832 | | 2 | |
| 225 | 766 | 26 | 1 | 0 | 0.491433 | | 0.106618 | | 0.605645 | | 0.39876 | | 2 | |
| 227 | 790 | 24 | 1 | 0 | 0.470957 | | 0.1148 | | 0.589792 | | 0.376066 | | 2 | |
| 239 | 1090 | 12 | 1 | 0 | 0.431711 | | 0.144065 | | 0.57256 | | 0.32551 | | 2 | |
| 246 | 1230 | 5 | 1 | 0 | 0.345368 | | 0.265998 | | 0.581702 | | 0.205053 | | 2 | |
| 247 | 1284 | 4 | 1 | 0 | 0.259026 | | 0.39254 | | 0.559081 | | 0.120009 | | 2 | |

As before, we highlight the largest smaller than 0.75, 0.5 and 0.25 for Chlamydia. The upper and lower confidence interval for the survival estimate for Chlamydia is displayed in Table 2. We then estimate the time to re-infection quartiles as below:

We calculate a 95% confidence interval using equation **[i]**, with the following result (α = 0.05):

Table 3 - Survival Estimates for Chlamydia and Gonorrhea

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| obs | t | nrisk | nevent | ncensored | |  | | σ | | upper | | lower | | strata | |
| 252 | 3 | 208 | 1 | 0 | 0.995192 | | 0.004819 | | 1 | | 0.985836 | | 3 | |
| 254 | 5 | 206 | 3 | 2 | 0.980699 | | 0.009745 | | 0.99961 | | 0.962146 | | 3 | |
| … | … | … | … | … | … | | … | | … | | … | | … | |
| 311 | 161 | 124 | 1 | 0 | 0.760723 | | 0.041756 | | 0.8256 | | 0.700944 | | 3 | |
| 313 | 164 | 122 | 1 | 0 | 0.754487 | | 0.04256 | | 0.820123 | | 0.694105 | | 3 | |
| 314 | 167 | 121 | 1 | 0 | 0.748252 | | 0.043361 | | 0.814624 | | 0.687288 | | 3 | |
| 316 | 177 | 119 | 1 | 1 | 0.741964 | | 0.044175 | | 0.809067 | | 0.680426 | | 3 | |
| 320 | 193 | 114 | 2 | 0 | 0.728947 | | 0.045914 | | 0.797586 | | 0.666215 | | 3 | |
| … | … | … | … | … | … | | … | | … | | … | | … | |
| 385 | 599 | 41 | 1 | 0 | 0.514905 | | 0.084437 | | 0.607575 | | 0.436369 | | 3 | |
| 386 | 604 | 40 | 1 | 0 | 0.502032 | | 0.088151 | | 0.596713 | | 0.422374 | | 3 | |
| 390 | 650 | 36 | 1 | 0 | 0.488087 | | 0.092543 | | 0.585154 | | 0.407122 | | 3 | |
| 391 | 663 | 35 | 1 | 0 | 0.474142 | | 0.096977 | | 0.573397 | | 0.392067 | | 3 | |
| 392 | 668 | 34 | 1 | 0 | 0.460196 | | 0.101468 | | 0.561453 | | 0.377201 | | 3 | |
| … | … | … | … | … | … | | … | | … | | … | | … | |
| 414 | 1138 | 12 | 1 | 0 | 0.296488 | | 0.184334 | | 0.425513 | | 0.206587 | | 3 | |
| 415 | 1168 | 11 | 1 | 1 | 0.269535 | | 0.207533 | | 0.404825 | | 0.179458 | | 3 | |
| 416 | 1172 | 9 | 1 | 0 | 0.239587 | | 0.23866 | | 0.382481 | | 0.150077 | | 3 | |
| 419 | 1327 | 6 | 1 | 0 | 0.199655 | | 0.300486 | | 0.359795 | | 0.110792 | | 3 | |
| 423 | 1517 | 2 | 1 | 0 | 0.099828 | | 0.768305 | | 0.450021 | | 0.022145 | | 3 | |

Again, we highlight the largest smaller than 0.75, 0.5 and 0.25 for both Chlamydia and Gonorrhea initial infection. The upper and lower confidence interval for the survival estimate is displayed in Table 3. We then estimate the time to re-infection quartiles as below:

We calculate a 95% confidence interval using equation **[i]**, with the following result (α = 0.05):

)

We summarize the results in the below table:

Table 4 - C.I. Summary

|  |  |  |  |
| --- | --- | --- | --- |
|  | 75th Percentile C.I. | Median C.I. | 25th Percentile C.I. |
| Gonorrhea | (60,315) | (144,1238) | (66,NA) |
| Both | (131,480) | (334,1284) | (NA,NA) |
| Chlamydia | (99,257) | (251,1138) | (242,NA) |

From Table 4 we can see that there is overlap for all confidence intervals, giving us an unclear indication whether or not the three curves do indeed differ. There is therefore not clear enough evidence to suggest whether time to re-infection is different for the three states of initial infection.

## Question 3

Conduct a single test for differences between the three survival curves. Justify your choice of the test. Also, give the complete notation for the test.

Testing for differences between the survival curves will involve equating the survival estimates for each of the three initial infections types under the null hypothesis, whereas under the alternative hypothesis at least one of the estimates should be different.

This means we set up our hypothesis like this:

Which translates to:

We employ a Fleming-Harrington test with p=1 and q=1, as we would like to place more weight on early and late re-infections, given the survival curves in Figure 1.

Table 5 - Fleming-Harrington Test

|  |  |  |  |
| --- | --- | --- | --- |
| Test of Equality over Strata | | | |
| Test | **ꭓ2** | **DF** | **p-value** |
| Fleming(1,1) | 6.5408 | 2 | 0.0380 |

Based on the Fleming-Harrington test, with a p-value of 0.038 we reject H0 and conclude that there is indeed a difference between the re-infection rates of the different initial STD infections.

## Question 4

Conduct a trend test for differences between the survival curves, using an ordering which seems natural.

We base our ordering on the evidence presented in Figure 1. This leads us to set up the hypothesis for the trend test as below:

Table 6 - Log-Rank statistics

|  |  |
| --- | --- |
| Rank Statistics | |
| Type | **Log-Rank** |
| 1 | 8.366 |
| 2 | -15.324 |
| 3 | 6.958 |

Using the log-rank statistics, we calculate with and z consisting of the log-rank statistics (i.e. the 3 is associated with the Gonorrhea hazard rates) and using the covariance matrix, we calculate

We then calculate:

This gives us a p-value of 0.4457149, so we do not reject the null hypothesis and can therefore not conclude that there is a trend to the re-infection times with the different initial infections.

## Question 5

Estimate the relative risks of re-infection for all the different risk groups (use as baseline, “gonorrhea alone” infection)

1. Assume first that these relative risks are constant over time. Find an estimator and confidence interval for these risks under this assumption

We specify the model as follows:

where,

)

Table 7 - Maximum likelihood estimates of the coefficients of the proportional hazards model for re-infection times using the Breslow method

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Analysis of Maximum Likelihood Estimates | | | | | | |
| Parameter | **DF** |  |  | **ꭓ2** | **p-value** | **RR** |
|  | 1 | -0.41698 | 0.19446 | 4.5978 | 0.0320 | 0.659 |
|  | 1 | -0.13952 | 0.18554 | 0.5655 | 0.4521 | 0.870 |

From Table 7 we can see that ( and the variable does not appear to be significant with a p-value of 0. 4521. We therefore do not reject at a 0.05 confidence level. As for , we have ( and the variable does appear to be significant with a p-value of (and thus we reject at a 0.05 confidence level).

For a 95% confidence interval for the relative risk of re-infection for someone who was initially infected by both gonorrhea and chlamydia compared to someone who was only infected with gonorrhea we define relative risk as:

Using the asymptotic normality of a 95% confidence interval for the relative risk is:

Which gives us:

Similarly for , we derive a 95% confidence interval for the relative risk as:

Which gives us:

1. Determine if there is evidence that these risks are indeed constant over time. Verify this with an appropriate hypothesis test procedure, as well as the appropriate graphical checks.

So we test time dependence with the following hypothesis:

Table 8 - Maximum Likelihood Estimates for time-dependence

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Analysis of Maximum Likelihood Estimates | | | | | | |
| Parameter | **DF** |  |  | **ꭓ2** | **p-value** | **RR** |
|  | 1 | 0.32190 | 0.68383 | 0.2216 | 0.6378 | 1.380 |
|  | 1 | 0.05620 | 0.67480 | 0.0069 | 0.9336 | 1.058 |
|  | 1 | -0.15046 | 0.13130 | 1.3133 | 0.2518 | 0.860 |
|  | 1 | -0.03724 | 0.12750 | 0.0853 | 0.7702 | 0.963 |

We see that for we have a p-value of which is greater than 0.05, so we do not reject . Again, for we see that the p-value is , which leads us to not reject and conclude that there is not enough evidence to suggest that there is some form of time-dependence with the type of initial infection and the risks are thus constant over time.

1. If the risks are not constant over time, propose a different model that fits the data better and estimate only the relative risks under this new model.

As stated with the previous question, the evidence suggests that the risks are constant over time.

# Part B

The investigator has a feeling that the use of condoms may play a role in the re-infection time.

## Question 1

Confounding for the variable “condom use”, repeat the analyses in part A, questions (1), (3) and (5a), by adjusting for and/or stratifying upon this factor “condom use”. Compare results briefly with those results in Part A.

We specify the model as follows:

where,

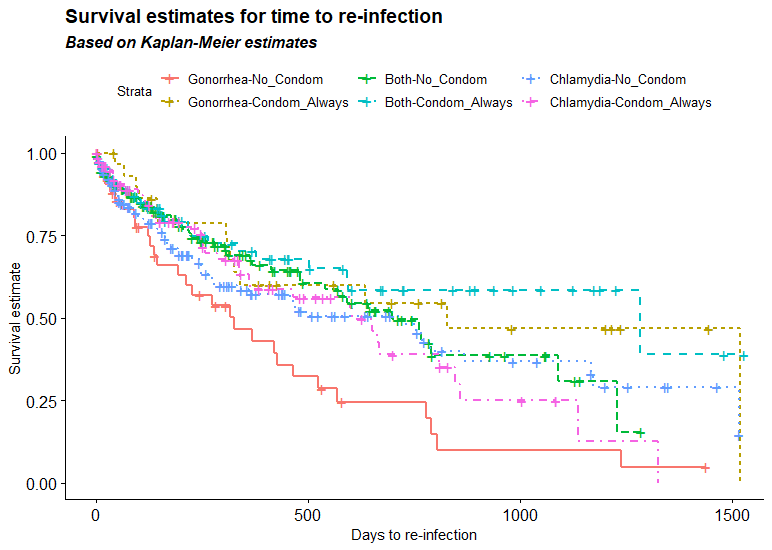


Figure 2 - Survival Estimates Confounding for Condom Use

Figure 2 is a bit messy, so to show the impact condom usage has, we separate out the different initial infections along with condom usage. We produce the following figures to illustrate the impact:

|  |  |
| --- | --- |
| Figure 3 - Gonorrhea – Condom | Figure 4 - Both – Condom |
| Figure 5 - Chlamydia - Condom | |

From Figure 3 we can see that there is quite the noticeable impact on the survival estimate curve for an initial infection of Gonorrhea and condom usage. For an initial infection of Chlamydia, from Figure 5, we see initially there does not appear to be an impact but in the longer times to re-infection, the graphs seem to separate. With an initial infection of both however, condom usage does not appear to have a noticeable effect and for the higher days to re-infection it even appears to possibly be detrimental.

Again, we aim to test the hypothesis:

We employ a Fleming-Harrington test with p=1 and q=1, as we would like to place more weight on early and long term re-infections, given the survival curves in Figure 2.

Table 9 - Fleming-Harrington Test

|  |  |  |  |
| --- | --- | --- | --- |
| Test of Equality over Strata | | | |
| Test | **ꭓ2** | **DF** | **p-value** |
| Fleming(1,1) | 20.8282 | 5 | 0.0009 |

Based on the Fleming-Harrington test, with a p-value of 0.0009 we reject H0 and conclude that there is indeed a difference between the re-infection rates of the different initial STD infections with condom use as a confounding factor.

We estimate the covariates using the maximum likelihood method obtaining the results in Table 10.

Table 10 - Maximum Likelihood Estimates confounding for condom usage

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Analysis of Maximum Likelihood Estimates | | | | | | |
| Parameter | **DF** |  |  | **ꭓ2** | **p-value** | **RR** |
|  | 1 | -0.18718 | 0.18684 | 1.0037 | 0.3164 | 0.829 |
|  | 1 | -0.46427 | 0.19576 | 5.6246 | 0.0177 | 0.629 |
|  | 1 | -0.30843 | 0.14978 | 4.2406 | 0.0395 | 0.735 |

Again, we see that ( and the variable does not appear to be significant with a p-value of . We therefore do not reject at a confidence level. As for , we have ( and the variable does appear to be significant with a p-value of (and thus we reject at a confidence level). Lastly, the condom usage confounding factor does appear to be significant with ( with a p-value of .

For a 95% confidence interval for the relative risk of re-infection for an individual who was initially infected by both gonorrhea and chlamydia compared to an individual who was only infected with gonorrhea, with both either rarely using condoms or always using condoms we define relative risk as:

Using the asymptotic normality of a 95% confidence interval for the relative risk is:

Which gives us:

Similarly for , we derive a 95% confidence interval for the relative risk as:

Which gives us:

We also calculate the 95% confidence interval for the relative risk for condom usage, , where both either have an initial infection of gonorrhea, chlamydia or both:

Which gives us:

## Question 2

Perform a statistical test, which determines what effect condom-use has on the survival curves for the three STD types (i.e. does condom-use have the same effect on all the three types of STD’s or are there different effects for the different users of condoms?)

So, we adjust the re-infection times for condom usage considering type of initial infection. The hypothesis we test is a local test and designed as follows:

We test this hypothesis with a likelihood ratio test. First we obtain the log likelihood of the model with just condom usage as variable:

Then we calculate the log likelihood of the model with all three variables:

We then calculate the likelihood ratio statistic:

With 2 degrees of freedom, the . We therefore do not reject in favor of the alternative and conclude that the are zero.

For specific impact of condom usage with the various initial infections, we include an interaction effect for each. We summarise the results below:

Table 11 - Likelihood ratio test for interactions

|  |  |  |  |
| --- | --- | --- | --- |
| Test Results | | | |
| Test |  | **DF** | **p-value** |
|  | 0.0126 | 1 | 0.9106 |
|  | 1.8492 | 1 | 0.1739 |

So we see that for neither of the interactions with one of the specific initial type infection variables the results are significant. For all the tests in table Table 11 is define as:

Where represents the coefficient of the variable being tested. The last test confirms to an extent what we saw in Figure 3, that condom usage appears to have more of an impact for an initial infection of Chlamydia, but not so much for an initial infection of both STD’s.

# Part C

Use a parametric model to estimate the mean time to re-infection for the three types of initial infection (use therefore the “condom use variable” in this parametric model).

## Question 1

Find the best single parametric model, with full justifications (include all relevant model fit statistics).

Table 12 - Model Fit Statistics

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Log Logistic Estimate |  | Weibull Estimate |  | Log Normal Estimate |  | Exponential Estimate |  | Gamma Estimate |  |
|  | 5.5296 | 0.3731 | 5.9969 | 0. 3374 | 5.5867 | 0.4105 | 6.0075 | 0.2677 | 6.0607 | 0.3895 |
|  | 1.0766 | 0.0622 | 2.0534 | 0.0725 | 1.9985 | 0.1028 | 1.0000 | 0.0000 | 1.1821 | 0.2878 |
|  | 0.2141 | 0.2747 | 0.2538 | 0. 2371 | 0.1994 | 0.3068 | 0.1890 | 0.1866 | 0.2531 | 0.2287 |
|  | 0.5956 | 0.2839 | 0.6191 | 0. 2511 | 0.5138 | 0.3133 | 0.4703 | 0.1953 | 0.6105 | 0.2461 |
|  | 0.3896 | 0.2097 | 0.3706 | 0. 1890 | 0.3968 | 0.2267 | 0.3312 | 0.1489 | 0.3630 | 0.1861 |
|  |  |  |  |  |  |  |  |  | 1.1410 | 0.4625 |
| AIC | 1147.003 |  | 1138.84 |  | 1156.75 |  | 1156.52 |  | 1140.64 |  |
| LL | -568.50 |  | -564.42 |  | -573.377‬ |  | -574.259 |  | -564.32 |  |

When we consider only AIC, we see that the Weibull model estimate has the smallest AIC. We use generalized gamma to further justify the choice of the model and pick the most appropriate model.

We test three hypotheses. The first one is the appropriateness of Weibull. The hypothesis is as follows:

Failure to reject implies that Weibull is preferred. We calculate the statistic as follows:

We do not reject and conclude that the Weibull is an appropriate model.

Next we test to see if an exponential model might be as good a fit as Weibull. Our hypothesis is thus as follows:

We calculate our test statistic as follows:

Again, we do reject and conclude that an exponential model could be a good fit. Lastly, we test for the fit of a lognormal. Our hypothesis is constructed as follows:

We calculate the statistic as follows:

We reject and conclude that a log normal won’t be a good fit.

Considering that Weibull and exponential would both be a good fit, we decide on exponential, as it has fewer parameters. We define our model as follows:

where W has the exponential and the Z parameters are as specified before.

## Question 2

Give a full interpretations of the estimated parameters (i.e. in terms of risk or acceleration).

Table 13 - Model Parameters

|  |  |  |
| --- | --- | --- |
| Parameter | Formula | Result |
|  |  | -0.189 |
|  |  | -0.4703 |
|  |  | -0.3312 |
|  |  | 1 |
|  |  | 0.002460231 |

This translates to relative risk as follows:

## Question 3

Summarise the means in one table for the different categories of condom-use within the STD-types.

## Question 4

Perform all relevant graphical checks to verify that all assumptions have been met (including influential observation- and outlier detection). Make relevant suggestions after investigating these plots.

|  |  |
| --- | --- |
| Figure 6 - Deviance Plot | Figure 7 - Score Residuals |
| Figure 8 - Cox-Snell Residuals | |

From Figure 6, we can see there are many outlying observations based on a threshold of ± 1.96. Further investigation needs to be done on the sample to understand why there are so many outliers. From Figure 7, we observe 3 influential observations. One could consider omitting the observations, refitting the model and comparing the two models to determine the extent of their influence, but I’ve unfortunately run out of time. Figure 8 shows us that the model fits relatively well as it follows the 45֯ line.

# Part D

Summarise your findings in about half a page, without mentioning any statistics (consider all the questions you have answered), such that the medical collaborator can understand what you have analysed. Focus on the differences between part A (pure non-parametric model vs proportional hazard assumption) and part B (condom-use included with full parametric model vs proportional hazards). Explain also the effect of condom use from your point of view.

Re-infection rates of individuals initially infected with gonorrhea, chlamydia or both gonorrhea and chlamydia were considered in the study. The different times to re-infection were compared to determine if there is a differentiation between the three initial states. One could not strictly conclude that there is a trend for re-infection between the different initial infections. This could be due to the high number of outliers.

Thereafter, condom usage was brought in to estimate the impact that this could possibly have on time to re-infection. Condom usage appears to only have a significant impact on the re-infection rate of gonorrhea. Considering the relative risk of re-infection for the different initial infections, time to re-infection with an individual who was initially infected with gonorrhea is impacted by a factor of about 1.5 compared to someone with chlamydia. An individual infected only with gonorrhea is impacted by a factor of 1.2 compared to an individual infected with both gonorrhea and chlamydia. Overall, considering all types of initial infection, condom usage appears to impact time to re-infection by a factor of close to 1.5.

# Appendix A

## SAS Code

/\*Part A\*/

/\*

Data import

\*/

title 'Re-infecion time of std patients';

**data** std;

label time ='Days to re-infection' type ='Infection Type';

infile 'H:\Werk\Survival Analysis\survival\_analysis\exam\_project\data\std\_2019\_pw\_altered.csv'

firstobs=**2** dlm=',';

input obs race\_B mar\_S mar\_D age school type part oral12 oral30 rec12 rec30 abdom dis dys condom

itch lesion rash lymph vag disexam node cens time @@;

**run**;

**proc** **print** data=std;

**run**;

**proc** **phreg** data=std;

model time\*cens(**0**)= type / ties=BRESLOW;

**run**;

/\*Question 3\*/

**proc** **lifetest** data=std;

time time\*cens(**0**);

strata type /test=FLEMING(**1**,**1**);

**run**;

/\*Question 4\*/

**proc** **lifetest** data=std plots=(s);

time time\*cens(**0**);

strata type;

**run**;

/\*Question 5\*/

**data** std\_rr;

label time ='Days to re-infection' type ='Infection Type';

infile 'H:\Werk\Survival Analysis\survival\_analysis\exam\_project\data\std\_2019\_pw\_rr.csv'

firstobs=**2** dlm=',';

input obs race mar age school type part oral12 oral30 rec12 rec30 abdom dis dys condom

itch lesion rash lymph vag disexam node cens time type\_chl type\_both condom\_always @@;

**run**;

**proc** **print** data=std\_rr;

**run**;

**proc** **phreg** data=std\_rr;

model time\*cens(**0**)=type\_both type\_chl /covb ;

**run**;

title 'Time to re-infection of STDs';

**proc** **phreg** data = std\_rr;

model time\*cens(**0**)= type\_both type\_chl X Y;

X=type\_both\*(log(time));

Y=type\_chl\*(log(time));

**run**;

**proc** **phreg** data = std\_rr;

model time\*cens(**0**)= type\_both type\_chl;

**run**;

/\*Part B\*/

/\*Question 1\*/

**proc** **lifetest** data=std;

time time\*cens(**0**);

strata type condom /test=FLEMING(**1**,**1**);

**run**;

**data** std\_rr;

label time ='Days to re-infection' type ='Infection Type';

infile 'H:\Werk\Survival Analysis\survival\_analysis\exam\_project\data\std\_2019\_pw\_rr.csv'

firstobs=**2** dlm=',';

input obs race mar age school type part oral12 oral30 rec12 rec30 abdom dis dys condom

itch lesion rash lymph vag disexam node cens time type\_chl type\_both condom\_always @@;

condom\_both = type\_both\*condom\_always;

condom\_chl = type\_chl\*condom\_always;

**run**;

**proc** **print** data=std\_rr;

**run**;

**proc** **phreg** data = std\_rr;

model time\*cens(**0**)= type\_both type\_chl condom\_always;

**run**;

**proc** **phreg** data=std\_rr;

model time\*cens(**0**)= condom\_always /covb ;

**run**;

**proc** **phreg** data=std\_rr;

model time\*cens(**0**)=type\_both type\_chl condom\_always /covb ;

test1: test type\_chl=type\_both=**0**/print;

**run**;

**proc** **phreg** data=std\_rr;

model time\*cens(**0**)=type\_both type\_chl condom\_both condom\_chl /covb ;

test1: test type\_chl=type\_both=**0**/print;

test2: test condom\_both=**0**/print;

test3: test condom\_chl=**0**/print;

**run**;

/\*Part C\*/

/\*Question 1\*/

/\* Weibull distribution model\*/

**proc** **lifereg** data=std\_rr;

model time\*cens(**0**)=type\_chl type\_both condom/ dist=weibull alpha=**0.05** covb;

**run**;

/\* Exponential distribution model\*/

**proc** **lifereg** data=std\_rr;

model time\*cens(**0**)=type\_chl type\_both condom/ dist=exponential alpha=**0.05** covb;

**run**;

/\* Log normal distribution\*/

**proc** **lifereg** data=std\_rr;

model time\*cens(**0**)=type\_chl type\_both condom/ dist=lognormal alpha=**0.05** covb;

**run**;

/\* Log logistic distribution model\*/

**proc** **lifereg** data=std\_rr;

model time\*cens(**0**)=type\_chl type\_both condom/ dist=lologistic alpha=**0.05** covb;

**run**;

/\* gamma distribution model\*/

**proc** **lifereg** data=std\_rr;

model time\*cens(**0**)=type\_chl type\_both condom/ dist=gamma alpha=**0.05** covb;

**run**;

# Appendix B

## R Code

---

title: "R Notebook"

output: html\_notebook

---

```{r echo=FALSE, warning=FALSE}

library(readxl)

library(survival)

library(survminer)

```

# Part A

## Question 1

```{r}

std <- read\_xlsx('data/std\_2019\_pw.xlsx')

kmp<-survfit(Surv(std$time,std$cens)~std$type,type="kaplan-meier")

ggsurv <- ggsurvplot(kmp , data = std, xlab="Days to re-infection",

ylab="Survival estimate",

legend.labs = c("Gonorrhea", "Chlamydia","Both"), linetype = 'strata') +

labs(title = "Survival estimates for time to re-infection",

subtitle = "Based on Kaplan-Meier estimates")

ggsurv <- ggpar(ggsurv, font.title = c(14, "bold"),

font.subtitle = c(12, "bold.italic"),

font.x = c(11, "plain"),

font.y = c(11, "plain"))

print(ggsurv)

```

From Figure 1 we can see that Chlamydia has an overall higher survival rate in terms of re-infection than does Gonorrhea. A person who has been infected with both appears to lie in between the two singular infections, perhaps being pulled up by the higher survival rate of Chlamydia

## Question 2

```{r}

library(ggfortify)

write.csv(fortify(kmp),file = 'std\_summary.csv')

print(0.747803 + (qnorm(0.975,0,1)\*0.071121))

print(0.747803 - (qnorm(0.975,0,1)\*0.071121))

print(0.484982 + (qnorm(0.975,0,1)\*0.133869))

print(0.484982 - (qnorm(0.975,0,1)\*0.133869))

print(0.205888 + (qnorm(0.975,0,1)\*0.343699))

print(0.205888 - (qnorm(0.975,0,1)\*0.343699))

print(0.746184802 + (qnorm(0.975,0,1)\*0.045501))

print(0.746184802 - (qnorm(0.975,0,1)\*0.045501))

print(0.491433433 + (qnorm(0.975,0,1)\*0.106618))

print(0.491433433 - (qnorm(0.975,0,1)\*0.106618))

print(0.748251879 + (qnorm(0.975,0,1)\*0.043361))

print(0.748251879 - (qnorm(0.975,0,1)\*0.043361))

print(0.488086846 + (qnorm(0.975,0,1)\*0.092543))

print(0.488086846 - (qnorm(0.975,0,1)\*0.092543))

print(0.2395865 + (qnorm(0.975,0,1)\*0.23866))

print(0.2395865 - (qnorm(0.975,0,1)\*0.23866))

```

Highlight biggest time where S(t) is just smaller than 0.75,0.5,0.25 for each infection type.

## Question 4

```{r}

dif <- survdiff(Surv(std$time,std$cens)~std$type,rho = 0)

a <- c(3,2,1)

z <- c(8.366,-15.324,6.958)

az <- a%\*%z

az

aaz <- t(a)%\*%dif$var%\*%a

aaz

az/sqrt(aaz[[1]])

1-pnorm(az/sqrt(aaz[[1]]))

```

## Question 5

### a

```{r}

std\_rr <- read.csv('data/std\_2019\_pw\_rr.csv')

cox <- coxph(Surv(std\_rr$time, std\_rr$cens)~std\_rr$type\_both+std\_rr$type\_chl, method = 'breslow')

cox

```

```{r}

exp(-0.41698+(1.96\*0.19446))

exp(-0.41698-(1.96\*0.19446))

exp(-0.13952+(1.96\*0.18554))

exp(-0.13952-(1.96\*0.18554))

```

```{r}

exp(-0.18718 +(1.96\*0.18684))

exp(-0.18718 -(1.96\*0.18684))

exp(-0.46427+(1.96\*0.19576))

exp(-0.46427-(1.96\*0.19576))

exp(-0.30843+(1.96\*0.14978))

exp(-0.30843-(1.96\*0.14978))

```

```{r}

1-pchisq(3.0945,2)

```

```{r}

res<-residuals(cox)

cox\_snell<-(std\_rr$cens-res)

aa <- Surv(std\_rr$time, std\_rr$cens)

plot(aa,fun="cumhaz",main="Cox-Snell residual plot",xlab="residuals",ylab="estimated cumulative H(t)")

abline(0,1,lty=6)

# Stratifying on initial infection type

surv\_obj\_strat <- Surv(cox\_snell,std\_rr$cens)~std\_rr$type

aa\_strat <-survfit(surv\_obj\_strat,conf.type = 'none')

plot(aa\_strat,fun="cumhaz",main="Cox-Snell residual plot",xlab="residuals",ylab="estimated cumulative H(t)",lty=c(1,2))

abline(0,1,lty=6)

legend(legend=c('Aneuploid','Diploid','45` Line'),lty = c(1,2,6),'topright')

```

```{r}

kmp<-survfit(Surv(std$time,std$cens)~std$type+std$condom,type="kaplan-meier")

summary(kmp)

ggsurv <- ggsurvplot(kmp , data = std, xlab="Days to re-infection",

ylab="Survival estimate",

legend.labs = c("Gonorrhea-No\_Condom","Gonorrhea-Condom\_Always","Both-No\_Condom","Both-Condom\_Always","Chlamydia-No\_Condom","Chlamydia-Condom\_Always"), linetype = 'strata') +

labs(title = "Survival estimates for time to re-infection",

subtitle = "Based on Kaplan-Meier estimates")

ggsurv <- ggpar(ggsurv, font.title = c(14, "bold"),

font.subtitle = c(12, "bold.italic"),

font.x = c(11, "plain"),

font.y = c(11, "plain"))

print(ggsurv)

kmp<-survfit(Surv(std$time,std$cens)~std$type+std$condom, subset = std$type==1,type="kaplan-meier")

ggsurv <- ggsurvplot(kmp , data = std, xlab="Days to re-infection",

ylab="Survival estimate",

legend.labs = c("Gonorrhea-No\_Condom","Gonorrhea-Condom\_Always"), linetype = 'strata') +

labs(title = "Survival estimates for time to re-infection",

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font.x = c(11, "plain"),

font.y = c(11, "plain"))

print(ggsurv)

std <- read\_xlsx('data/std\_2019\_pw.xlsx')

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ggsurv <- ggsurvplot(kmp , data = std, xlab="Days to re-infection",

ylab="Survival estimate",

legend.labs = c("Both-No\_Condom","Both-Condom\_Always"), linetype = 'strata') +

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font.x = c(11, "plain"),

font.y = c(11, "plain"))

print(ggsurv)

kmp<-survfit(Surv(std$time,std$cens)~std$type+std$condom, subset = std$type==3,type="kaplan-meier")

ggsurv <- ggsurvplot(kmp , data = std, xlab="Days to re-infection",

ylab="Survival estimate",

legend.labs = c("Chlamydia-No\_Condom","Chlamydia-Condom\_Always"), linetype = 'strata') +

labs(title = "Survival estimates for time to re-infection",

subtitle = "Based on Kaplan-Meier estimates")

ggsurv <- ggpar(ggsurv, font.title = c(14, "bold"),

font.subtitle = c(12, "bold.italic"),

font.x = c(11, "plain"),

font.y = c(11, "plain"))

print(ggsurv)

```

```{r}

exp(0.0023+1.96\*0.0004209)

exp(0.0023-1.96\*0.0004209)

exp(0.0007958+1.96\*0.0004560)

exp(0.0007958-1.96\*0.0004560)

```

---

title: "R Notebook"

output: html\_notebook

---

```{r echo=FALSE, warning=FALSE}

library(readxl)

library(survival)

library(survminer)

```

# Part A

## Question 1

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legend.labs = c("Gonorrhea", "Chlamydia","Both"), linetype = 'strata') +

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font.subtitle = c(12, "bold.italic"),

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print(ggsurv)

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```

Highlight biggest time where S(t) is just smaller than 0.75,0.5,0.25 for each infection type.

## Question 4

```{r}

dif <- survdiff(Surv(std$time,std$cens)~std$type,rho = 0)

a <- c(3,2,1)

z <- c(8.366,-15.324,6.958)

az <- a%\*%z

az

aaz <- t(a)%\*%dif$var%\*%a

aaz

az/sqrt(aaz[[1]])

1-pnorm(az/sqrt(aaz[[1]]))

```

## Question 5

### a

```{r}

std\_rr <- read.csv('data/std\_2019\_pw\_rr.csv')

cox <- coxph(Surv(std\_rr$time, std\_rr$cens)~std\_rr$type\_both+std\_rr$type\_chl, method = 'breslow')

cox

```

```{r}

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exp(-0.41698-(1.96\*0.19446))

exp(-0.13952+(1.96\*0.18554))

exp(-0.13952-(1.96\*0.18554))

```

```{r}

exp(-0.18718 +(1.96\*0.18684))

exp(-0.18718 -(1.96\*0.18684))

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exp(-0.46427-(1.96\*0.19576))

exp(-0.30843+(1.96\*0.14978))

exp(-0.30843-(1.96\*0.14978))

```

```{r}

1-pchisq(3.0945,2)

```

```{r}

res<-residuals(cox)

cox\_snell<-(std\_rr$cens-res)

aa <- Surv(std\_rr$time, std\_rr$cens)

plot(aa,fun="cumhaz",main="Cox-Snell residual plot",xlab="residuals",ylab="estimated cumulative H(t)")

abline(0,1,lty=6)

# Stratifying on initial infection type

surv\_obj\_strat <- Surv(cox\_snell,std\_rr$cens)~std\_rr$type

aa\_strat <-survfit(surv\_obj\_strat,conf.type = 'none')

plot(aa\_strat,fun="cumhaz",main="Cox-Snell residual plot",xlab="residuals",ylab="estimated cumulative H(t)",lty=c(1,2))

abline(0,1,lty=6)

legend(legend=c('Aneuploid','Diploid','45` Line'),lty = c(1,2,6),'topright')

```

```{r}

kmp<-survfit(Surv(std$time,std$cens)~std$type+std$condom,type="kaplan-meier")

summary(kmp)

ggsurv <- ggsurvplot(kmp , data = std, xlab="Days to re-infection",

ylab="Survival estimate",

legend.labs = c("Gonorrhea-No\_Condom","Gonorrhea-Condom\_Always","Both-No\_Condom","Both-Condom\_Always","Chlamydia-No\_Condom","Chlamydia-Condom\_Always"), linetype = 'strata') +

labs(title = "Survival estimates for time to re-infection",

subtitle = "Based on Kaplan-Meier estimates")

ggsurv <- ggpar(ggsurv, font.title = c(14, "bold"),

font.subtitle = c(12, "bold.italic"),

font.x = c(11, "plain"),

font.y = c(11, "plain"))

print(ggsurv)

kmp<-survfit(Surv(std$time,std$cens)~std$type+std$condom, subset = std$type==1,type="kaplan-meier")

ggsurv <- ggsurvplot(kmp , data = std, xlab="Days to re-infection",

ylab="Survival estimate",

legend.labs = c("Gonorrhea-No\_Condom","Gonorrhea-Condom\_Always"), linetype = 'strata') +

labs(title = "Survival estimates for time to re-infection",

subtitle = "Based on Kaplan-Meier estimates")

ggsurv <- ggpar(ggsurv, font.title = c(14, "bold"),

font.subtitle = c(12, "bold.italic"),

font.x = c(11, "plain"),

font.y = c(11, "plain"))

print(ggsurv)

std <- read\_xlsx('data/std\_2019\_pw.xlsx')

kmp<-survfit(Surv(std$time,std$cens)~std$type+std$condom, subset = std$type==2,type="kaplan-meier")

ggsurv <- ggsurvplot(kmp , data = std, xlab="Days to re-infection",

ylab="Survival estimate",

legend.labs = c("Both-No\_Condom","Both-Condom\_Always"), linetype = 'strata') +

labs(title = "Survival estimates for time to re-infection",

subtitle = "Based on Kaplan-Meier estimates")

ggsurv <- ggpar(ggsurv, font.title = c(14, "bold"),

font.subtitle = c(12, "bold.italic"),

font.x = c(11, "plain"),

font.y = c(11, "plain"))

print(ggsurv)

kmp<-survfit(Surv(std$time,std$cens)~std$type+std$condom, subset = std$type==3,type="kaplan-meier")

ggsurv <- ggsurvplot(kmp , data = std, xlab="Days to re-infection",

ylab="Survival estimate",

legend.labs = c("Chlamydia-No\_Condom","Chlamydia-Condom\_Always"), linetype = 'strata') +

labs(title = "Survival estimates for time to re-infection",

subtitle = "Based on Kaplan-Meier estimates")

ggsurv <- ggpar(ggsurv, font.title = c(14, "bold"),

font.subtitle = c(12, "bold.italic"),

font.x = c(11, "plain"),

font.y = c(11, "plain"))

print(ggsurv)

```

```{r}

exp(0.0023+1.96\*0.0004209)

exp(0.0023-1.96\*0.0004209)

exp(0.0007958+1.96\*0.0004560)

exp(0.0007958-1.96\*0.0004560)

library(readxl)

library(survival)

library(survminer)

std <- read\_xlsx('data/std\_2019\_pw.xlsx')

summary(std)

head(std)

kmp<-survfit(Surv(std$time,std$cens)~std$type,type="kaplan-meier")

ggsurv <- ggsurvplot(kmp , data = std, xlab="Days to re-infection",

ylab="Survival estimate",

legend.labs = c("Gonorrhea", "Chlamydia","Both"), linetype = 'strata') +

labs(title = "Survival estimates for time to re-infection",

subtitle = "Based on Kaplan-Meier estimates")

ggsurv <- ggpar(ggsurv, font.title = c(14, "bold"),

font.subtitle = c(12, "bold.italic"),

font.x = c(11, "plain"),

font.y = c(11, "plain"))

print(ggsurv)

res<-residuals(cox)

cox\_snell<-(std\_rr$cens-res)

surv\_obj <- Surv(cox\_snell,std\_rr$cens)~std\_rr$type\_both+std\_rr$type\_chl

aa<-survfit(surv\_obj,conf.type = 'none')

plot(aa,fun="cumhaz",main="Cox-Snell residual plot",xlab="residuals",ylab="estimated cumulative H(t)")

abline(0,1,lty=6)

# Stratifying on initial infection type

surv\_obj\_strat <- Surv(cox\_snell,std\_rr$cens)~std\_rr$type

aa\_strat <-survfit(surv\_obj\_strat,conf.type = 'none')

plot(aa\_strat,fun="cumhaz",main="Cox-Snell residual plot",xlab="residuals",ylab="estimated cumulative H(t)",lty=c(1,2,3),col=c('green','blue','red'))

abline(0,1,lty=6,col='orange')

legend(legend=c('Gonorrhea', 'Chlamydia','Both','45` Line'),lty = c(1,2,3,6),col=c('green','blue','red','orange'),'topright')

#######################################

## Part B

######################################

kmp<-survfit(Surv(std$time,std$cens)~std$type+std$condom,type="kaplan-meier")

summary(kmp)

ggsurv <- ggsurvplot(kmp , data = std, xlab="Days to re-infection",

ylab="Survival estimate",

legend.labs = c("Gonorrhea-No\_Condom","Gonorrhea-Condom\_Always","Chlamydia-No\_Condom","Chlamydia-Condom\_Always","Both-No\_Condom","Both-Condom\_Always"), linetype = 'strata') +

labs(title = "Survival estimates for time to re-infection",

subtitle = "Based on Kaplan-Meier estimates")

ggsurv <- ggpar(ggsurv, font.title = c(14, "bold"),

font.subtitle = c(12, "bold.italic"),

font.x = c(11, "plain"),

font.y = c(11, "plain"))

print(ggsurv)

kmp<-survfit(Surv(std$time,std$cens)~std$type+std$condom, subset = std$type==1,type="kaplan-meier")

ggsurv <- ggsurvplot(kmp , data = std, xlab="Days to re-infection",

ylab="Survival estimate",

legend.labs = c("Gonorrhea-No\_Condom","Gonorrhea-Condom\_Always"), linetype = 'strata') +

labs(title = "Survival estimates for time to re-infection",

subtitle = "Based on Kaplan-Meier estimates")

ggsurv <- ggpar(ggsurv, font.title = c(14, "bold"),

font.subtitle = c(12, "bold.italic"),

font.x = c(11, "plain"),

font.y = c(11, "plain"))

print(ggsurv)

kmp<-survfit(Surv(std$time,std$cens)~std$type+std$condom, subset = std$type==2,type="kaplan-meier")

ggsurv <- ggsurvplot(kmp , data = std, xlab="Days to re-infection",

ylab="Survival estimate",

legend.labs = c("Chlamydia-No\_Condom","Chlamydia-Condom\_Always"), linetype = 'strata') +

labs(title = "Survival estimates for time to re-infection",

subtitle = "Based on Kaplan-Meier estimates")

ggsurv <- ggpar(ggsurv, font.title = c(14, "bold"),

font.subtitle = c(12, "bold.italic"),

font.x = c(11, "plain"),

font.y = c(11, "plain"))

print(ggsurv)

kmp<-survfit(Surv(std$time,std$cens)~std$type+std$condom, subset = std$type==3,type="kaplan-meier")

ggsurv <- ggsurvplot(kmp , data = std, xlab="Days to re-infection",

ylab="Survival estimate",

legend.labs = c("Both-No\_Condom","Both-Condom\_Always"), linetype = 'strata') +

labs(title = "Survival estimates for time to re-infection",

subtitle = "Based on Kaplan-Meier estimates")

ggsurv <- ggpar(ggsurv, font.title = c(14, "bold"),

font.subtitle = c(12, "bold.italic"),

font.x = c(11, "plain"),

font.y = c(11, "plain"))

print(ggsurv)

exp(0.0023+1.96\*0.0004209)

exp(0.0023-1.96\*0.0004209)

exp(0.0007958+1.96\*0.0004560)

exp(0.0007958-1.96\*0.0004560)

kmp<-survfit(Surv(std$time,std$cens)~std$type+std$condom, subset = std$type==3,type="kaplan-meier")

cox <- coxph(Surv(std$time,std$cens)~std$condom, subset = std\_rr$type==3, method = 'breslow')

cox$coefficients

1-pchisq(0.0929 ,1)

1-pchisq(0.4003 ,1)

1-pchisq(9.2943 ,1)

exp(-6.0075)

exp(-0.189)

exp(-0.4703)

1/exp(-0.3312)

std\_rr <- read.csv('data/std\_2019\_pw\_rr.csv')

fit <- survreg(Surv(std\_rr$time,std\_rr$cen)~ as.factor(std\_rr$type)+std\_rr$condom\_always, dist="exponential", data=std\_rr)

resids <- residuals(fit, type = "deviance")

par(mfrow=c(1,1))

plot(x=std\_rr$obs,y=resids, main="Deviance plot for exponential model - STD study", xlab="Observations",ylab="Deviance residuals", col=std\_rr$type)

abline(h=c(-1.96,1.96),lty=7)

legend(legend=c('Gonorrhea', 'Chlamydia','Both'),col=unique(std\_rr$type),'topright',pch=1)

#influential

score.res <- residuals(fit,type="dfbeta")

plot(1:length(std\_rr$obs),y=score.res[,1],main="Score residuals for exponential model - STD study",xlab="Observations",ylab="Difference in betas", col=std\_rr$type)

abline(h=c(-0.03,0.03),lty=7)

legend(legend=c('Gonorrhea', 'Chlamydia','Both'),col=unique(std\_rr$type),'topright',pch=1)

res=sort((score.res[,1]))

##### Cox Snell

surv\_reg\_obj <- survreg(Surv(std\_rr$time, std\_rr$cens)~ std\_rr$type\_chl+std\_rr$type\_both+std\_rr$condom\_always, dist="weibull")

hat\_sig <- surv\_reg\_obj$scale

hat\_alpha <- 1/hat\_sig

reg\_linear <- surv\_reg\_obj$linear.predictor

reg\_linear\_mdf <- -reg\_linear/hat\_sig

tt <- cbind(Surv(std\_rr$time, std\_rr$cens))[,1]

cs\_resid <- exp(reg\_linear\_mdf)\*tt^(hat\_alpha)

cs\_fit = survfit(Surv(cs\_resid,std\_rr$cens)~1,type="kaplan-meier")

par(mfrow=c(1,1))

plot(x=cs\_fit$time, y=-log(cs\_fit$surv),type ="s",

ylab = "Estimated Cumulative H(t)",

xlab= "Cox–Snell Residuals",

main="Cox–Snell residuals to assess the fit of the Weibull regression model")

lines(c(0,3),c(0,3), lty=2)

legend(legend=c('Estimated H(t)','45` Line'),lty = c(1,2),'topright')

```