

Bayesian parametric models for survival prediction in medical applications

Sample size calculation

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Setup

```
library(pwr)  
library(TOSTER)
```

Assumptions

- This study involves multiple testing of certain performance thresholds. Bonferroni correction is used to account for multiple testing.

Sample size for comparative experiments

```
sample_sd <- 0.025
mu_diff <- 0.02
n_comparisons <- 15

pwr.calc <- pwr.t.test(
  d = mu_diff / sample_sd,
  power = 0.8,
  sig.level = 0.05 / n_comparisons,
  type = 'two.sample',
  alternative = 'two.sided'
)

pwr.calc$n_comparisons <- n_comparisons
pwr.calc$n_adjusted <- pwr.calc$n * 1.15

pwr.calc
```

Two-sample t test power calculation

```
      n = 46.75793
      d = 0.8
sig.level = 0.003333333
power = 0.8
alternative = two.sided
n_comparisons = 15
n_adjusted = 53.77161
```

NOTE: n is number in *each* group

Sample size for model re-training

```
sample_sd <- 0.025
n_comparisons <- 3

pwr.calc <- power_t_TOST(
  n = NULL,
  delta = 0,
  sd = sample_sd,
  low_eqbound = -0.01,
  high_eqbound = 0.01,
  alpha = 0.05 / n_comparisons ,
  power = 0.8,
  type = "two.sided"
)

pwr.calc$n_comparisons <- n_comparisons
pwr.calc$n_adjusted <- pwr.calc$n * 1.15

pwr.calc
```

TOST power calculation

```
power = 0.8
beta = 0.2
alpha = 0.01666667
n = 74.95133
delta = 0
sd = 0.025
bounds = -0.01, 0.01
n_comparisons = 3
n_adjusted = 86.19403
```