

# BIOST/EPI 537 Final Group Project

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**1. Provide an estimate of disease-free survival time for patients enrolled in this study. What are the main characteristics of this summary?**

```
library(survival)
library(survminer)
```

```
## Loading required package: ggplot2
```

```
## Loading required package: ggpubr
```

```
##
```

```
## Attaching package: 'survminer'
```

```
## The following object is masked from 'package:survival':
```

```
##
```

```
##      myeloma
```

```
library(ggplot2)
library(dplyr)
```

```
##
```

```
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':
```

```
##
```

```
##      filter, lag
```

```
## The following objects are masked from 'package:base':
```

```
##
```

```
##      intersect, setdiff, setequal, union
```

```
library(knitr)
library(broom)
library(table1)
```

```
##  
## Attaching package: 'table1'
```

```
## The following objects are masked from 'package:base':  
##  
##      units, units<-
```

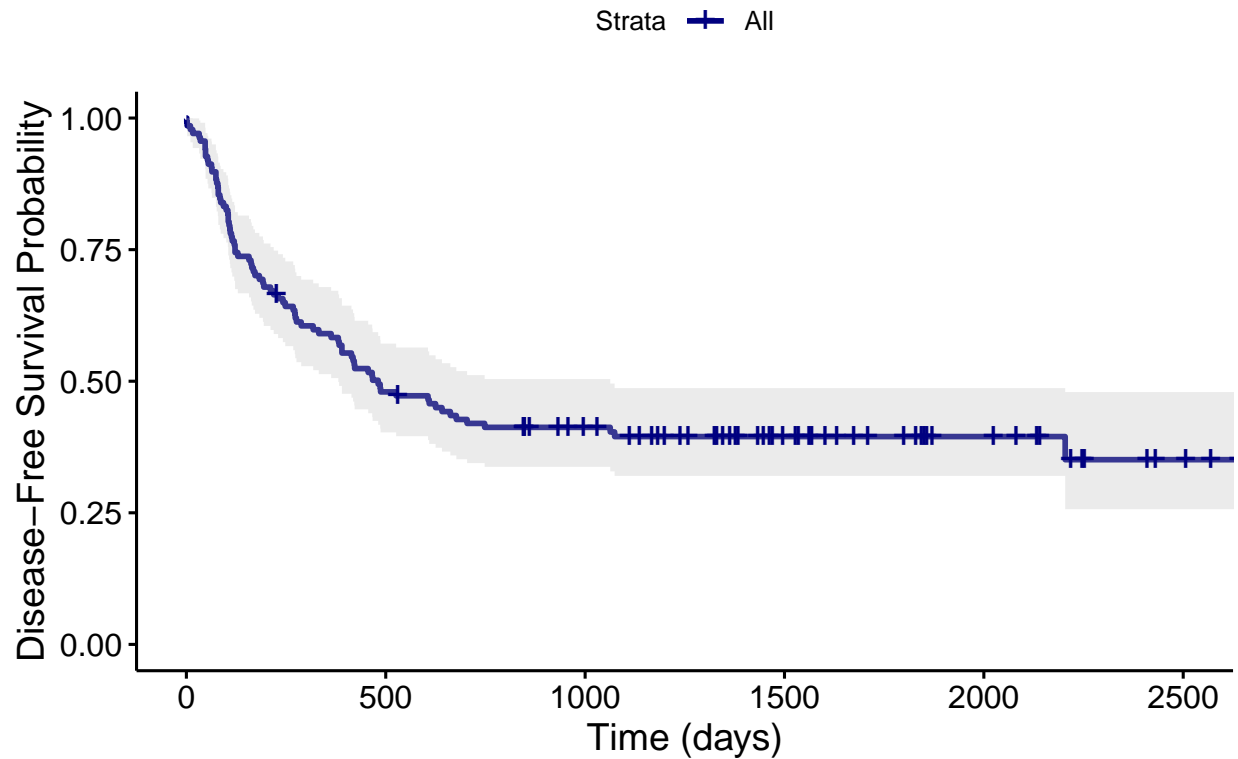
```
library(kableExtra)
```

```
##  
## Attaching package: 'kableExtra'
```

```
## The following object is masked from 'package:dplyr':  
##  
##      group_rows
```

```
#bmt <- read.csv("~/Documents/UW classes/survival analysis/bmt.csv")  
bmt <- read.csv("~/Downloads/bmt.csv")  
  
dfs_surv <- Surv(time = bmt$tdfs, event = bmt$deltadfs)  
km_fit <- survfit(dfs_surv ~ 1)  
  
survminer::ggsurvplot(  
  fit = km_fit,  
  data = bmt,  
  conf.int = T,  
  palette = "navy",  
  xlab = "Time (days)",  
  ylab = "Disease-Free Survival Probability",  
  title = "Kaplan-Meier Curve for Disease-Free Survival of All Participants"  
)
```

## Kaplan–Meier Curve for Disease–Free Survival of All Partic



```
summary(km_fit)
```

```
## Call: survfit(formula = dfs_surv ~ 1)
##
##      time  n.risk  n.event  survival  std.err  lower 95% CI  upper 95% CI
##      1      137       1    0.993 0.00727    0.979    1.000
##      2      136       1    0.985 0.01025    0.966    1.000
##     10      135       1    0.978 0.01250    0.954    1.000
##     16      134       1    0.971 0.01438    0.943    0.999
##     32      133       1    0.964 0.01602    0.933    0.995
##     35      132       1    0.956 0.01748    0.923    0.991
##     47      131       2    0.942 0.02003    0.903    0.982
##     48      129       2    0.927 0.02222    0.884    0.972
##     53      127       1    0.920 0.02322    0.875    0.966
##     55      126       1    0.912 0.02415    0.866    0.961
##     63      125       1    0.905 0.02504    0.857    0.956
##     64      124       1    0.898 0.02588    0.848    0.950
##     74      123       2    0.883 0.02744    0.831    0.939
##     76      121       1    0.876 0.02817    0.822    0.933
##     79      120       1    0.869 0.02886    0.814    0.927
##     80      119       2    0.854 0.03017    0.797    0.915
##     84      117       1    0.847 0.03078    0.788    0.909
##     86      116       1    0.839 0.03137    0.780    0.903
##     93      115       1    0.832 0.03193    0.772    0.897
##    100      114       1    0.825 0.03248    0.764    0.891
```

##	104	113	1	0.818	0.03300	0.755	0.885
##	105	112	2	0.803	0.03399	0.739	0.872
##	107	110	1	0.796	0.03445	0.731	0.866
##	109	109	1	0.788	0.03490	0.723	0.860
##	110	108	1	0.781	0.03533	0.715	0.853
##	113	107	1	0.774	0.03575	0.707	0.847
##	115	106	1	0.766	0.03615	0.699	0.841
##	120	105	1	0.759	0.03653	0.691	0.834
##	122	104	2	0.745	0.03726	0.675	0.821
##	129	102	1	0.737	0.03760	0.667	0.815
##	157	101	1	0.730	0.03793	0.659	0.808
##	162	100	1	0.723	0.03825	0.651	0.802
##	164	99	1	0.715	0.03855	0.644	0.795
##	168	98	1	0.708	0.03884	0.636	0.788
##	172	97	1	0.701	0.03912	0.628	0.782
##	183	96	1	0.693	0.03939	0.620	0.775
##	192	95	1	0.686	0.03965	0.613	0.768
##	194	94	1	0.679	0.03989	0.605	0.762
##	211	93	1	0.672	0.04013	0.597	0.755
##	219	92	1	0.664	0.04035	0.590	0.748
##	230	90	1	0.657	0.04057	0.582	0.741
##	242	89	1	0.649	0.04078	0.574	0.735
##	248	88	1	0.642	0.04098	0.567	0.728
##	268	87	1	0.635	0.04117	0.559	0.721
##	272	86	1	0.627	0.04134	0.551	0.714
##	273	85	1	0.620	0.04151	0.544	0.707
##	276	84	1	0.613	0.04167	0.536	0.700
##	288	83	1	0.605	0.04181	0.529	0.693
##	318	82	1	0.598	0.04195	0.521	0.686
##	332	81	1	0.590	0.04208	0.513	0.679
##	363	80	1	0.583	0.04219	0.506	0.672
##	381	79	1	0.576	0.04230	0.498	0.665
##	383	78	1	0.568	0.04240	0.491	0.658
##	390	77	2	0.554	0.04256	0.476	0.644
##	414	75	1	0.546	0.04263	0.469	0.636
##	418	74	1	0.539	0.04269	0.461	0.629
##	421	73	1	0.531	0.04273	0.454	0.622
##	422	72	1	0.524	0.04277	0.447	0.615
##	456	71	1	0.517	0.04280	0.439	0.608
##	466	70	1	0.509	0.04282	0.432	0.600
##	467	69	1	0.502	0.04283	0.425	0.593
##	481	68	1	0.494	0.04284	0.417	0.586
##	486	67	1	0.487	0.04283	0.410	0.579
##	487	66	1	0.480	0.04281	0.403	0.571
##	526	65	1	0.472	0.04278	0.396	0.564
##	606	63	1	0.465	0.04275	0.388	0.557
##	609	62	1	0.457	0.04272	0.381	0.549
##	625	61	1	0.450	0.04267	0.374	0.542
##	641	60	1	0.442	0.04261	0.366	0.534
##	662	59	1	0.435	0.04254	0.359	0.527
##	677	58	1	0.427	0.04247	0.352	0.519
##	704	57	1	0.420	0.04238	0.345	0.512
##	748	56	1	0.412	0.04228	0.337	0.504
##	1063	47	1	0.404	0.04228	0.329	0.496

```
## 1074      46      1    0.395 0.04226      0.320      0.487
## 2204      9      1    0.351 0.05587      0.257      0.479
```

2. How do patients in different disease groups or in different FAB classifications compare to each other with respect to other available baseline measurements?

```
baseline_vars <- c("age", "donorage", "waittime")
cat_vars <- c("male", "cmv", "donormale", "donorcmv", "mtx")
# do hospital on its own since it is 4 categories

group_summary <- bmt %>%
  group_by(disgroup) %>%
  summarise(n = n(), across(all_of(baseline_vars), list(mean = mean, sd = sd, median = median), na.rm = TRUE),
    across(all_of(cat_vars), ~ mean(. == 1, na.rm = TRUE) * 100, .names = "percent_{.col}"),
    percent_Ohio=mean(hospital == 1, na.rm = TRUE) * 100,
    percent_Melbourne=mean(hospital == 2, na.rm = TRUE) * 100,
    percent_Sydney=mean(hospital == 3, na.rm = TRUE) * 100,
    percent_Philadelphia=mean(hospital == 4, na.rm = TRUE) * 100) %>%
  mutate(disgroup=case_when(disgroup==1 ~ "ALL",
    disgroup==2 ~ "Low risk AML",
    disgroup==3 ~ "High risk AML"))
```

```
## Warning: There was 1 warning in 'summarise()'.
## i In argument: 'across(...)'.
```

```
## i In group 1: 'disgroup = 1'.
```

```
## Caused by warning:
```

```
## ! The '...' argument of 'across()' is deprecated as of dplyr 1.1.0.
```

```
## Supply arguments directly to '.fns' through an anonymous function instead.
```

```
##
```

```
## # Previously
```

```
## across(a:b, mean, na.rm = TRUE)
```

```
##
```

```
## # Now
```

```
## across(a:b, \(x) mean(x, na.rm = TRUE))
```

```
kable(group_summary, caption = "Baseline Summary by Disease Group (disgroup)")
```

Table 1: Baseline Summary by Disease Group (disgroup)

disgroup	age	age_sd	age_median	donorage	donorage_sd	donorage_median	waittime	waittime_sd	waittime_median	male	cmv	donormale	donormale_sd	donormale_median	donorcmv	donorcmv_sd	donorcmv_median	mtx	percent_Ohio	percent_Melbourne	percent_Sydney	percent_Philadelphia
ALL	38	24.42	21.05	22.23	26.78	9.47	32.06	5.50	47.71	50.85	50.95	68.42	10.54	76.88	12.10	1.73	68.44	7.35	42.63	21.05	23.26	84.00
Low risk AML	54	29.40	27.16	29.17	28.07	4.07	44.28	8.85	138.05	56.48	190.0	55.55	15.61	46.25	96.29	10.74	72.22	30.20	90.05	59.25	12.96	27.77
High risk AML	45	30.44	14.22	20.02	29.93	13.30	52.93	8.38	268.86	17.70	108.0	53.33	33.00	00.00	22.22	22.22	22.44	62.22	28.88	15.55	56.33	33.33

```
# Continuous variables - ANOVA or Kruskal-Wallis  
kruskal.test(age ~ disgroup, data = bmt)
```

```
##  
## Kruskal-Wallis rank sum test  
##  
## data: age by disgroup  
## Kruskal-Wallis chi-squared = 10.486, df = 2, p-value = 0.005284
```

```
kruskal.test(donorage ~ disgroup, data = bmt)
```

```
##  
## Kruskal-Wallis rank sum test  
##  
## data: donorage by disgroup  
## Kruskal-Wallis chi-squared = 2.4723, df = 2, p-value = 0.2905
```

```
kruskal.test(waittime ~ disgroup, data = bmt)
```

```
##  
## Kruskal-Wallis rank sum test  
##  
## data: waittime by disgroup  
## Kruskal-Wallis chi-squared = 26.105, df = 2, p-value = 2.145e-06
```

```
# Categorical variables - Chi-square test  
table_male <- table(bmt$male, bmt$disgroup)  
chisq.test(table_male)
```

```
##  
## Pearson's Chi-squared test  
##  
## data: table_male  
## X-squared = 2.226, df = 2, p-value = 0.3286
```

```
table_cmv <- table(bmt$cmv, bmt$disgroup)  
chisq.test(table_cmv)
```

```
##  
## Pearson's Chi-squared test  
##  
## data: table_cmv  
## X-squared = 3.5512, df = 2, p-value = 0.1694
```

```
table_hospital <- table(bmt$hospital, bmt$disgroup)  
fisher.test(table_hospital)
```

```
##  
## Fisher's Exact Test for Count Data
```

```
table_mtx <- table(bmt$mtx, bmt$disgroup)
chisq.test(table_mtx)
```

```
fab_summary <- bmt %>%
  group_by(fab) %>%
  summarise(n = n(), across(all_of(baseline_vars), list(mean = mean, sd = sd, median = median), na.rm =
    across(all_of(cat_vars), ~ mean(. == 1, na.rm = TRUE) * 100, .names = "percent_{.col}"),
    percent_Ohio=mean(hospital == 1, na.rm = TRUE) * 100,
    percent_Melbourne=mean(hospital == 2, na.rm = TRUE) * 100,
    percent_Sydney=mean(hospital == 3, na.rm = TRUE) * 100,
    percent_Philadelphia=mean(hospital == 4, na.rm = TRUE) * 100) %>%
  mutate(fab=case_when(fab==0 ~ "Otherwise",
    fab==1 ~ "FAB Grade 4 or 5 & AML"))

kable(fab_summary, caption = "Baseline Summary by FAB Classification (fab)")
```

fab	n	age	age <sub>2</sub>	age <sub>3</sub>	double	diagnose	diagnose <sub>2</sub>	diagnose <sub>3</sub>	attained	attained <sub>2</sub>	attained <sub>3</sub>	survived	survived <sub>2</sub>	survived <sub>3</sub>	comp	comp <sub>2</sub>	comp <sub>3</sub>	comp <sub>4</sub>	comp <sub>5</sub>	comp <sub>6</sub>	comp <sub>7</sub>	comp <sub>8</sub>	comp <sub>9</sub>	comp <sub>10</sub>	comp <sub>11</sub>	comp <sub>12</sub>	comp <sub>13</sub>	comp <sub>14</sub>	comp <sub>15</sub>	comp <sub>16</sub>	comp <sub>17</sub>	comp <sub>18</sub>	comp <sub>19</sub>	comp <sub>20</sub>	comp <sub>21</sub>	comp <sub>22</sub>	comp <sub>23</sub>	comp <sub>24</sub>	comp <sub>25</sub>	comp <sub>26</sub>	comp <sub>27</sub>	comp <sub>28</sub>	comp <sub>29</sub>	comp <sub>30</sub>	comp <sub>31</sub>	comp <sub>32</sub>	comp <sub>33</sub>	comp <sub>34</sub>	comp <sub>35</sub>	comp <sub>36</sub>	comp <sub>37</sub>	comp <sub>38</sub>	comp <sub>39</sub>	comp <sub>40</sub>	comp <sub>41</sub>	comp <sub>42</sub>	comp <sub>43</sub>	comp <sub>44</sub>	comp <sub>45</sub>	comp <sub>46</sub>	comp <sub>47</sub>	comp <sub>48</sub>	comp <sub>49</sub>	comp <sub>50</sub>	comp <sub>51</sub>	comp <sub>52</sub>	comp <sub>53</sub>	comp <sub>54</sub>	comp <sub>55</sub>	comp <sub>56</sub>	comp <sub>57</sub>	comp <sub>58</sub>	comp <sub>59</sub>	comp <sub>60</sub>	comp <sub>61</sub>	comp <sub>62</sub>	comp <sub>63</sub>	comp <sub>64</sub>	comp <sub>65</sub>	comp <sub>66</sub>	comp <sub>67</sub>	comp <sub>68</sub>	comp <sub>69</sub>	comp <sub>70</sub>	comp <sub>71</sub>	comp <sub>72</sub>	comp <sub>73</sub>	comp <sub>74</sub>	comp <sub>75</sub>	comp <sub>76</sub>	comp <sub>77</sub>	comp <sub>78</sub>	comp <sub>79</sub>	comp <sub>80</sub>	comp <sub>81</sub>	comp <sub>82</sub>	comp <sub>83</sub>	comp <sub>84</sub>	comp <sub>85</sub>	comp <sub>86</sub>	comp <sub>87</sub>	comp <sub>88</sub>	comp <sub>89</sub>	comp <sub>90</sub>	comp <sub>91</sub>	comp <sub>92</sub>	comp <sub>93</sub>	comp <sub>94</sub>	comp <sub>95</sub>	comp <sub>96</sub>	comp <sub>97</sub>	comp <sub>98</sub>	comp <sub>99</sub>	comp <sub>100</sub>	comp <sub>101</sub>	comp <sub>102</sub>	comp <sub>103</sub>	comp <sub>104</sub>	comp <sub>105</sub>	comp <sub>106</sub>	comp <sub>107</sub>	comp <sub>108</sub>	comp <sub>109</sub>	comp <sub>110</sub>	comp <sub>111</sub>	comp <sub>112</sub>	comp <sub>113</sub>	comp <sub>114</sub>	comp <sub>115</sub>	comp <sub>116</sub>	comp <sub>117</sub>	comp <sub>118</sub>	comp <sub>119</sub>	comp <sub>120</sub>	comp <sub>121</sub>	comp <sub>122</sub>	comp <sub>123</sub>	comp <sub>124</sub>	comp <sub>125</sub>	comp <sub>126</sub>	comp <sub>127</sub>	comp <sub>128</sub>	comp <sub>129</sub>	comp <sub>130</sub>	comp <sub>131</sub>	comp <sub>132</sub>	comp <sub>133</sub>	comp <sub>134</sub>	comp <sub>135</sub>	comp <sub>136</sub>	comp <sub>137</sub>	comp <sub>138</sub>	comp <sub>139</sub>	comp <sub>140</sub>	comp <sub>141</sub>	comp <sub>142</sub>	comp <sub>143</sub>	comp <sub>144</sub>	comp <sub>145</sub>	comp <sub>146</sub>	comp <sub>147</sub>	comp <sub>148</sub>	comp <sub>149</sub>	comp <sub>150</sub>	comp <sub>151</sub>	comp <sub>152</sub>	comp <sub>153</sub>	comp <sub>154</sub>	comp <sub>155</sub>	comp <sub>156</sub>	comp <sub>157</sub>	comp <sub>158</sub>	comp <sub>159</sub>	comp <sub>160</sub>	comp <sub>161</sub>	comp <sub>162</sub>	comp <sub>163</sub>	comp <sub>164</sub>	comp <sub>165</sub>	comp <sub>166</sub>	comp <sub>167</sub>	comp <sub>168</sub>	comp <sub>169</sub>	comp <sub>170</sub>	comp <sub>171</sub>	comp <sub>172</sub>	comp <sub>173</sub>	comp <sub>174</sub>	comp <sub>175</sub>	comp <sub>176</sub>	comp <sub>177</sub>	comp <sub>178</sub>	comp <sub>179</sub>	comp <sub>180</sub>	comp <sub>181</sub>	comp <sub>182</sub>	comp <sub>183</sub>	comp <sub>184</sub>	comp <sub>185</sub>	comp <sub>186</sub>	comp <sub>187</sub>	comp <sub>188</sub>	comp <sub>189</sub>	comp <sub>190</sub>	comp <sub>191</sub>	comp <sub>192</sub>	comp <sub>193</sub>	comp <sub>194</sub>	comp <sub>195</sub>	comp <sub>196</sub>	comp <sub>197</sub>	comp <sub>198</sub>	comp <sub>199</sub>	comp <sub>200</sub>	comp <sub>201</sub>	comp <sub>202</sub>	comp <sub>203</sub>	comp <sub>204</sub>	comp <sub>205</sub>	comp <sub>206</sub>	comp <sub>207</sub>	comp <sub>208</sub>	comp <sub>209</sub>	comp <sub>210</sub>	comp <sub>211</sub>	comp <sub>212</sub>	comp <sub>213</sub>	comp <sub>214</sub>	comp <sub>215</sub>	comp <sub>216</sub>	comp <sub>217</sub>	comp <sub>218</sub>	comp <sub>219</sub>	comp <sub>220</sub>	comp <sub>221</sub>	comp <sub>222</sub>	comp <sub>223</sub>	comp <sub>224</sub>	comp <sub>225</sub>	comp <sub>226</sub>	comp <sub>227</sub>	comp <sub>228</sub>	comp <sub>229</sub>	comp <sub>230</sub>	comp <sub>231</sub>	comp <sub>232</sub>	comp <sub>233</sub>	comp <sub>234</sub>	comp <sub>235</sub>	comp <sub>236</sub>	comp <sub>237</sub>	comp <sub>238</sub>	comp <sub>239</sub>	comp <sub>240</sub>	comp <sub>241</sub>	comp <sub>242</sub>	comp <sub>243</sub>	comp <sub>244</sub>	comp <sub>245</sub>	comp <sub>246</sub>	comp <sub>247</sub>	comp <sub>248</sub>	comp <sub>249</sub>	comp <sub>250</sub>	comp <sub>251</sub>	comp <sub>252</sub>	comp <sub>253</sub>	comp <sub>254</sub>	comp <sub>255</sub>	comp <sub>256</sub>	comp <sub>257</sub>	comp <sub>258</sub>	comp <sub>259</sub>	comp <sub>260</sub>	comp <sub>261</sub>	comp <sub>262</sub>	comp <sub>263</sub>	comp <sub>264</sub>	comp <sub>265</sub>	comp <sub>266</sub>	comp <sub>267</sub>	comp <sub>268</sub>	comp <sub>269</sub>	comp <sub>270</sub>	comp <sub>271</sub>	comp <sub>272</sub>	comp <sub>273</sub>	comp <sub>274</sub>	comp <sub>275</sub>	comp <sub>276</sub>	comp <sub>277</sub>	comp <sub>278</sub>	comp <sub>279</sub>	comp <sub>280</sub>	comp <sub>281</sub>	comp <sub>282</sub>	comp <sub>283</sub>	comp <sub>284</sub>	comp <sub>285</sub>	comp <sub>286</sub>	comp <sub>287</sub>	comp <sub>288</sub>	comp <sub>289</sub>
-----	---	-----	------------------	------------------	--------	----------	-----------------------	-----------------------	----------	-----------------------	-----------------------	----------	-----------------------	-----------------------	------	-------------------	-------------------	-------------------	-------------------	-------------------	-------------------	-------------------	-------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	--------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	---------------------	-------------------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```
wilcox.test(donorage ~ fab, data = bmt)
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: donorage by fab
## W = 2212, p-value = 0.5164
## alternative hypothesis: true location shift is not equal to 0
```

```
wilcox.test(waittime ~ fab, data = bmt)
```

```
##
## Wilcoxon rank sum test with continuity correction
##
## data: waittime by fab
## W = 2244.5, p-value = 0.4244
## alternative hypothesis: true location shift is not equal to 0
```

```
# Categorical variables - Chi-square test
table_male_fab <- table(bmt$male, bmt$fab)
chisq.test(table_male_fab)
```

```
##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: table_male_fab
## X-squared = 0.43028, df = 1, p-value = 0.5119
```

```
table_cmv_fab <- table(bmt$cmv, bmt$fab)
chisq.test(table_cmv_fab)
```

```
##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: table_cmv_fab
## X-squared = 0.17943, df = 1, p-value = 0.6719
```

```
table_hospital_fab <- table(bmt$hospital, bmt$fab)
fisher.test(table_hospital_fab)
```

```
##
## Fisher's Exact Test for Count Data
##
## data: table_hospital_fab
## p-value = 0.2222
## alternative hypothesis: two.sided
```

```
table_mtx_fab <- table(bmt$mtx, bmt$fab)
chisq.test(table_mtx_fab)
```

```
##
## Pearson's Chi-squared test with Yates' continuity correction
##
## data: table_mtx_fab
## X-squared = 3.4444, df = 1, p-value = 0.06346
```



```

# table 1 by disease or FAB classification
bmt <- bmt %>%
  mutate(disgroupCat = factor(disgroup,
                                levels = c(1, 2, 3),
                                labels = c("All", "Low Risk AML", "High Risk AML")),
    maleCat = factor(male,
                      levels = c(0, 1),
                      labels = c("Female", "Male")),
    cmvCat = factor(cmv,
                     levels = c(0, 1),
                     labels = c("CMV Negative", "CMV Positive")),
    donormaleCat = factor(donormale,
                           levels = c(0, 1),
                           labels = c("Female Donor", "Male Donor")),
    donorcmvCat = factor(donorcmv,
                           levels = c(0, 1),
                           labels = c("CMV Negative Donor", "CMV Positive Donor")),
    fabCat = factor(fab,
                     levels = c(0, 1),
                     labels = c("Otherwise", "FAB Grade 4 or 5 and AML")),
    hospitalCat = factor(hospital,
                           levels = c(1, 2, 3, 4),
                           labels = c("OSU", "Alfred", "St. Vincent", "Hahnemann")),
    mtxCat = factor(mtx,
                     levels = c(0, 1),
                     labels = c("No", "Yes")),
    deltasCat = factor(deltas,
                        levels = c(0, 1),
                        labels = c("Alive", "Dead")),
    deltarCat = factor(deltar,
                        levels = c(0, 1),
                        labels = c("Disease-free", "Relapse")),
    deltadfsCat = factor(deltadfs,
                          levels = c(0, 1),
                          labels = c("Alive and Disease-free", "Dead or Relapsed")),
    deltaaCat = factor(deltaa,
                         levels = c(0, 1),
                         labels = c("No aGVHD", "aGVHD")),
    deltapCat = factor(deltap,
                        levels = c(0, 1),
                        labels = c("Not Recovered", "Recovered")))

label(bmt$deltarCat) <- "Replase"
label(bmt$deltasCat) <- "Death"
label(bmt$deltadfsCat) <- "Disease-free Survival"
label(bmt$deltaaCat) <- "aGVHD"
label(bmt$deltapCat) <- "Recovery of Normal Platelet Levels"
label(bmt$age) <- "Patient Age"
label(bmt$maleCat) <- "Patient Sex"
label(bmt$cmvCat) <- "Patient CMV Status"
label(bmt$donorage) <- "Donor Age"
label(bmt$donormaleCat) <- "Donor Sex"
label(bmt$donorcmvCat) <- "Donor CMV Status"

```

```

label(bmt$waittime) <- "Wait Time until Transplant (Days)"
label(bmt$fabCat) <- "Disease Subtype"
label(bmt$hospitalCat) <- "Recruitment Center"
label(bmt$mtxCat) <- "Prophylactic Methotrexate Use"

# by disease group
disgroup_tab1 <- table1(~ deltarCat + deltadfsCat + deltaaCat + deltasCat + deltapCat + age + donorage + waittime,
                        data = bmt,
                        caption = "Baseline Descriptive Statistics by Disease Group")
disgroup_tab1

```

```

# by fab classification
fab_tab1 <- table1(~ deltarCat + deltadfsCat + deltaaCat + deltasCat + deltapCat + age + donorage + waittime,
                  data = bmt,
                  caption = "Baseline Descriptive Statistics by FAB Classification")
fab_tab1

```

### 3. Are any of the measured baseline variables associated with differences in disease-free survival?

```

baseline_vars <- c("age", "maleCat", "cmvCat", "disgroupCat",
                  "donorage", "donormaleCat", "donorcmvCat",
                  "waittime", "hospitalCat", "mtxCat")

univariate_results <- lapply(baseline_vars, function(var) {
  formula <- as.formula(paste("dfs_surv ~", var))
  cox_model <- coxph(formula, data = bmt)
  result <- tidy(cox_model, conf.int = TRUE, exponentiate=TRUE) # Ensure confidence intervals are in
  result$variable <- var
  return(result)
})

univariate_results <- do.call(rbind, univariate_results)

colnames(univariate_results)

## [1] "term"      "estimate" "std.error" "statistic" "p.value"   "conf.low"
## [7] "conf.high" "variable"

univariate_results <- univariate_results[, c("variable", "term", "estimate", "conf.low", "conf.high", "p.value")]
kable(univariate_results, digits = 3, caption = "Univariate Cox Regression Results for Disease-Free Survival")

```

Table 3: Baseline Descriptive Statistics by Disease Group

	All	Low Risk AML	High Risk AML	Overall
	(N=38)	(N=54)	(N=45)	(N=137)
<b>Replase</b>				
Disease-free	26 (68.4%)	45 (83.3%)	24 (53.3%)	95 (69.3%)
Relapse	12 (31.6%)	9 (16.7%)	21 (46.7%)	42 (30.7%)
<b>Disease-free Survival</b>				
Alive and Disease-free	14 (36.8%)	29 (53.7%)	11 (24.4%)	54 (39.4%)
Dead or Relapsed	24 (63.2%)	25 (46.3%)	34 (75.6%)	83 (60.6%)
<b>aGVHD</b>				
No aGVHD	29 (76.3%)	43 (79.6%)	39 (86.7%)	111 (81.0%)
aGVHD	9 (23.7%)	11 (20.4%)	6 (13.3%)	26 (19.0%)
<b>Death</b>				
Alive	14 (36.8%)	31 (57.4%)	11 (24.4%)	56 (40.9%)
Dead	24 (63.2%)	23 (42.6%)	34 (75.6%)	81 (59.1%)
<b>Recovery of Normal Platelet Levels</b>				
Not Recovered	4 (10.5%)	6 (11.1%)	7 (15.6%)	17 (12.4%)
Recovered	34 (89.5%)	48 (88.9%)	38 (84.4%)	120 (87.6%)
<b>Patient Age</b>				
Mean (SD)	24.4 (7.30)	29.4 (8.76)	30.4 (11.2)	28.4 (9.56)
Median [Min, Max]	22.5 [15.0, 42.0]	29.5 [13.0, 50.0]	32.0 [7.00, 52.0]	28.0 [7.00, 52.0]
<b>Donor Age</b>				
Mean (SD)	26.8 (8.93)	28.1 (9.24)	29.9 (12.1)	28.3 (10.2)
Median [Min, Max]	26.0 [5.00, 48.0]	29.5 [12.0, 54.0]	29.0 [2.00, 56.0]	28.0 [2.00, 56.0]
<b>Wait Time until Transplant (Days)</b>				
Mean (SD)	477 (599)	138 (74.5)	269 (211)	275 (365)
Median [Min, Max]	200 [74.0, 2620]	120 [30.0, 450]	210 [24.0, 900]	178 [24.0, 2620]
<b>Patient Sex</b>				
Female	12 (31.6%)	24 (44.4%)	21 (46.7%)	57 (41.6%)
Male	26 (68.4%)	30 (55.6%)	24 (53.3%)	80 (58.4%)
<b>Patient CMV Status</b>				
CMV Negative	23 (60.5%)	28 (51.9%)	18 (40.0%)	69 (50.4%)
CMV Positive	15 (39.5%)	26 (48.1%)	27 (60.0%)	68 (49.6%)
<b>Recruitment Center</b>				
OSU	21 (55.3%)	27 (50.0%)	28 (62.2%)	76 (55.5%)
Alfred	8 (21.1%)	5 (9.3%)	4 (8.9%)	17 (12.4%)
St. Vincent	9 (23.7%)	7 (13.0%)	7 (15.6%)	23 (16.8%)
Hahnemann	0 (0%)	15 (27.8%)	6 (13.3%)	21 (15.3%)
<b>Prophylactic Methotrexate Use</b>				
No	21 (55.3%)	42 (77.8%)	34 (75.6%)	97 (70.8%)
Yes	17 (44.7%)	12 (22.2%)	11 (24.4%)	40 (29.2%)

Table 4: Baseline Descriptive Statistics by FAB Classification

	Otherwise (N=92)	FAB Grade 4 or 5 and AML (N=45)	Overall (N=137)
<b>Replase</b>			
Disease-free	72 (78.3%)	23 (51.1%)	95 (69.3%)
Relapse	20 (21.7%)	22 (48.9%)	42 (30.7%)
<b>Disease-free Survival</b>			
Alive and Disease-free	44 (47.8%)	10 (22.2%)	54 (39.4%)
Dead or Relapsed	48 (52.2%)	35 (77.8%)	83 (60.6%)
<b>aGVHD</b>			
No aGVHD	74 (80.4%)	37 (82.2%)	111 (81.0%)
aGVHD	18 (19.6%)	8 (17.8%)	26 (19.0%)
<b>Death</b>			
Alive	45 (48.9%)	11 (24.4%)	56 (40.9%)
Dead	47 (51.1%)	34 (75.6%)	81 (59.1%)
<b>Recovery of Normal Platelet Levels</b>			
Not Recovered	12 (13.0%)	5 (11.1%)	17 (12.4%)
Recovered	80 (87.0%)	40 (88.9%)	120 (87.6%)
<b>Patient Age</b>			
Mean (SD)	28.6 (9.48)	27.9 (9.81)	28.4 (9.56)
Median [Min, Max]	27.0 [13.0, 52.0]	28.0 [7.00, 50.0]	28.0 [7.00, 52.0]
<b>Donor Age</b>			
Mean (SD)	29.0 (9.67)	27.0 (11.1)	28.3 (10.2)
Median [Min, Max]	28.5 [5.00, 56.0]	28.0 [2.00, 48.0]	28.0 [2.00, 56.0]
<b>Wait Time until Transplant (Days)</b>			
Mean (SD)	309 (427)	206 (164)	275 (365)
Median [Min, Max]	180 [24.0, 2620]	150 [60.0, 780]	178 [24.0, 2620]
<b>Patient Sex</b>			
Female	36 (39.1%)	21 (46.7%)	57 (41.6%)
Male	56 (60.9%)	24 (53.3%)	80 (58.4%)
<b>Patient CMV Status</b>			
CMV Negative	48 (52.2%)	21 (46.7%)	69 (50.4%)
CMV Positive	44 (47.8%)	24 (53.3%)	68 (49.6%)
<b>Recruitment Center</b>			
OSU	48 (52.2%)	28 (62.2%)	76 (55.5%)
Alfred	14 (15.2%)	3 (6.7%)	17 (12.4%)
St. Vincent	18 (19.6%)	5 (11.1%)	23 (16.8%)
Hahnemann	12 (13.0%)	9 (20.0%)	21 (15.3%)
<b>Prophylactic Methotrexate Use</b>			
No	60 (65.2%)	37 (82.2%)	97 (70.8%)
Yes	32 (34.8%)	8 (17.8%)	40 (29.2%)

Table 5: Univariate Cox Regression Results for Disease-Free Survival

variable	term	estimate	conf.low	conf.high	p.value
age	age	1.011	0.988	1.035	0.338
maleCat	maleCatMale	0.795	0.514	1.228	0.301
cmvCat	cmvCatCMV Positive	1.167	0.759	1.796	0.482
disgroupCat	disgroupCatLow Risk AML	0.563	0.321	0.989	0.046
disgroupCat	disgroupCatHigh Risk AML	1.467	0.869	2.478	0.152
donorage	donorage	1.014	0.990	1.040	0.252
donormaleCat	donormaleCatMale Donor	0.991	0.633	1.552	0.970
donorcmvCat	donorcmvCatCMV Positive Donor	1.047	0.677	1.620	0.836
waittime	waittime	1.000	0.999	1.001	0.791
hospitalCat	hospitalCatAlfred	2.122	1.148	3.922	0.016
hospitalCat	hospitalCatSt. Vincent	0.912	0.495	1.681	0.768
hospitalCat	hospitalCatHahnemann	0.421	0.191	0.930	0.032
mtxCat	mtxCatYes	1.489	0.934	2.373	0.094

4. It is generally thought that aGVHD has an anti-leukemic effect. Based on the available data, is occurrence of aGVHD after transplantation associated with improved disease-free survival? Is it associated with a decreased risk of relapse? In view of this, do you consider aGVHD as an important prognostic event?

```
dfs_surv <- Surv(time = bmt$tdfs, event = bmt$deltadfs)

relapse_surv <- Surv(time = bmt$tdfs, event = bmt$deltar)

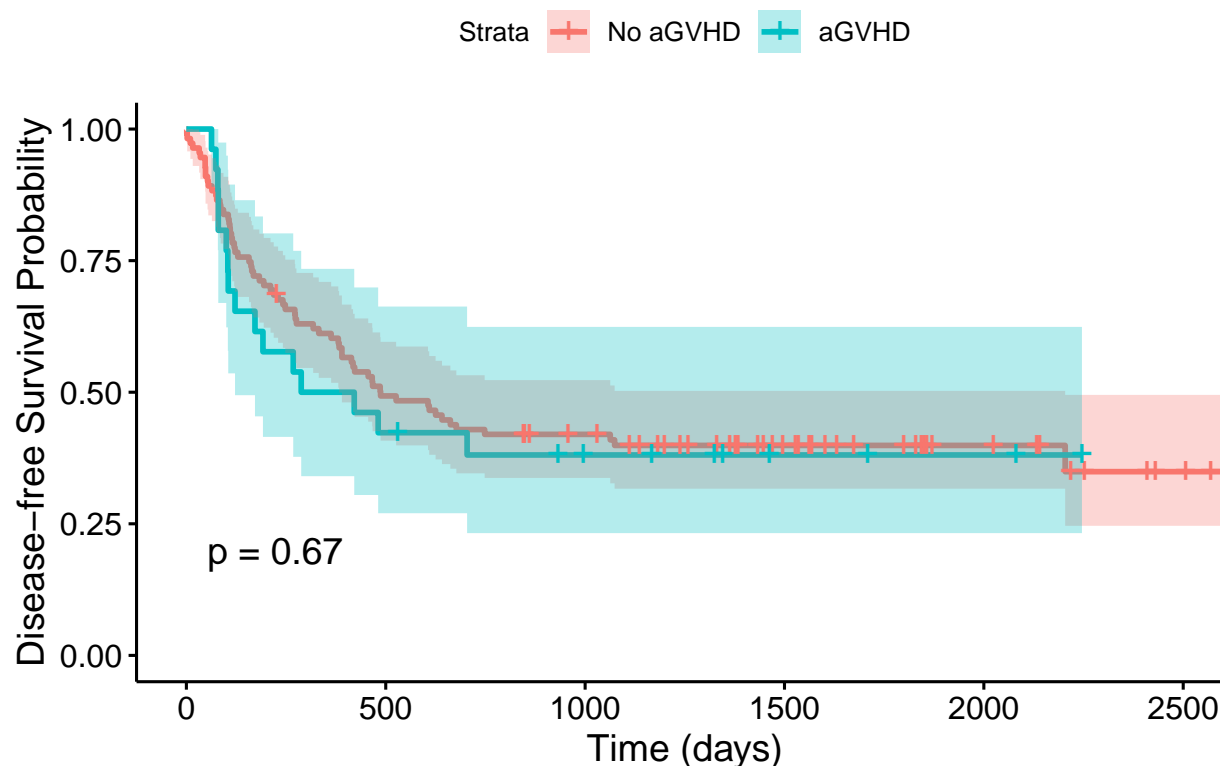
## univariate Cox for disease-free survival
cox_dfs_unadj <- coxph(dfs_surv ~ deltaa, data = bmt)
dfs_summary <- tidy(cox_dfs_unadj, conf.int = TRUE, exponentiate = TRUE)
dfs_summary
```

```
## # A tibble: 1 x 7
##   term      estimate std.error statistic p.value conf.low conf.high
##   <chr>      <dbl>    <dbl>    <dbl>   <dbl>   <dbl>    <dbl>
## 1 deltaa      1.13      0.279      0.428   0.668    0.653     1.94
```

```
km_dfs <- survfit(dfs_surv ~ deltaa, data = bmt)

ggsurvplot(km_dfs, conf.int = TRUE, pval = TRUE,
            xlab = "Time (days)",
            ylab = "Disease-free Survival Probability",
            legend.labs = c("No aGVHD", "aGVHD"),
            title = "Disease-free Survival by aGVHD Status")
```

## Disease-free Survival by aGVHD Status



```
## multivariable Cox for dfs
cox_dfs_adj <- coxph(dfs_surv ~ deltaa + age + as.factor(hospital) + male, data = bmt)
dfs_summary_adj <- tidy(cox_dfs_adj, conf.int = T, exponentiate = T)
dfs_summary_adj
```

```
## # A tibble: 6 x 7
##   term                estimate std.error statistic p.value conf.low conf.high
##   <chr>              <dbl>    <dbl>    <dbl>   <dbl>   <dbl>   <dbl>
## 1 deltaa              1.24      0.288     0.742  0.458    0.704    2.18
## 2 age                 1.02      0.0129    1.44   0.150    0.993    1.04
## 3 as.factor(hospital)2 1.88      0.328     1.93  0.0541    0.989    3.58
## 4 as.factor(hospital)3 0.805     0.325    -0.668  0.504    0.425    1.52
## 5 as.factor(hospital)4 0.342     0.423    -2.54  0.0112    0.149    0.783
## 6 male                0.828     0.234    -0.807  0.419    0.524    1.31
```

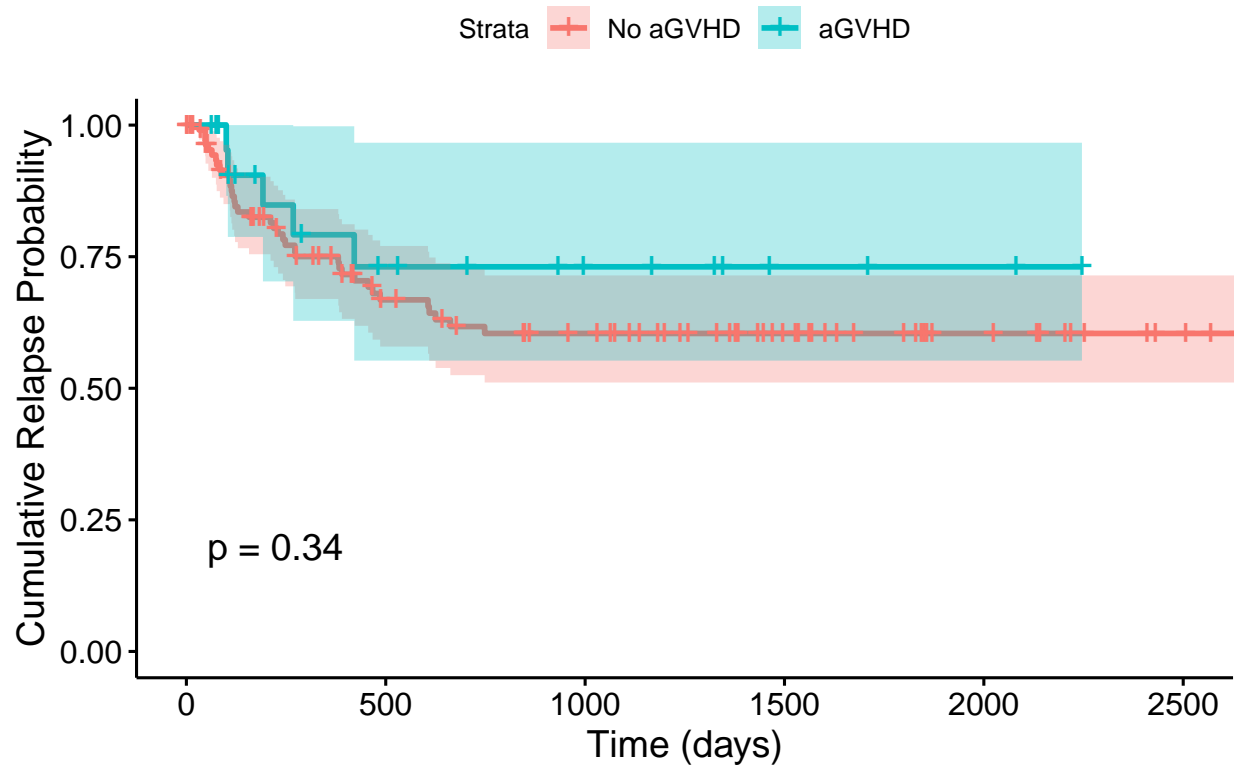
```
## univariate Cox for relapse
cox_relapse_unadj <- coxph(relapse_surv ~ deltaa, data = bmt)
relapse_summary <- tidy(cox_relapse_unadj, conf.int = TRUE, exponentiate=TRUE)
relapse_summary
```

```
## # A tibble: 1 x 7
##   term    estimate std.error statistic p.value conf.low conf.high
##   <chr>    <dbl>    <dbl>    <dbl>   <dbl>   <dbl>   <dbl>
## 1 deltaa   0.638     0.477    -0.944  0.345    0.250    1.62
```

```
km_relapse <- survfit(relapse_surv ~ deltaa, data = bmt)

ggsurvplot(km_relapse, conf.int = TRUE, pval = TRUE,
  xlab = "Time (days)",
  ylab = "Cumulative Relapse Probability",
  legend.labs = c("No aGVHD", "aGVHD"),
  title = "Relapse by aGVHD Status")
```

## Relapse by aGVHD Status



```
## multivariable Cox for relapse
cox_relapse_adj <- coxph(relapse_surv ~ deltaa + age + as.factor(hospital) + male, data = bmt)
relapse_summary_adj <- tidy(cox_relapse_adj, conf.int = T, exponentiate = T)
relapse_summary_adj
```

```
## # A tibble: 6 x 7
##   term                estimate std.error statistic p.value conf.low conf.high
##   <chr>                <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>
## 1 deltaa                0.682     0.491    -0.778    0.437    0.260    1.79
## 2 age                  1.01     0.0182    0.587    0.557    0.975    1.05
## 3 as.factor(hospital)2  1.21     0.555     0.350    0.726    0.409    3.60
## 4 as.factor(hospital)3  1.11     0.413     0.243    0.808    0.492    2.48
## 5 as.factor(hospital)4  0.588     0.513    -1.04     0.300    0.215    1.61
## 6 male                 0.673     0.320    -1.24     0.216    0.359    1.26
```

## 5. Among the patients who develop aGVHD, are any of the measured baseline factors associated with differences in disease-free survival?

```
bmt_agvhd <- subset(bmt, deltaa == 1)

dfs_surv_agvhd <- Surv(time = bmt_agvhd$tdfs, event = bmt_agvhd$deltadfs)

baseline_vars <- c("age", "maleCat", "cmvCat", "disgroupCat",
                  "donorage", "donormaleCat", "donorcmvCat",
                  "waittime", "hospitalCat", "mtxCat")

uni_agvhd <- lapply(baseline_vars, function(var) {
  formula <- as.formula(paste("dfs_surv_agvhd ~", var))
  cox_model <- coxph(formula, data = bmt_agvhd)
  result <- tidy(cox_model, conf.int = TRUE, exponentiate=TRUE)
  result$variable <- var
  return(result)
})

uni_agvhd <- do.call(rbind, uni_agvhd)

uni_agvhd <- uni_agvhd[, c("variable", "term", "estimate", "conf.low", "conf.high", "p.value")]
kable(uni_agvhd, digits = 3, caption = "Univariate Cox Regression Results for DFS (aGVHD Patients Only)")
```

Table 6: Univariate Cox Regression Results for DFS (aGVHD Patients Only)

variable	term	estimate	conf.low	conf.high	p.value
age	age	1.024	0.978	1.073	0.307
maleCat	maleCatMale	1.323	0.478	3.661	0.590
cmvCat	cmvCatCMV Positive	0.787	0.295	2.102	0.632
disgroupCat	disgroupCatLow Risk AML	1.450	0.424	4.966	0.554
disgroupCat	disgroupCatHigh Risk AML	3.854	1.022	14.531	0.046
donorage	donorage	1.072	0.996	1.153	0.063
donormaleCat	donormaleCatMale Donor	0.837	0.311	2.255	0.725
donorcmvCat	donorcmvCatCMV Positive Donor	1.878	0.647	5.453	0.247
waittime	waittime	1.000	1.000	1.001	0.375
hospitalCat	hospitalCatAlfred	1.147	0.251	5.239	0.859
hospitalCat	hospitalCatSt. Vincent	1.014	0.223	4.612	0.986
hospitalCat	hospitalCatHahnemann	0.118	0.015	0.929	0.042
mtxCat	mtxCatYes	1.718	0.551	5.350	0.351



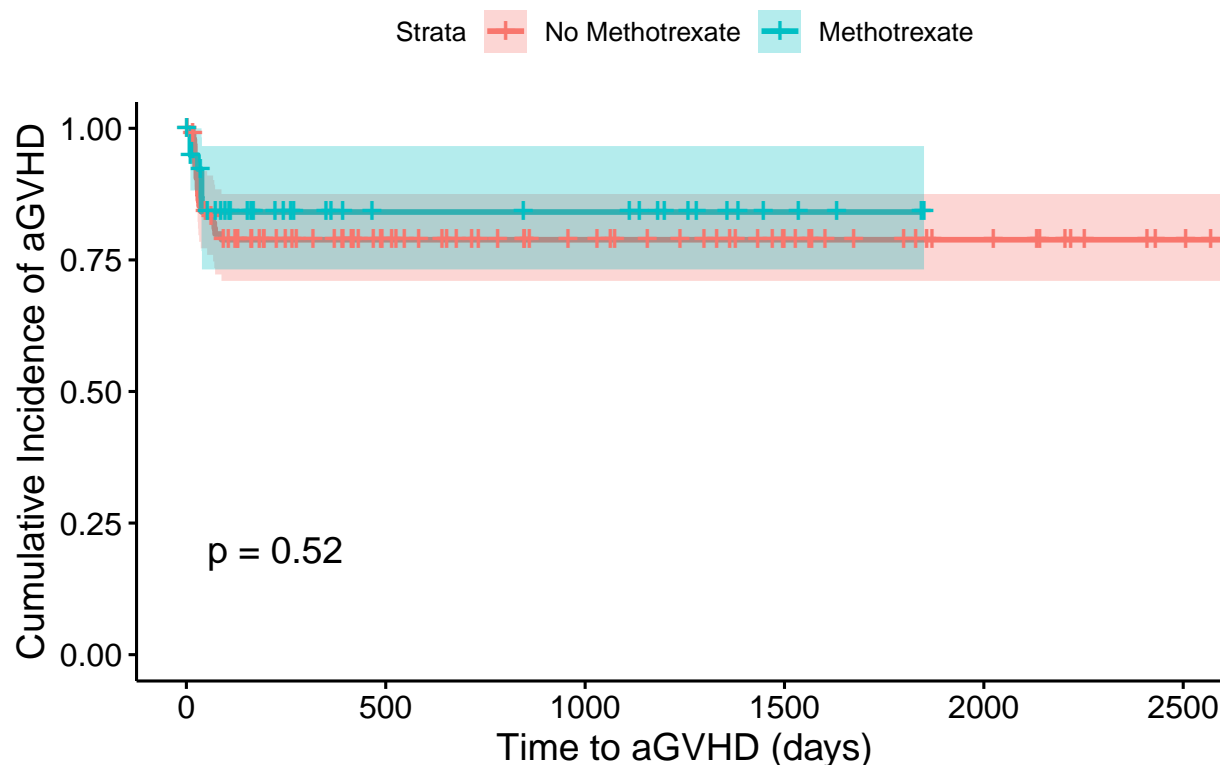
6. Is prophylactic use of methotrexate associated with an increased or decreased risk of developing aGVHD? Provide an estimate of the survival function of time from transplant until onset of aGVHD separately for patients either administered methotrexate or not. In doing so, consider the importance of accounting for relevant confounding factors.

```
agvhd_surv <- Surv(time = bmt$ta, event = bmt$deltaa)

## unadjusted KM
km_agvhd <- survfit(agvhd_surv ~ mtx, data = bmt)

ggsurvplot(km_agvhd, conf.int = TRUE, pval = TRUE,
  xlab = "Time to aGVHD (days)",
  ylab = "Cumulative Incidence of aGVHD",
  legend.labs = c("No Methotrexate", "Methotrexate"),
  title = "Time to aGVHD by Prophylactic Methotrexate Use")
```

Time to aGVHD by Prophylactic Methotrexate Use



```
## univariate Cox
cox_mtx <- coxph(agvhd_surv ~ mtx, data = bmt)
univariate_mtx <- tidy(cox_mtx, conf.int = TRUE, exponentiate=TRUE)
```

```
kable(univariate_mtx[, c("term", "estimate", "conf.low", "conf.high", "p.value")],
      digits = 3, caption = "Univariate Cox Regression: Methotrexate and aGVHD Risk")
```

Table 7: Univariate Cox Regression: Methotrexate and aGVHD Risk

term	estimate	conf.low	conf.high	p.value
mtx	0.742	0.298	1.847	0.521

```
## multivariable Cox w/ confounders
cox_adj <- coxph(agvhd_surv ~ mtx + age + maleCat + disgroupCat + waittime + hospitalCat, data = bmt)
multivariable_mtx <- tidy(cox_adj, conf.int = TRUE, exponentiate=TRUE)

kable(multivariable_mtx[, c("term", "estimate", "conf.low", "conf.high", "p.value")],
      digits = 3, caption = "Multivariable Cox Regression: Methotrexate and aGVHD Risk")
```

Table 8: Multivariable Cox Regression: Methotrexate and aGVHD Risk

term	estimate	conf.low	conf.high	p.value
mtx	0.470	0.131	1.682	0.246
age	1.074	1.027	1.123	0.002
maleCatMale	0.882	0.390	1.996	0.764
disgroupCatLow Risk AML	0.528	0.177	1.580	0.254
disgroupCatHigh Risk AML	0.303	0.093	0.986	0.047
waittime	1.000	0.999	1.001	0.470
hospitalCatAlfred	1.632	0.316	8.417	0.558
hospitalCatSt. Vincent	NA	NA	NA	NA
hospitalCatHahnemann	1.606	0.563	4.586	0.376

7. Based on the available data, is recovery of normal platelet levels associated with improved disease- free survival? Is it associated with a decreased risk of relapse?

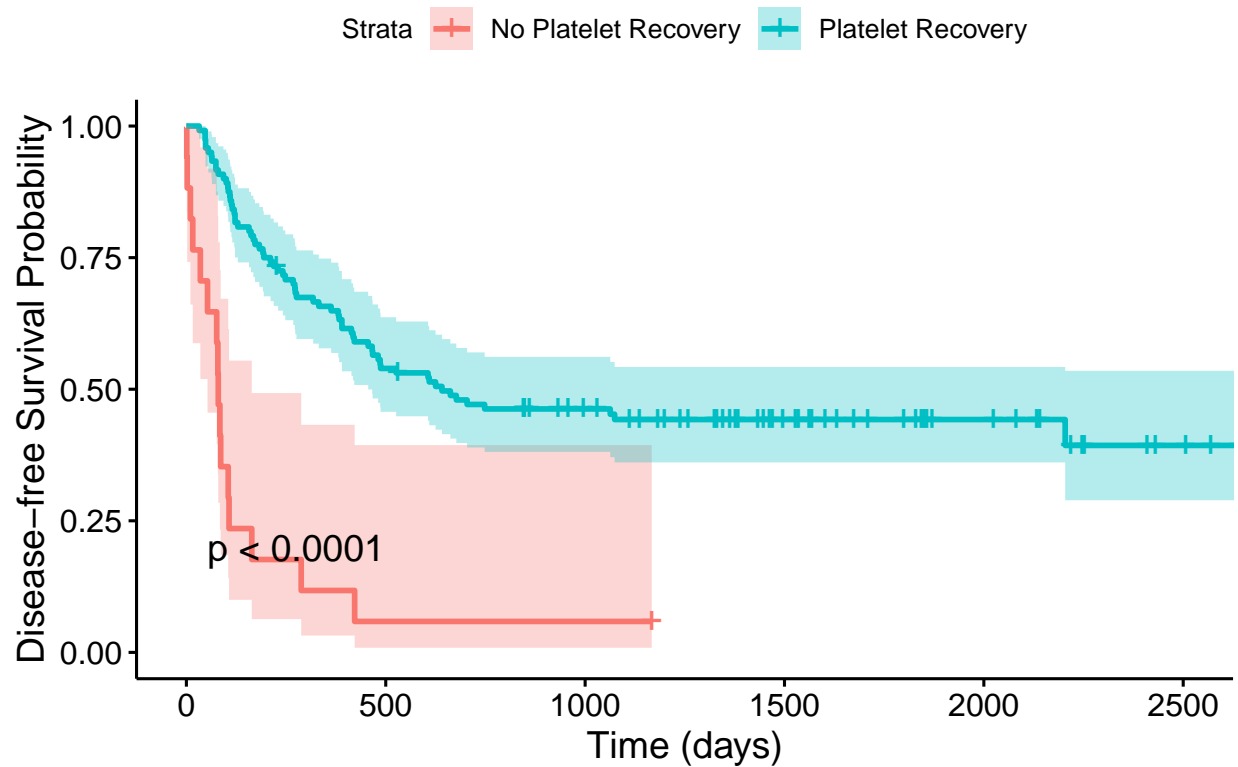
```
dfs_surv <- Surv(time = bmt$tdfs, event = bmt$deltadfs)

relapse_surv <- Surv(time = bmt$tdfs, event = bmt$deltar)

## KM for dfs
km_dfs <- survfit(dfs_surv ~ deltap, data = bmt)

ggsurvplot(km_dfs, conf.int = TRUE, pval = TRUE,
            xlab = "Time (days)",
            ylab = "Disease-free Survival Probability",
            legend.labs = c("No Platelet Recovery", "Platelet Recovery"),
            title = "Disease-free Survival by Platelet Recovery")
```

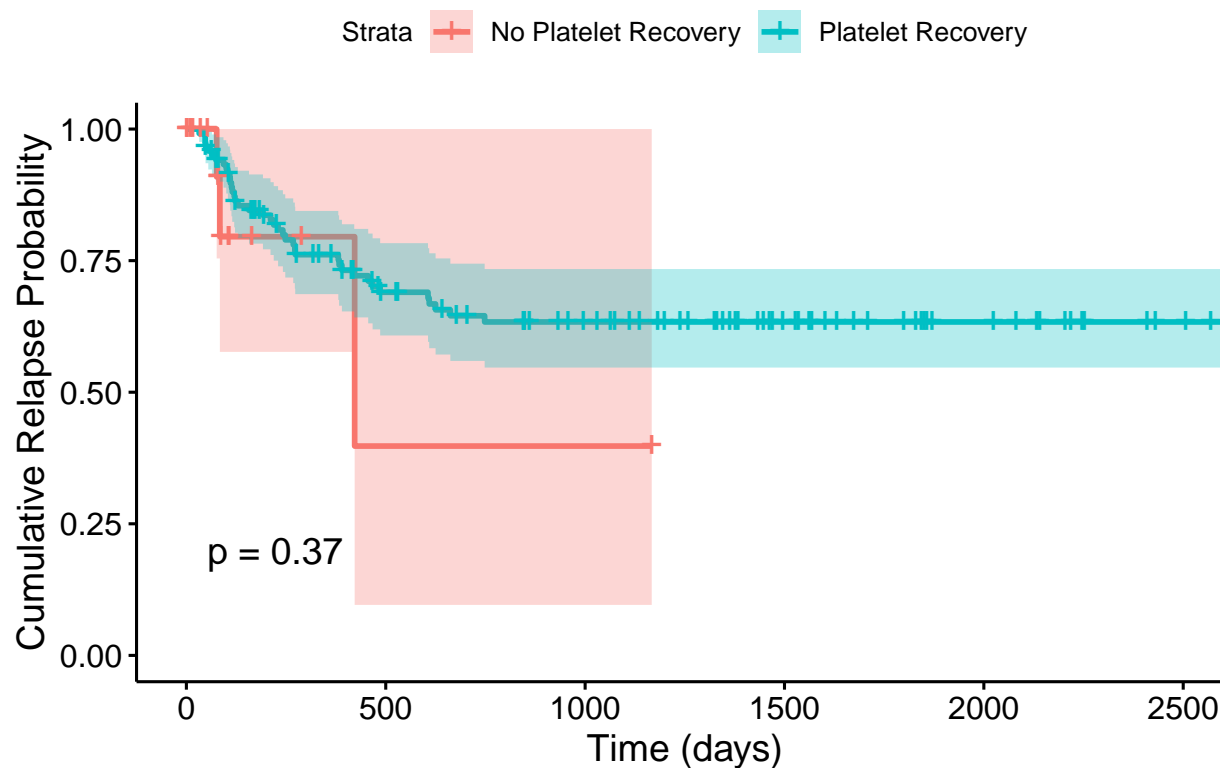
## Disease-free Survival by Platelet Recovery



```
## KM for relapse
km_relapse <- survfit(relapse_surv ~ deltap, data = bmt)

ggsurvplot(km_relapse, conf.int = TRUE, pval = TRUE,
  xlab = "Time (days)",
  ylab = "Cumulative Relapse Probability",
  legend.labs = c("No Platelet Recovery", "Platelet Recovery"),
  title = "Relapse by Platelet Recovery")
```

## Relapse by Platelet Recovery



```
## univariate Cox for dfs
cox_dfs <- coxph(dfs_surv ~ deltap, data = bmt)
cox_dfs

## Call:
## coxph(formula = dfs_surv ~ deltap, data = bmt)
##
##              coef exp(coef) se(coef)      z      p
## deltap -1.6729    0.1877   0.2884 -5.801 6.6e-09
##
## Likelihood ratio test=24.39  on 1 df, p=7.874e-07
## n= 137, number of events= 83
```

```
univariate_dfs <- tidy(cox_dfs, conf.int = TRUE, exponentiate=TRUE)

kable(univariate_dfs[, c("term", "estimate", "conf.low", "conf.high", "p.value")],
      digits = 3, caption = "Univariate Cox: Platelet Recovery and DFS")
```

Table 9: Univariate Cox: Platelet Recovery and DFS

term	estimate	conf.low	conf.high	p.value
deltap	0.188	0.107	0.33	0

```
## multivariable Cox for dfs
cox_dfs_adj <- coxph(dfs_surv ~ deltap + age + as.factor(hospital) + as.factor(disgroup) + male, data =
multi_dfs <- tidy(cox_dfs_adj, conf.int = T, exponentiate = T)

kable(multi_dfs[, c("term", "estimate", "conf.low", "conf.high", "p.value")],
      digits = 3, caption = "Multivariable Cox: Platelet Recovery and DFS")
```

Table 10: Multivariable Cox: Platelet Recovery and DFS

term	estimate	conf.low	conf.high	p.value
deltap	0.256	0.138	0.476	0.000
age	1.017	0.992	1.044	0.189
as.factor(hospital)2	1.347	0.662	2.739	0.411
as.factor(hospital)3	0.869	0.453	1.667	0.672
as.factor(hospital)4	0.477	0.206	1.102	0.083
as.factor(disgroup)2	0.702	0.375	1.312	0.267
as.factor(disgroup)3	1.496	0.835	2.680	0.176
male	0.928	0.580	1.484	0.756

```
## univariate Cox for relapse
cox_relapse <- coxph(relapse_surv ~ deltap, data = bmt)
univariate_relapse <- tidy(cox_relapse, conf.int = TRUE, exponentiate = TRUE)

kable(univariate_relapse[, c("term", "estimate", "conf.low", "conf.high", "p.value")],
      digits = 3, caption = "Univariate Cox: Platelet Recovery and Relapse Risk")
```

Table 11: Univariate Cox: Platelet Recovery and Relapse Risk

term	estimate	conf.low	conf.high	p.value
deltap	0.583	0.178	1.916	0.374

```
## multivariable Cox for relapse
cox_relapse_adj <- coxph(relapse_surv ~ deltap + age + as.factor(hospital) + + as.factor(disgroup) + mal
multi_relapse <- tidy(cox_relapse_adj, conf.int = T, exponentiate = T)

kable(multi_relapse[, c("term", "estimate", "conf.low", "conf.high", "p.value")],
      digits = 3, caption = "Multivariable Cox: Platelet Recovery and DFS")
```

Table 12: Multivariable Cox: Platelet Recovery and DFS

term	estimate	conf.low	conf.high	p.value
deltap	0.895	0.256	3.134	0.863
age	0.998	0.960	1.038	0.937
as.factor(hospital)2	1.100	0.359	3.374	0.868
as.factor(hospital)3	1.324	0.575	3.051	0.509
as.factor(hospital)4	0.783	0.274	2.241	0.649
as.factor(disgroup)2	0.415	0.163	1.057	0.065
as.factor(disgroup)3	1.836	0.821	4.106	0.139

term	estimate	conf.low	conf.high	p.value
male	0.637	0.335	1.213	0.170