

# How to Create One- and Multi-Arm Simulation Result Plots with rpact

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## Summary

This R Markdown document provides many different examples for creating one- and multi-arm as well as enrichment simulation result plots with rpact and ggplot2.

## 1 Preparation

First, load the rpact package

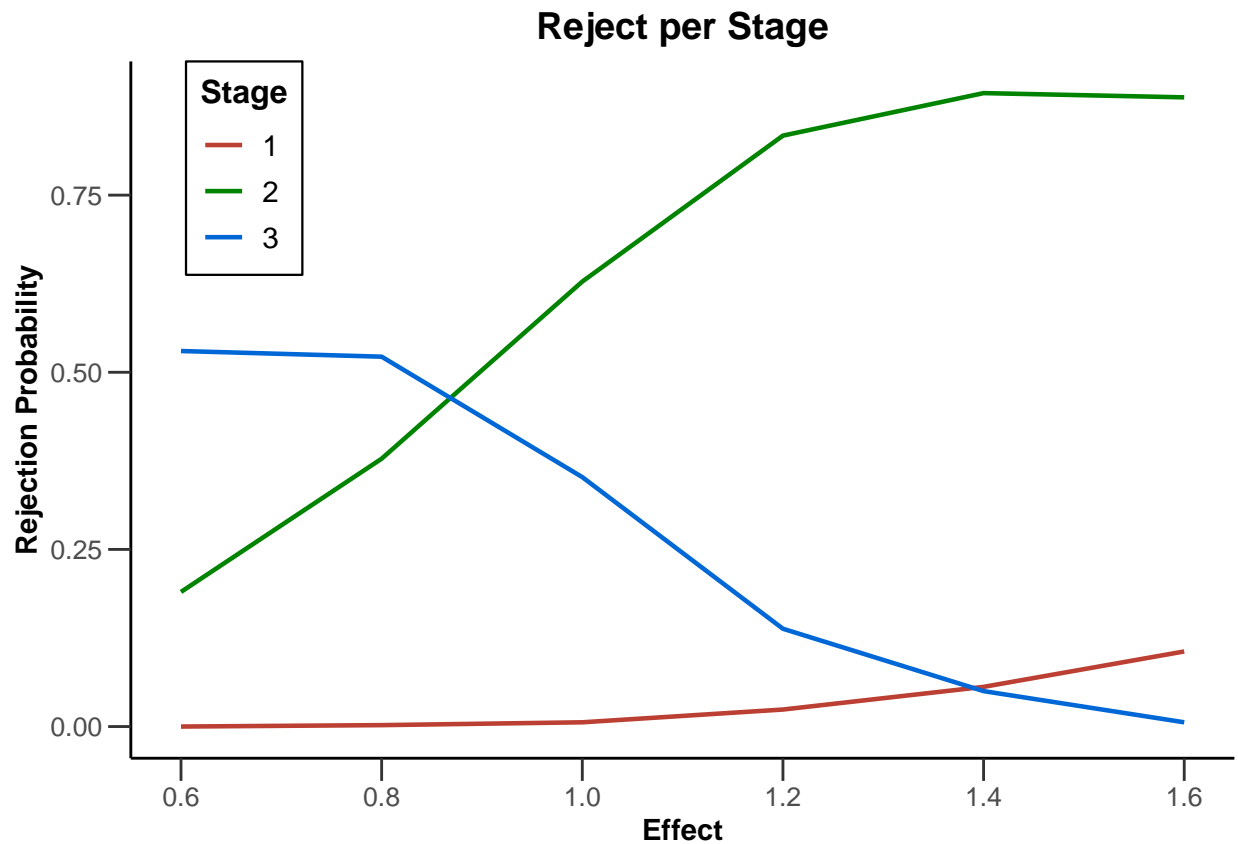
```
library(rpact)
packageVersion("rpact") # version should be version 3.0 or later

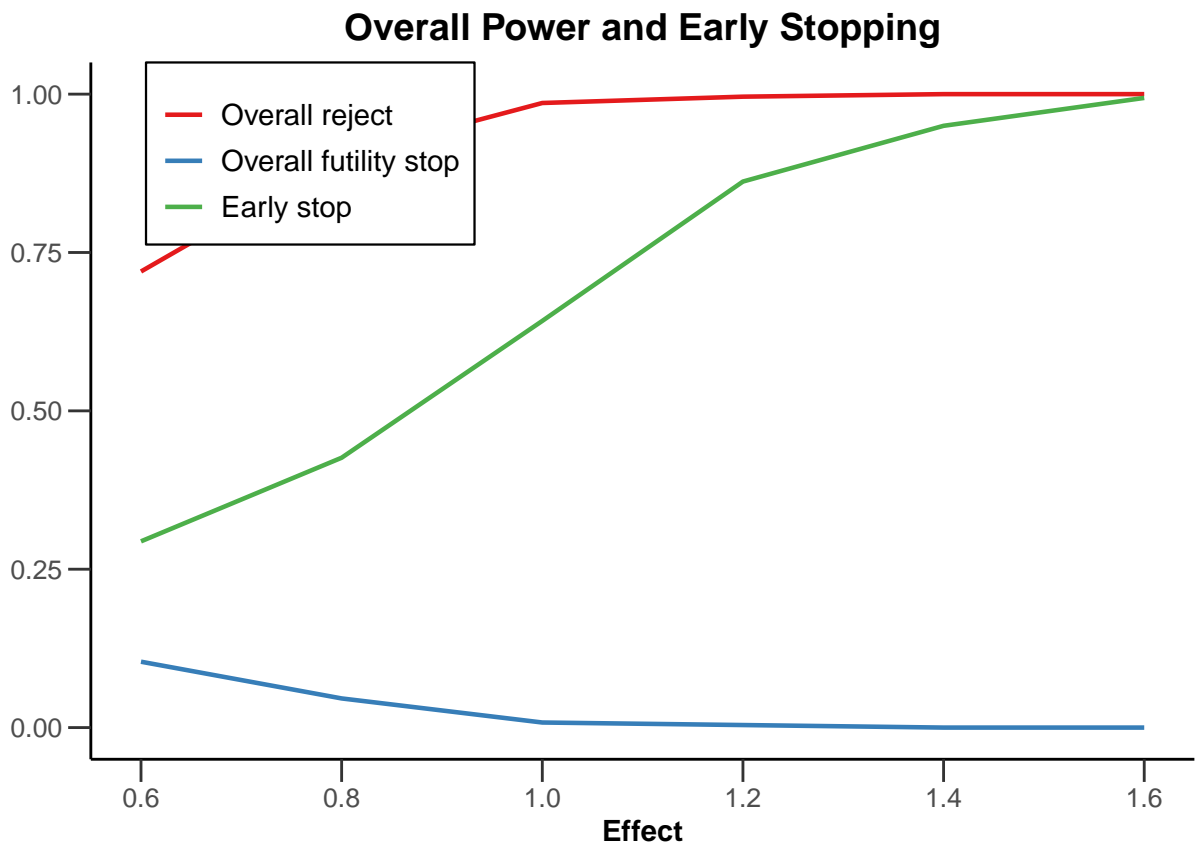
## [1] '3.3.2'
```

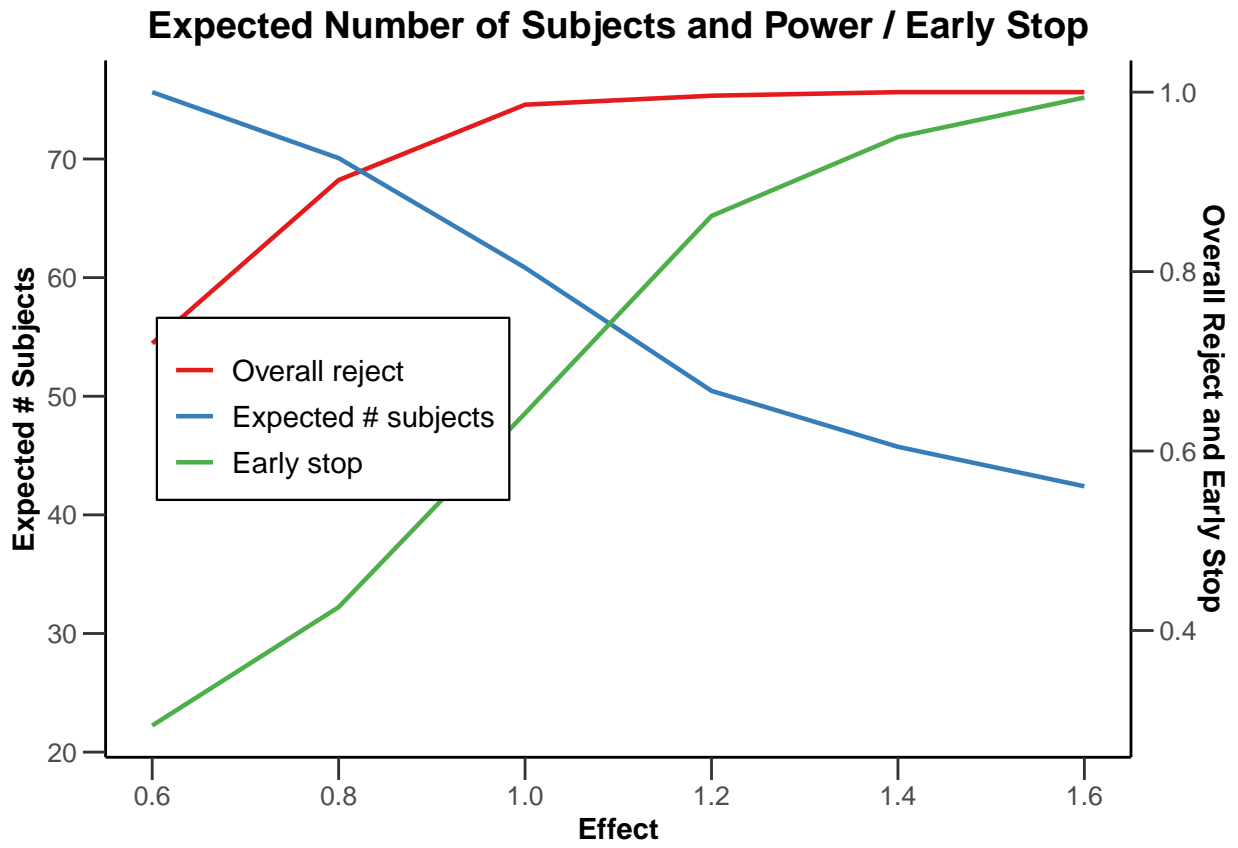
## 2 Simulation results base

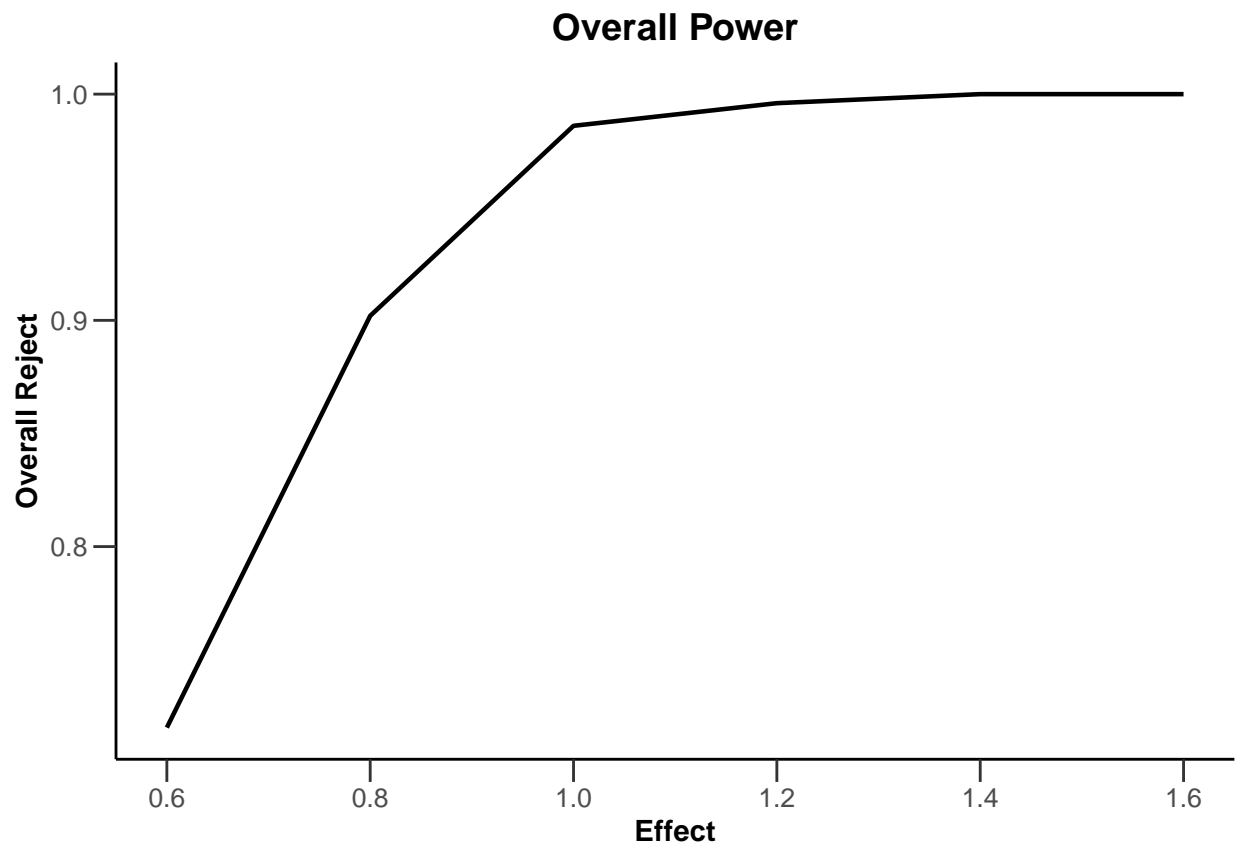
### 2.1 Simulation results base - means

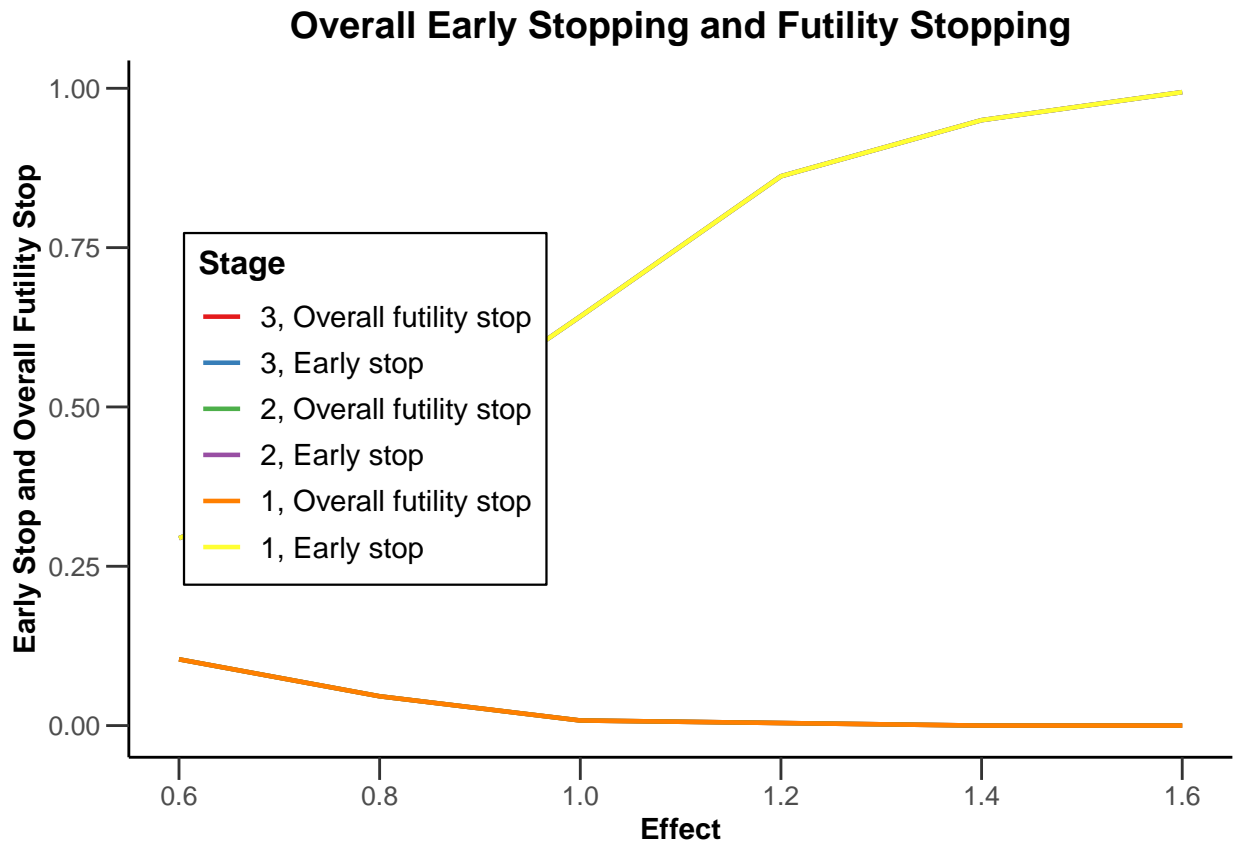
```
maxNumberOfSubjects <- 90
informationRates <- c(0.2, 0.5, 1)
plannedSubjects <- round(informationRates * maxNumberOfSubjects)
design <- getDesignInverseNormal(
  futilityBounds = c(-0.5, 0.5),
  informationRates = informationRates
)
x <- getSimulationMeans(
  design = design, groups = 2, meanRatio = TRUE,
  thetaH0 = 0.4, plannedSubjects = plannedSubjects,
  maxNumberOfIterations = 500, allocationRatioPlanned = 3,
  stDev = 1.5, seed = 1234567890
)
plot(x, type = "all", grid = 0)
```

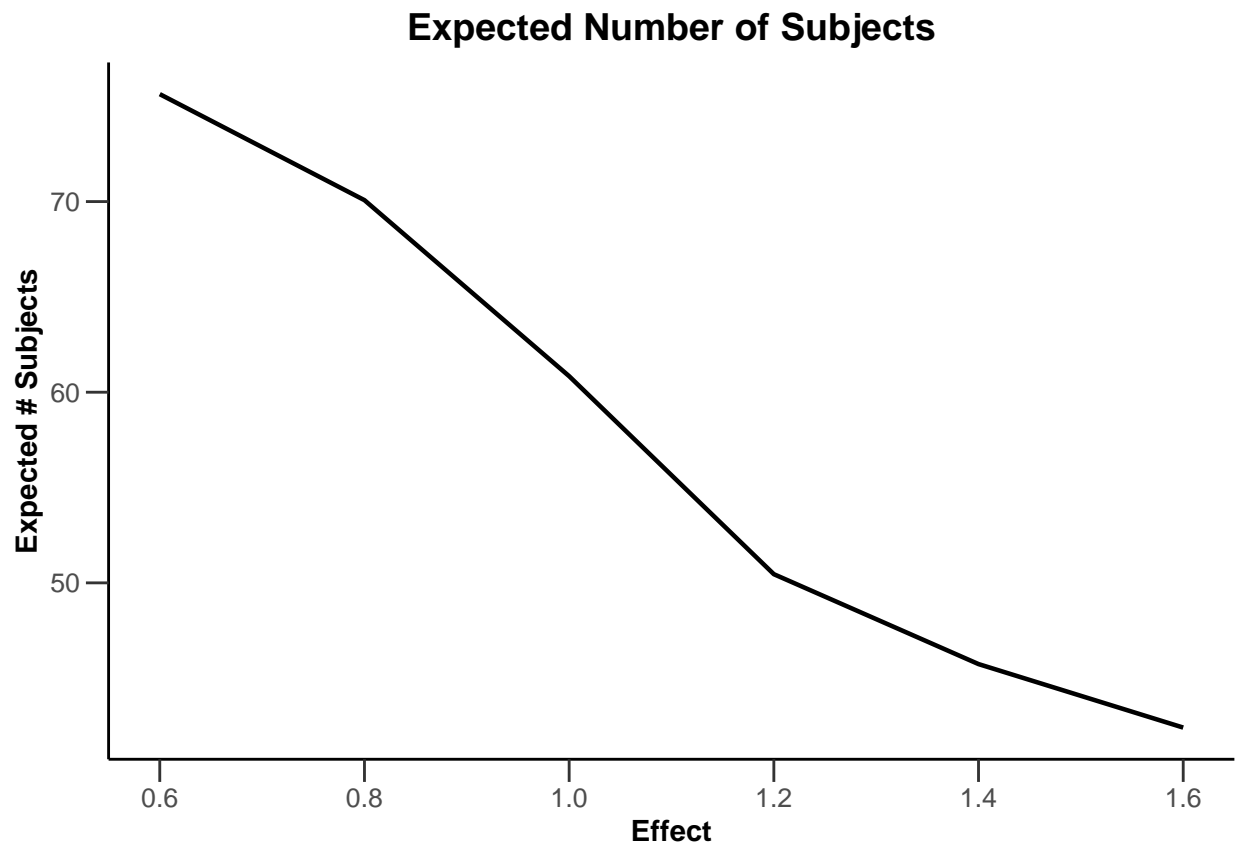






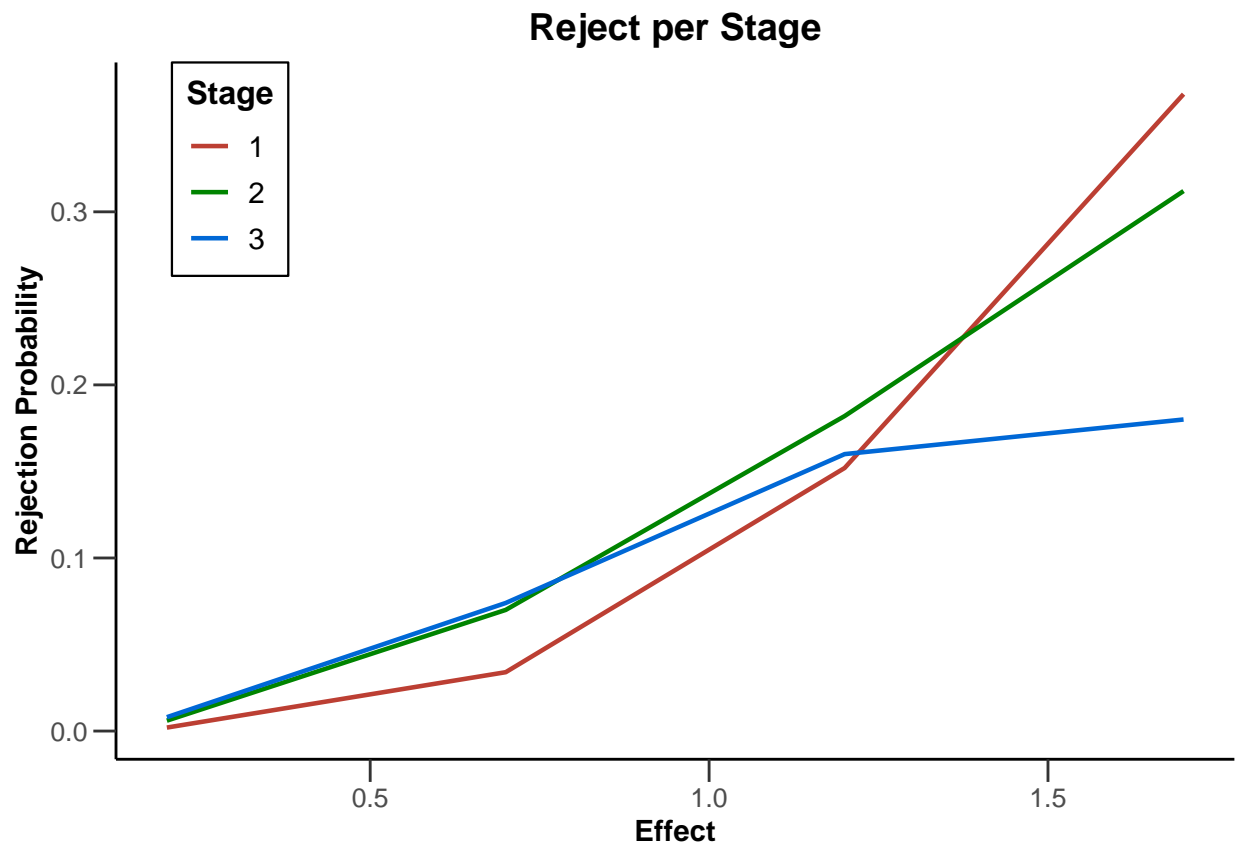




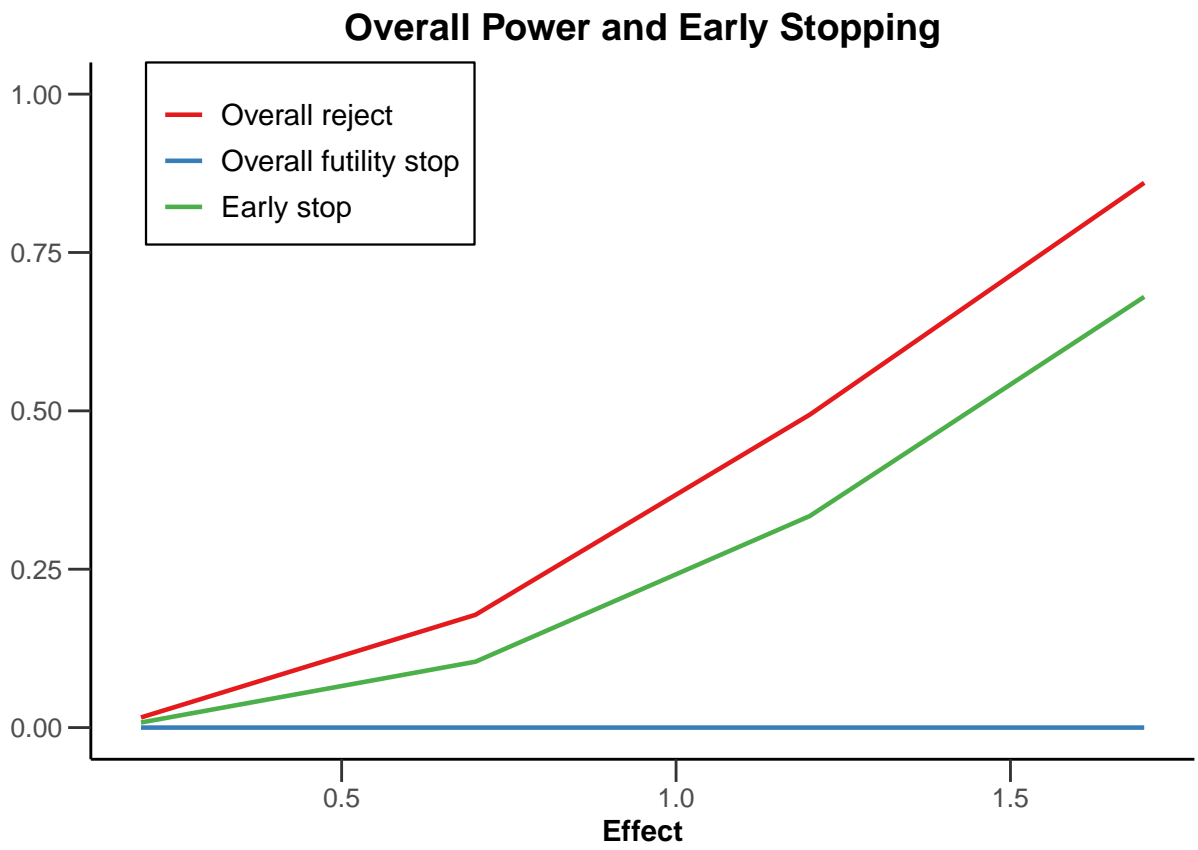


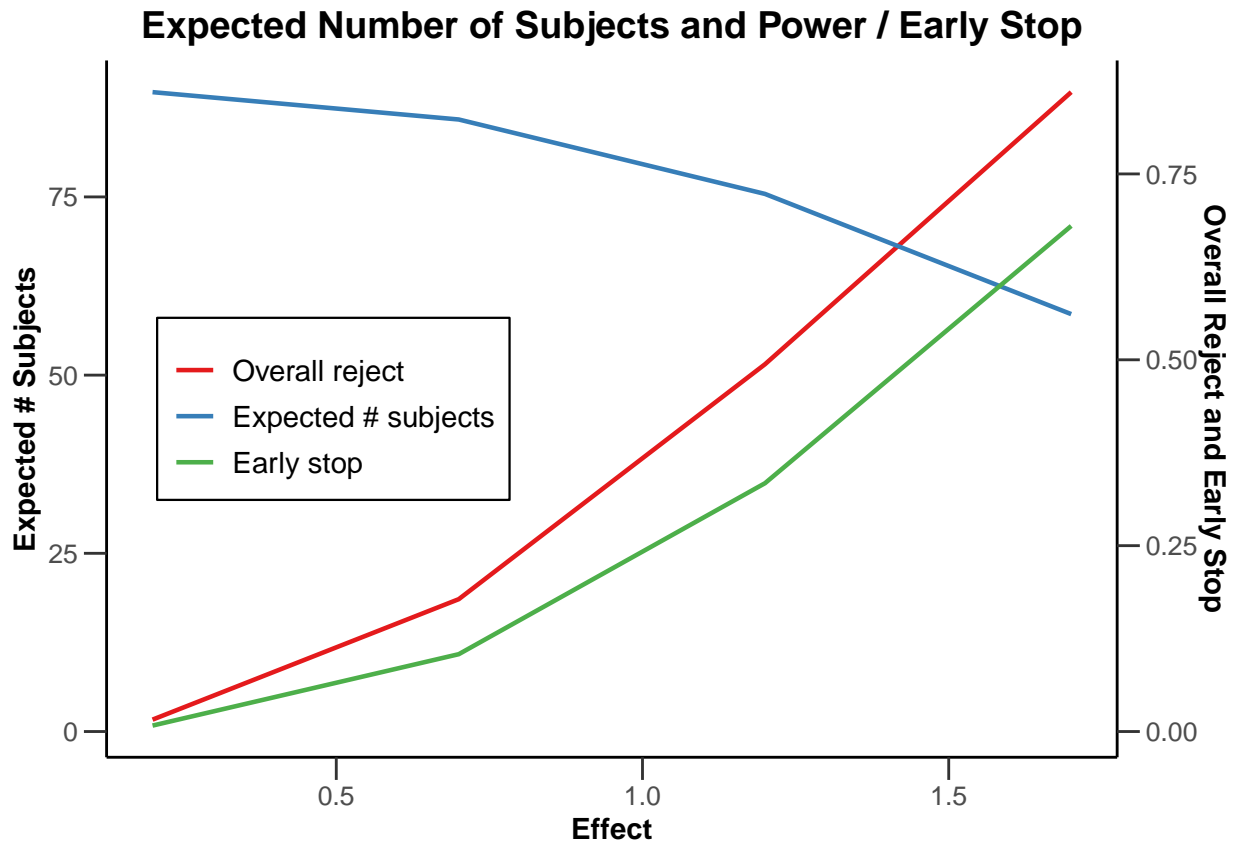
## 2.2 Simulation results base - rates

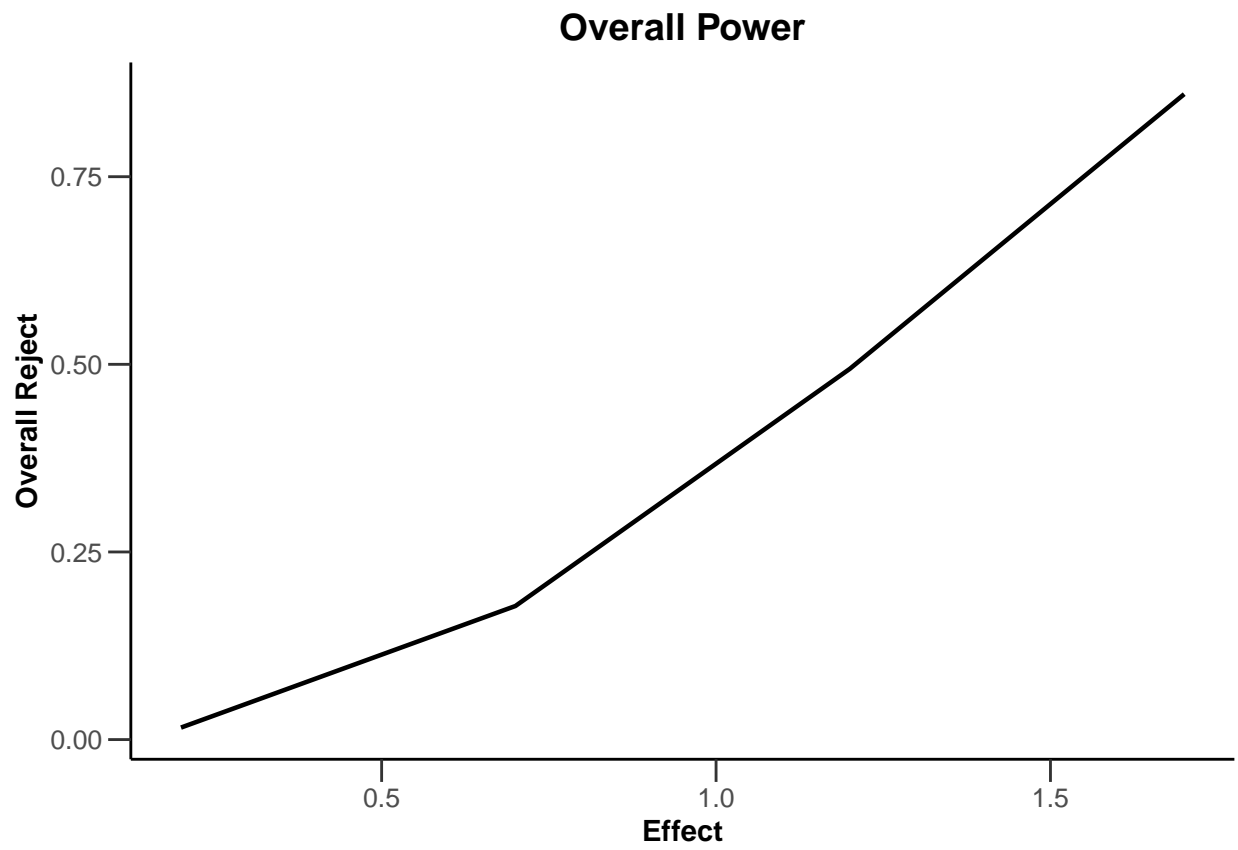
```
maxNumberOfSubjects <- 90
informationRates <- (1:3) / 3
plannedSubjects <- round(informationRates * maxNumberOfSubjects)
design <- getDesignInverseNormal(
  futilityBounds = c(-0.5, 0.5),
  informationRates = informationRates
)
x <- getSimulationRates(
  design = getDesignFisher(),
  groups = 2, riskRatio = TRUE,
  thetaH0 = 0.8, plannedSubjects = plannedSubjects,
  maxNumberOfIterations = 500, allocationRatioPlanned = 3,
  seed = 1234567890
)
plot(x, type = "all", grid = 0)
```

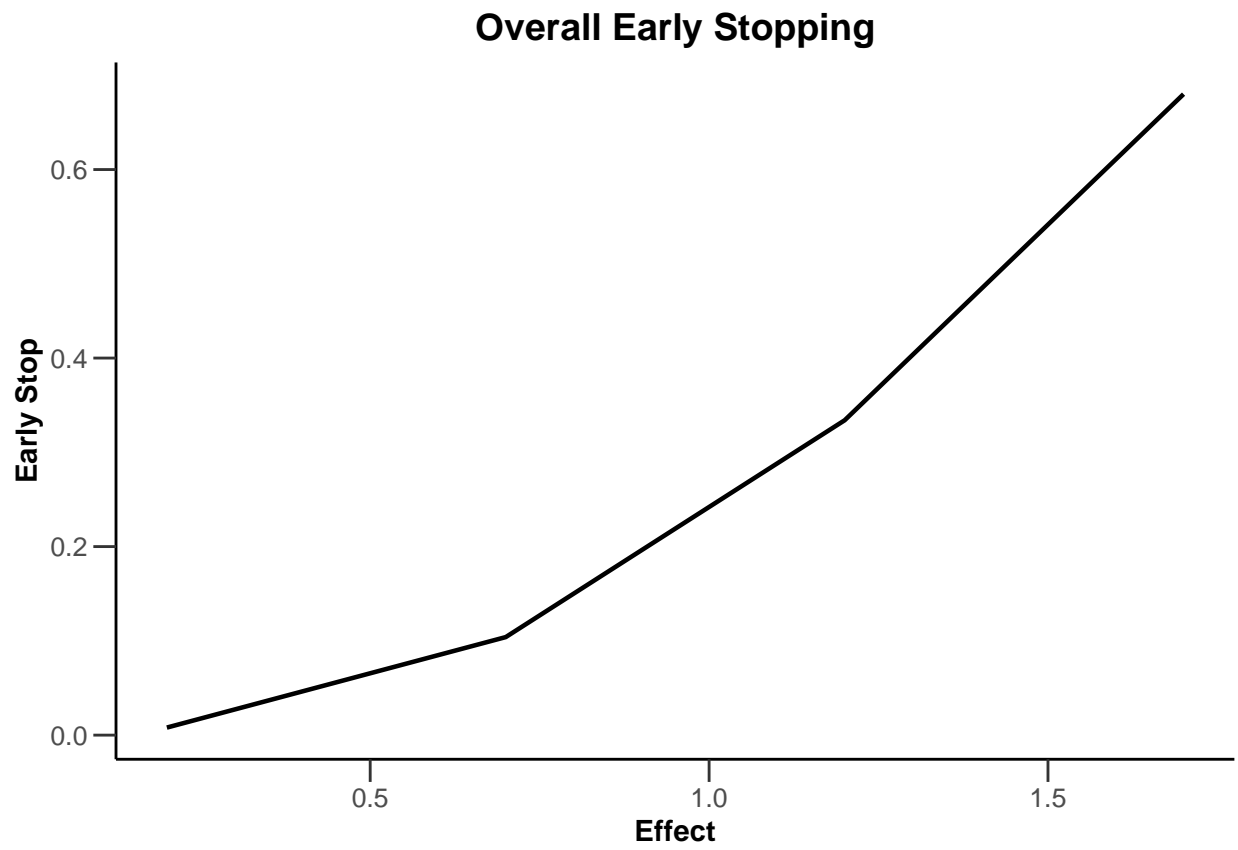


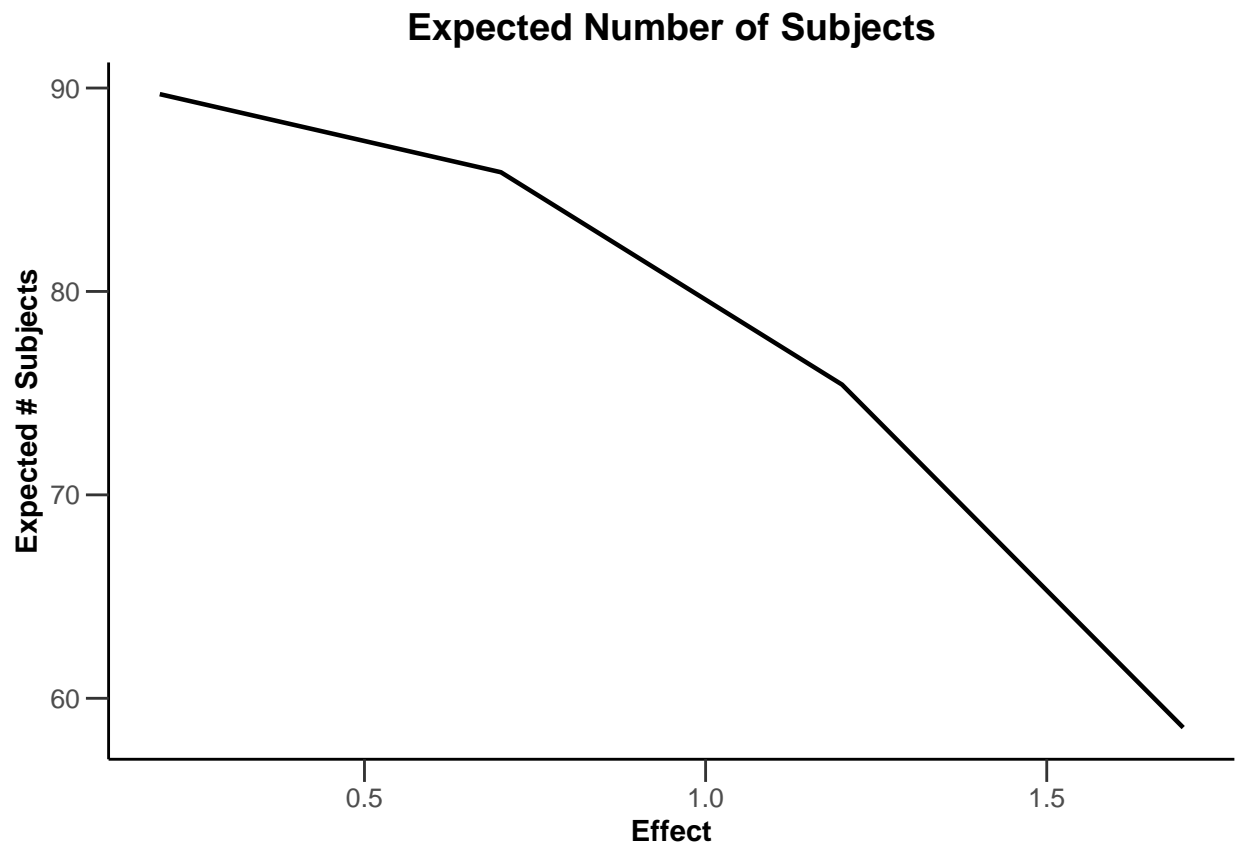










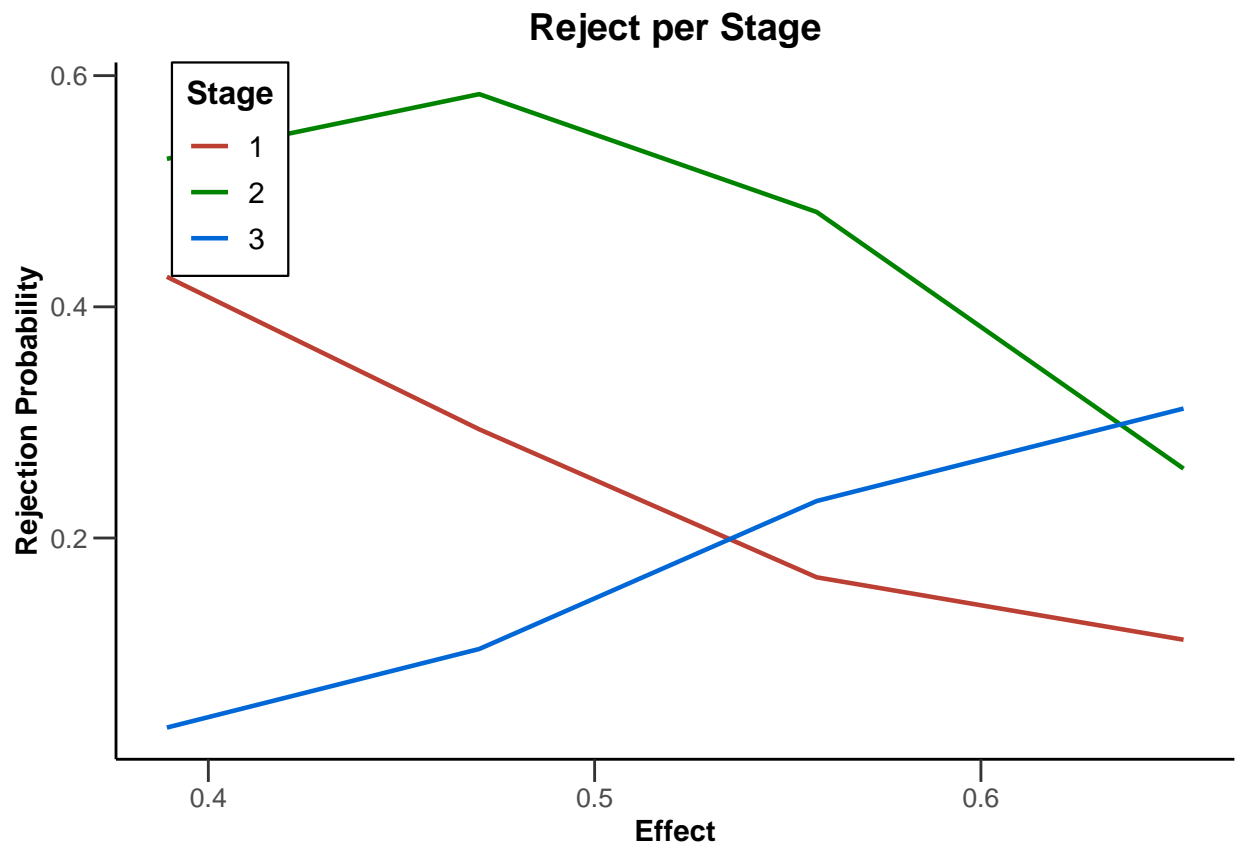


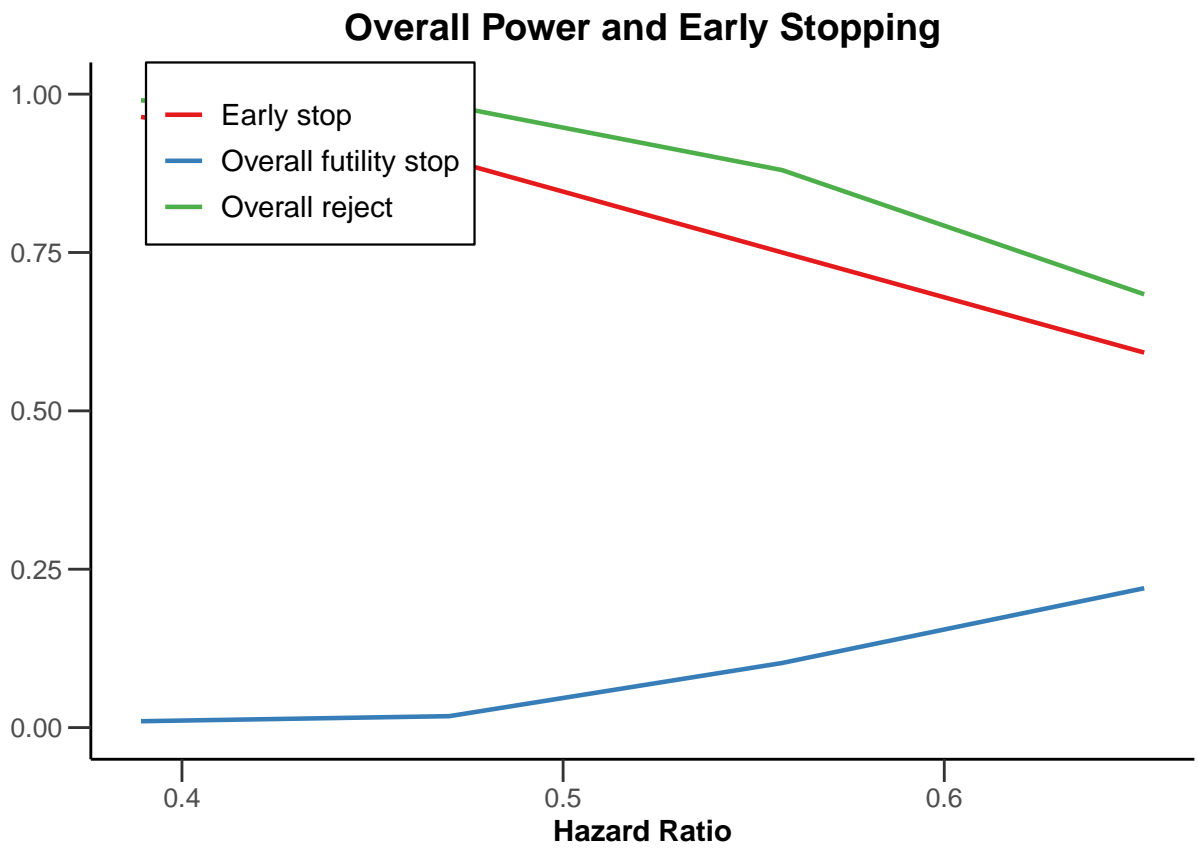
### 2.3 Simulation results base - survival

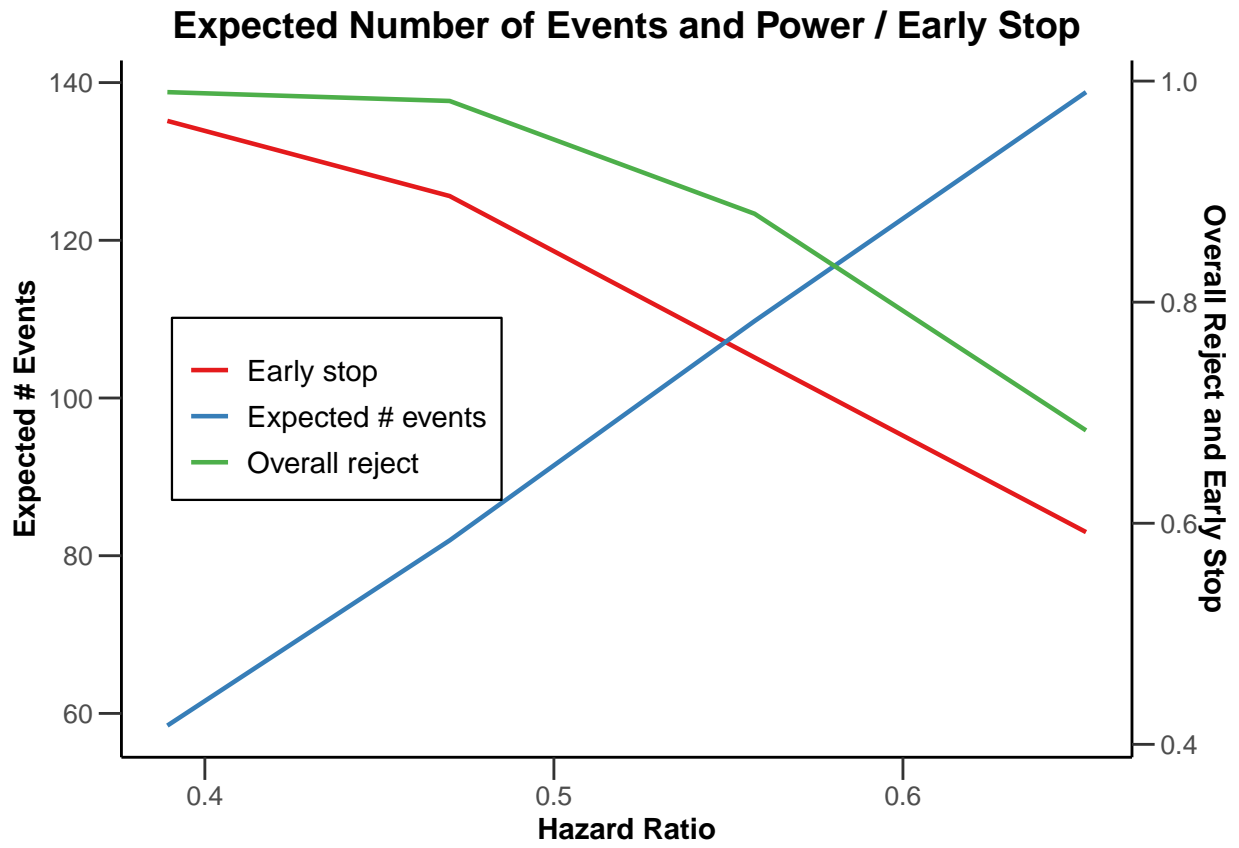
```

design <- getDesignFisher(kMax = 3, alpha0Vec = c(0.5, 0.5))
x <- getSimulationSurvival(
  design = design, pi2 = 0.6,
  pi1 = seq(0.3, 0.45, 0.05), directionUpper = FALSE,
  maxNumberOfSubjects = 500, plannedEvents = (1:design$kMax) * 20,
  allocation1 = 1, allocation2 = 1, accrualTime = c(0, 3, 6, 12),
  accrualIntensity = c(0.1, 0.2, 0.2), dropoutRate1 = 0,
  dropoutRate2 = 0, dropoutTime = 12, conditionalPower = 0.8,
  minNumberOfEventsPerStage = c(NA_real_, 10, 10),
  maxNumberOfEventsPerStage = c(NA_real_, 100, 200),
  maxNumberOfIterations = 500, seed = 1234567890
)
plot(x, type = "all", grid = 0)

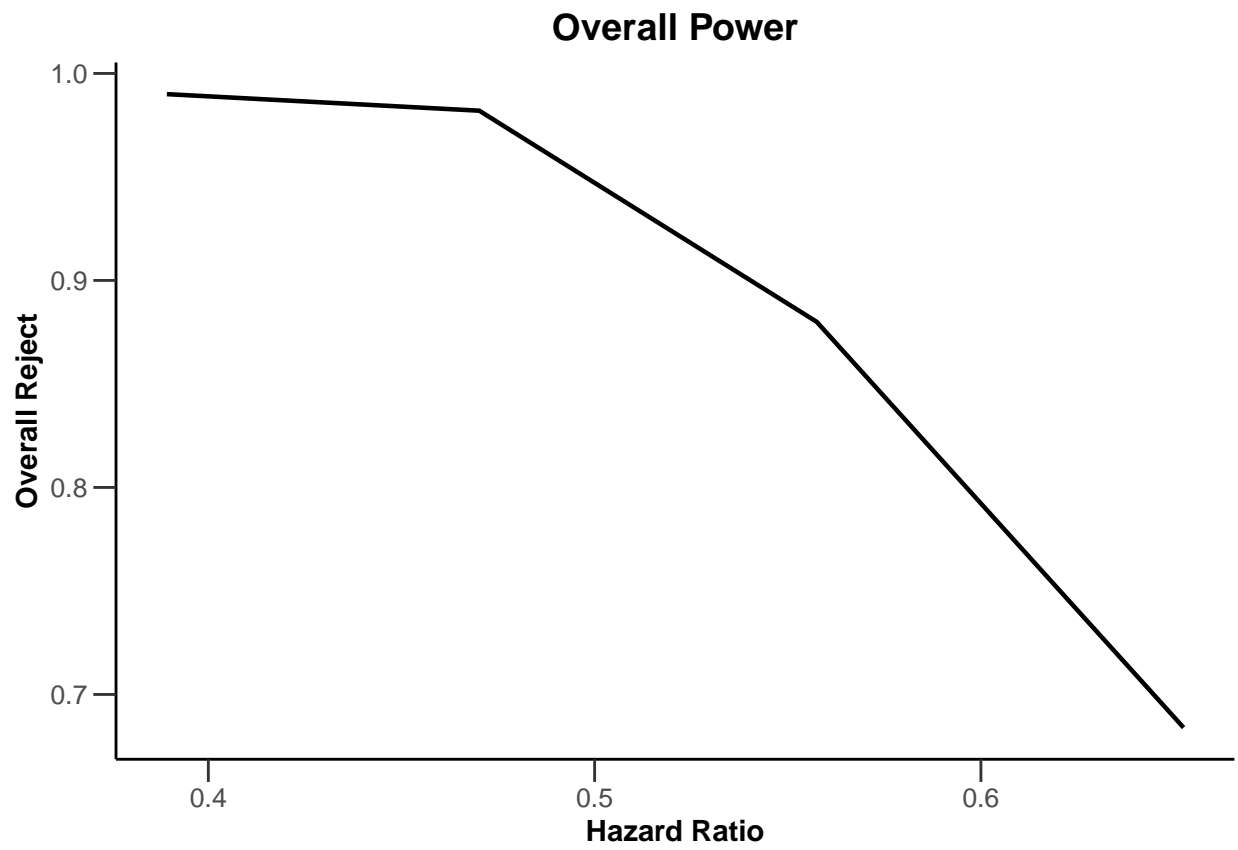
```

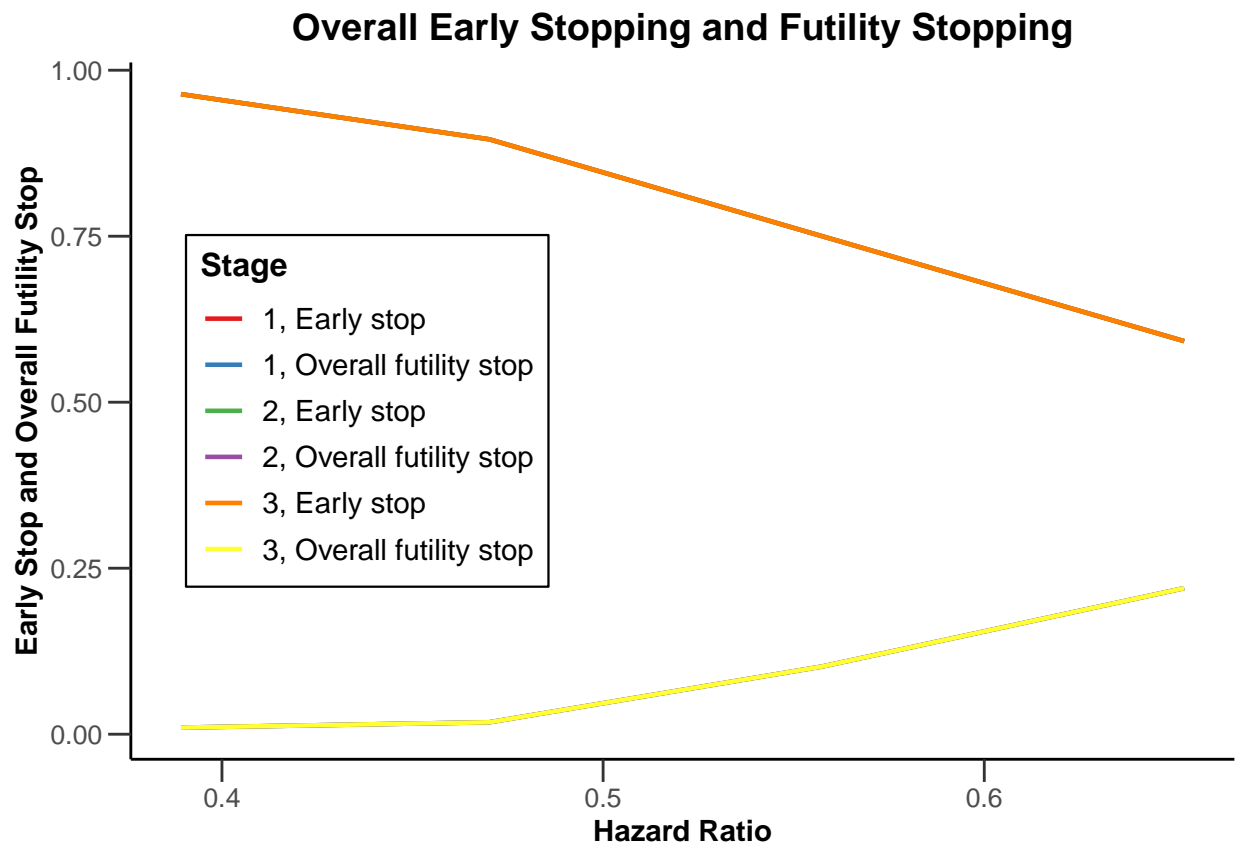


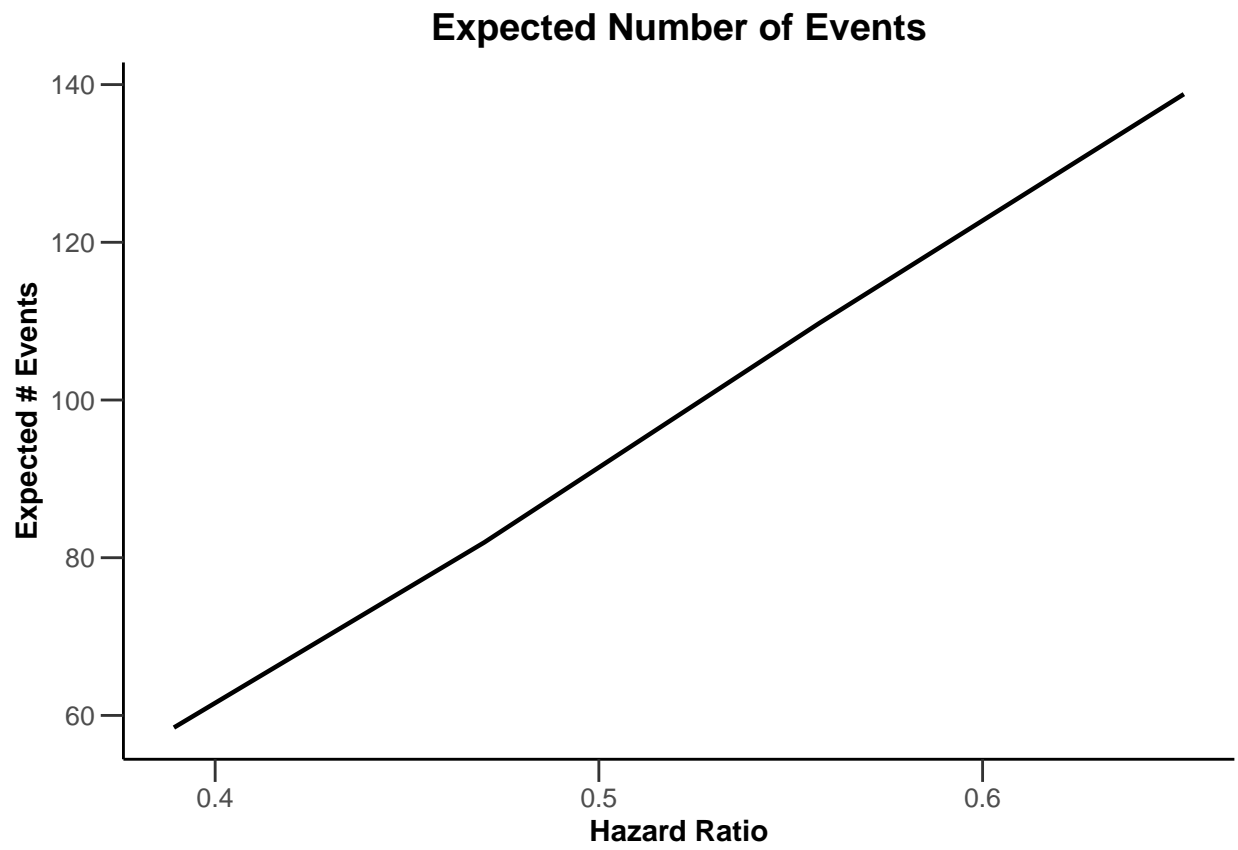


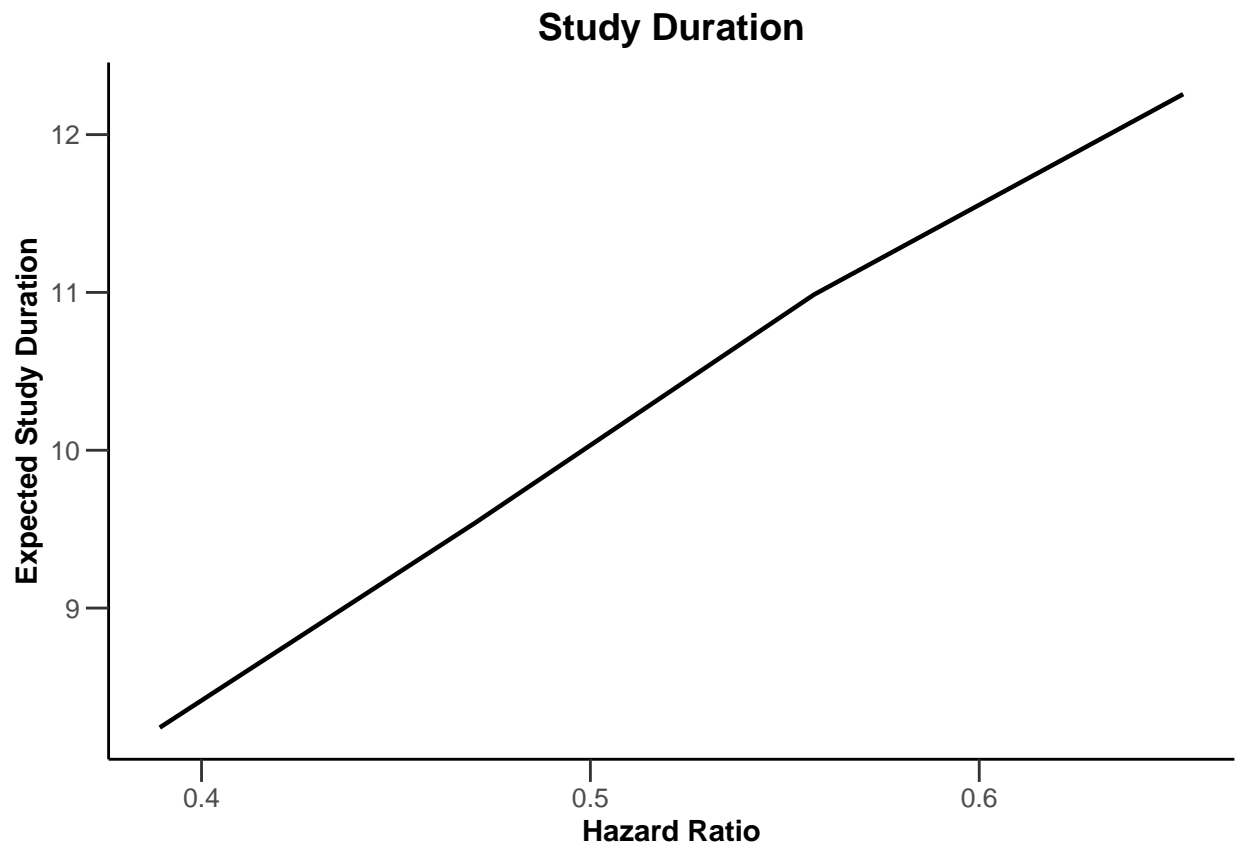


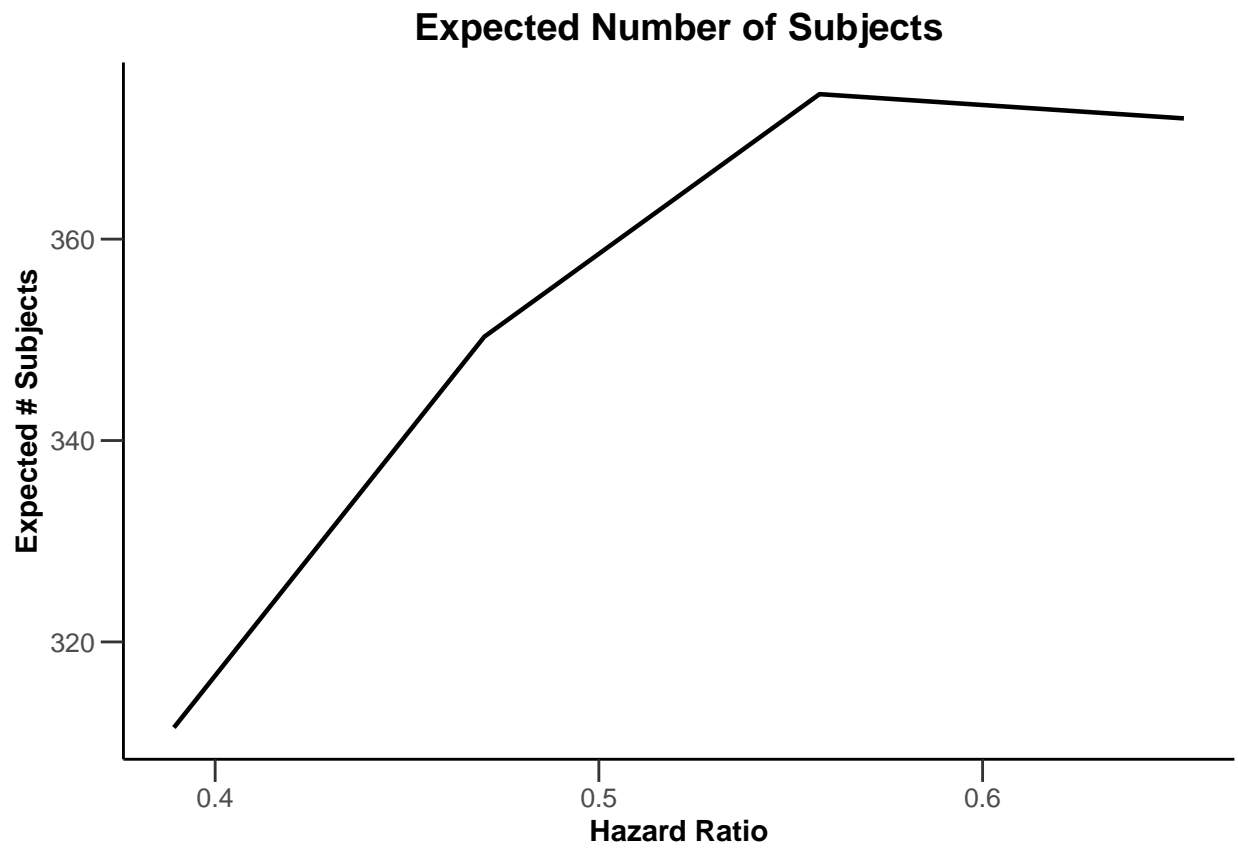


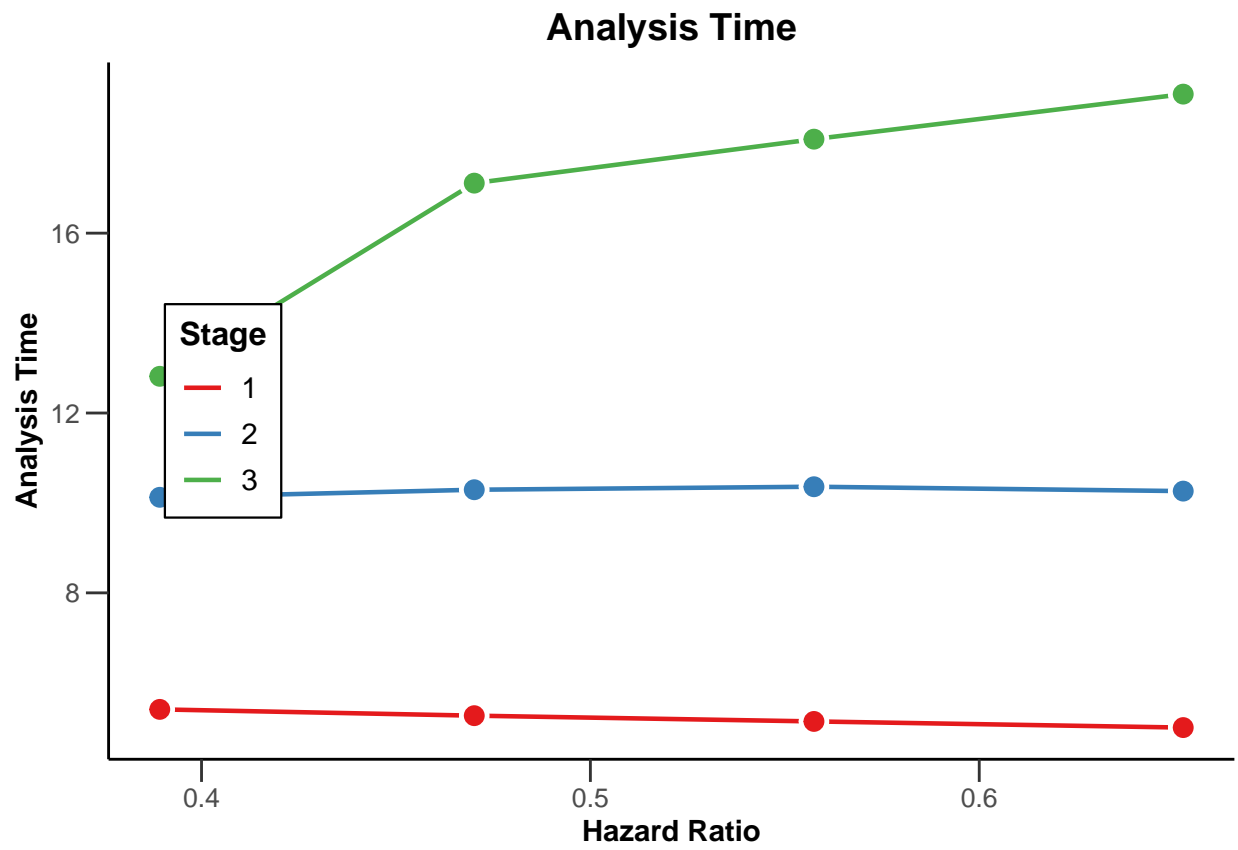


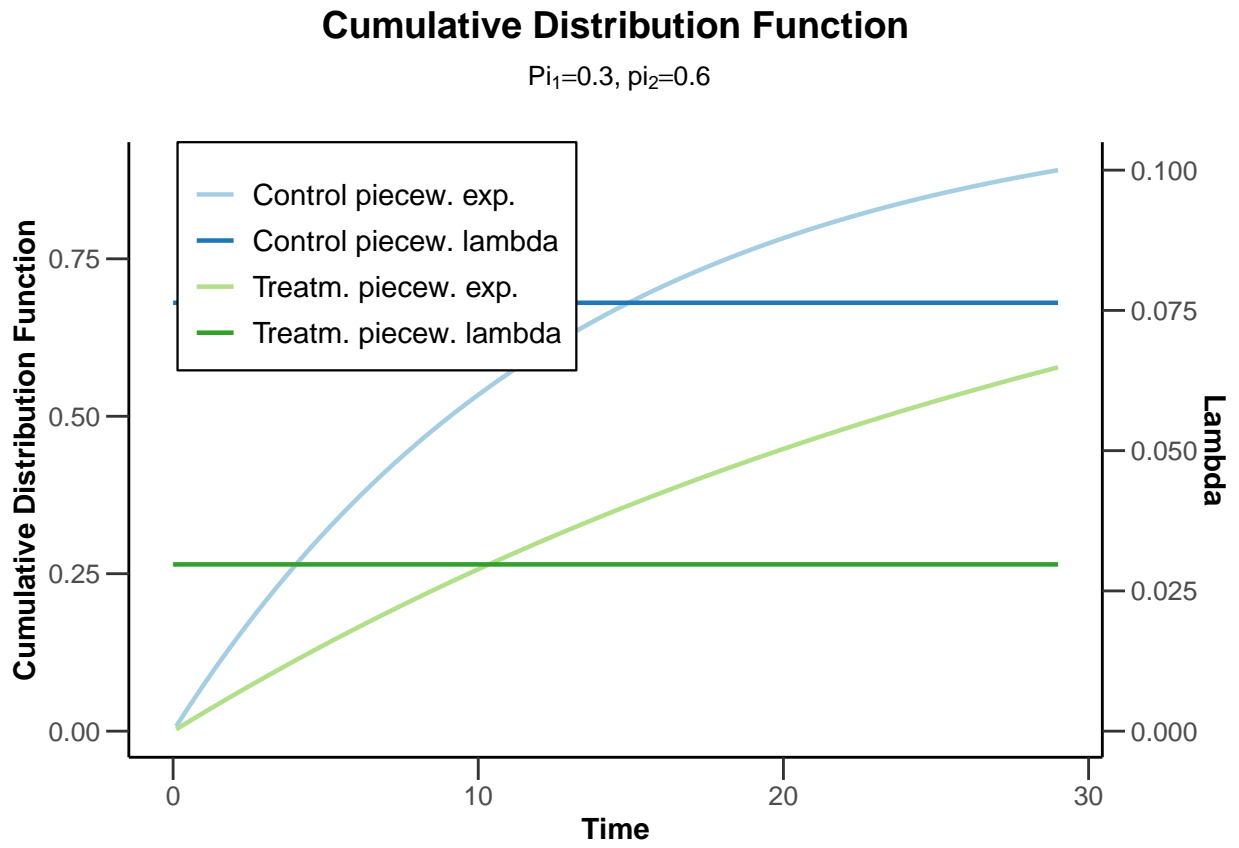


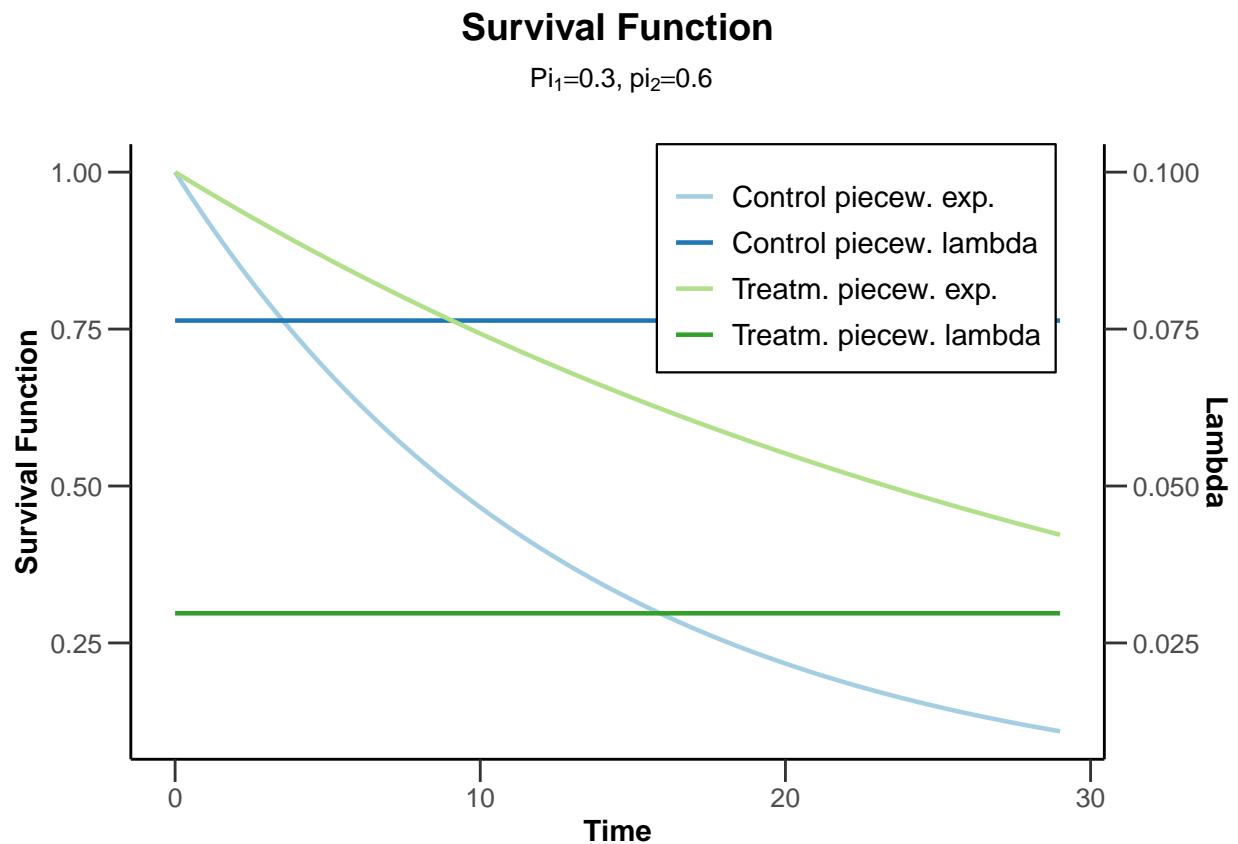












```
design <- getDesignGroupSequential(kMax = 3, typeOfDesign = "WT", deltaWT = 0.25)
piecewiseSurvivalTime <- list(
  "<6" = 0.025,
  "6 - <9" = 0.04,
  "9 - <15" = 0.015,
  "15 - <21" = 0.01,
  ">=21" = 0.007
)
x <- getSimulationSurvival(
  design = design,
  directionUpper = TRUE, maxNumberOfSubjects = 500,
  plannedEvents = (1:design$kMax) * 20, allocation1 = 1,
  allocation2 = 1, accrualTime = c(0, 3, 6, 12),
  piecewiseSurvivalTime = piecewiseSurvivalTime, hazardRatio = 1.7,
  accrualIntensity = c(0.1, 0.2, 0.2), dropoutRate1 = 0,
  dropoutRate2 = 0, dropoutTime = 12, conditionalPower = 0.8,
  minNumberOfEventsPerStage = c(NA_real_, 10, 10),
  maxNumberOfEventsPerStage = c(NA_real_, 100, 200),
  maxNumberOfIterations = 500, seed = 1234567890
)
plot(x, type = "all", grid = 0)
```

```
## Warning in !is.null(lambda1) && !is.na(lambda1): 'length(x) = 5 > 1' in coercion
## to 'logical(1)'
```

```
## Warning in !is.null(lambda1) && !is.na(lambda1): 'length(x) = 5 > 1' in coercion
```



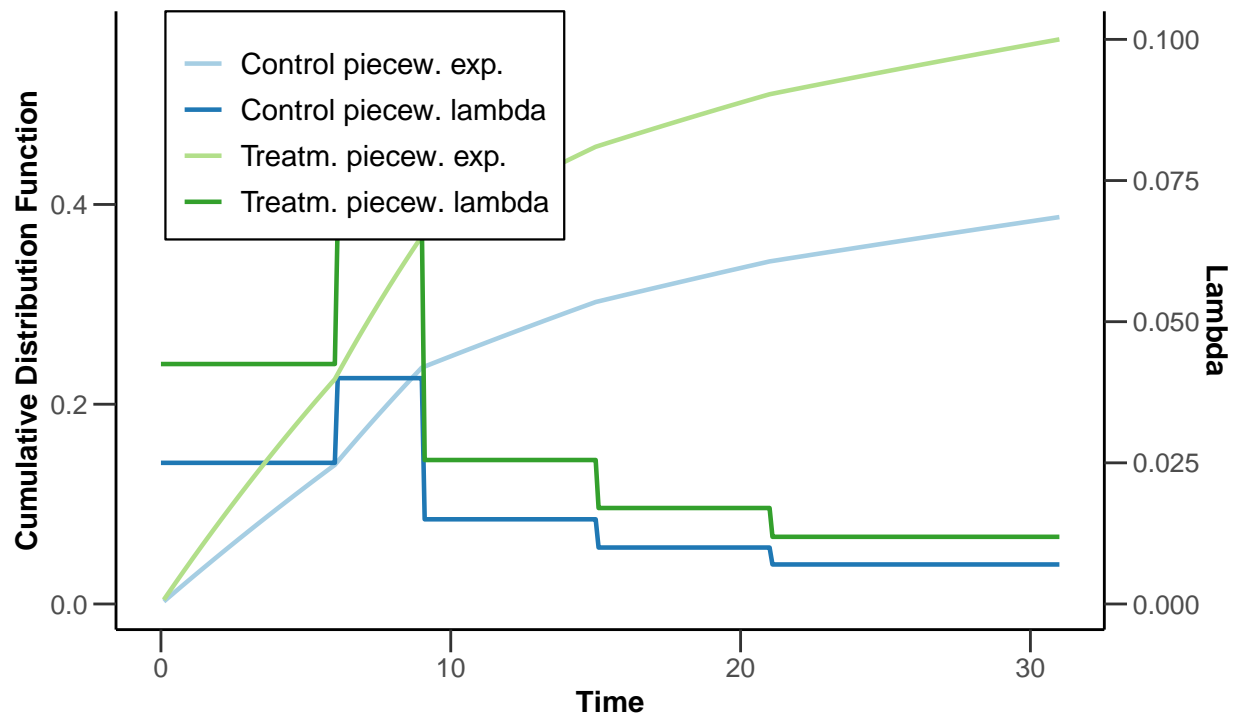
```
## to 'logical(1)'
```

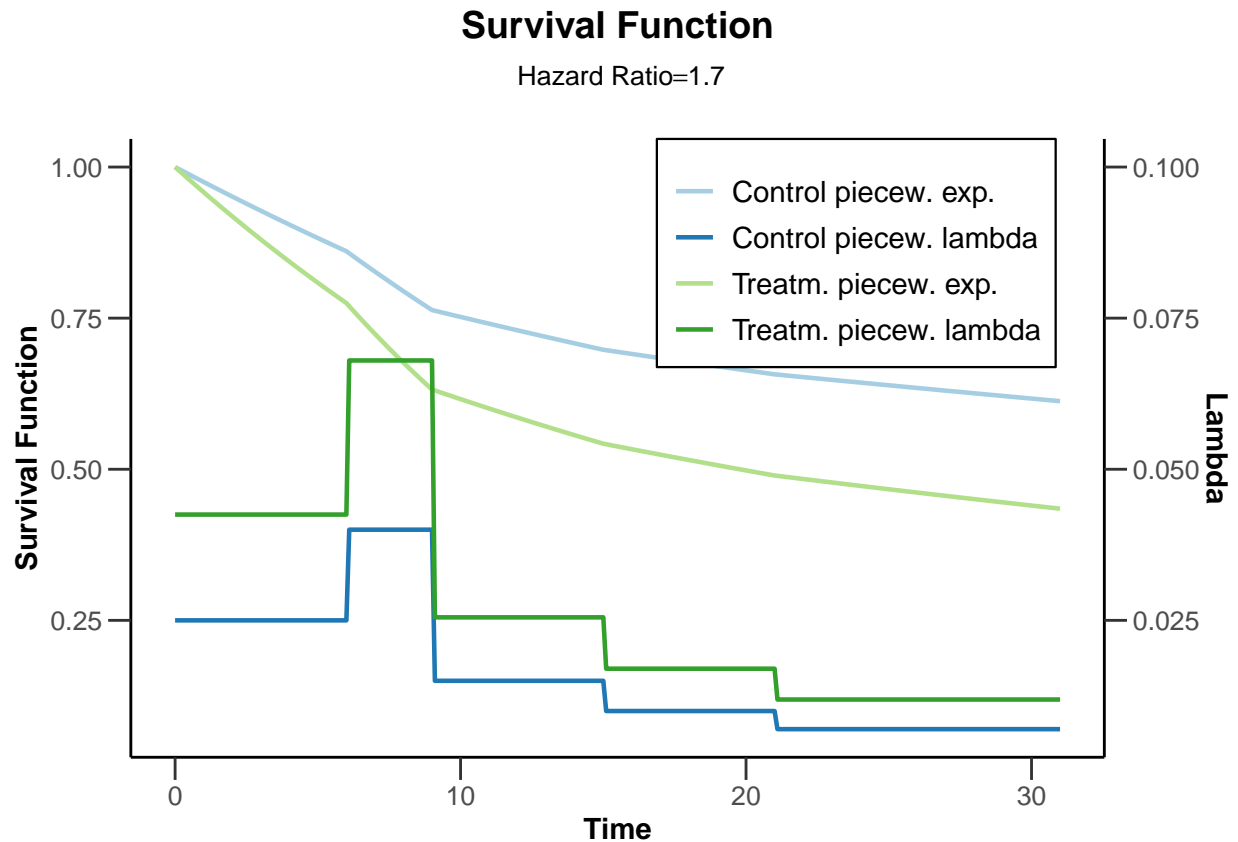
```
## Warning in !is.null(lambda1) && !is.na(lambda1): 'length(x) = 5 > 1' in coercion  
## to 'logical(1)'
```

```
## Warning in !is.null(lambda1) && !is.na(lambda1): 'length(x) = 5 > 1' in coercion  
## to 'logical(1)'
```

## Cumulative Distribution Function

Hazard Ratio=1.7

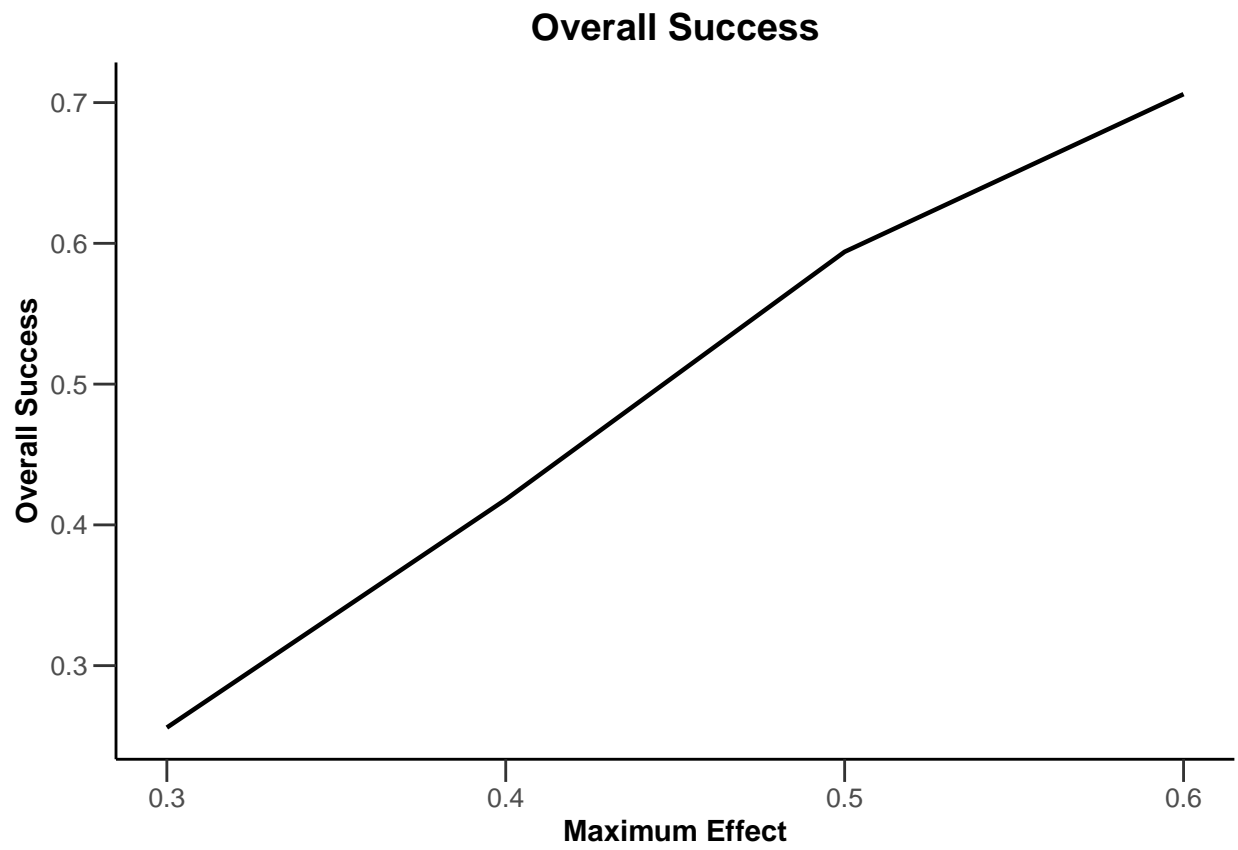


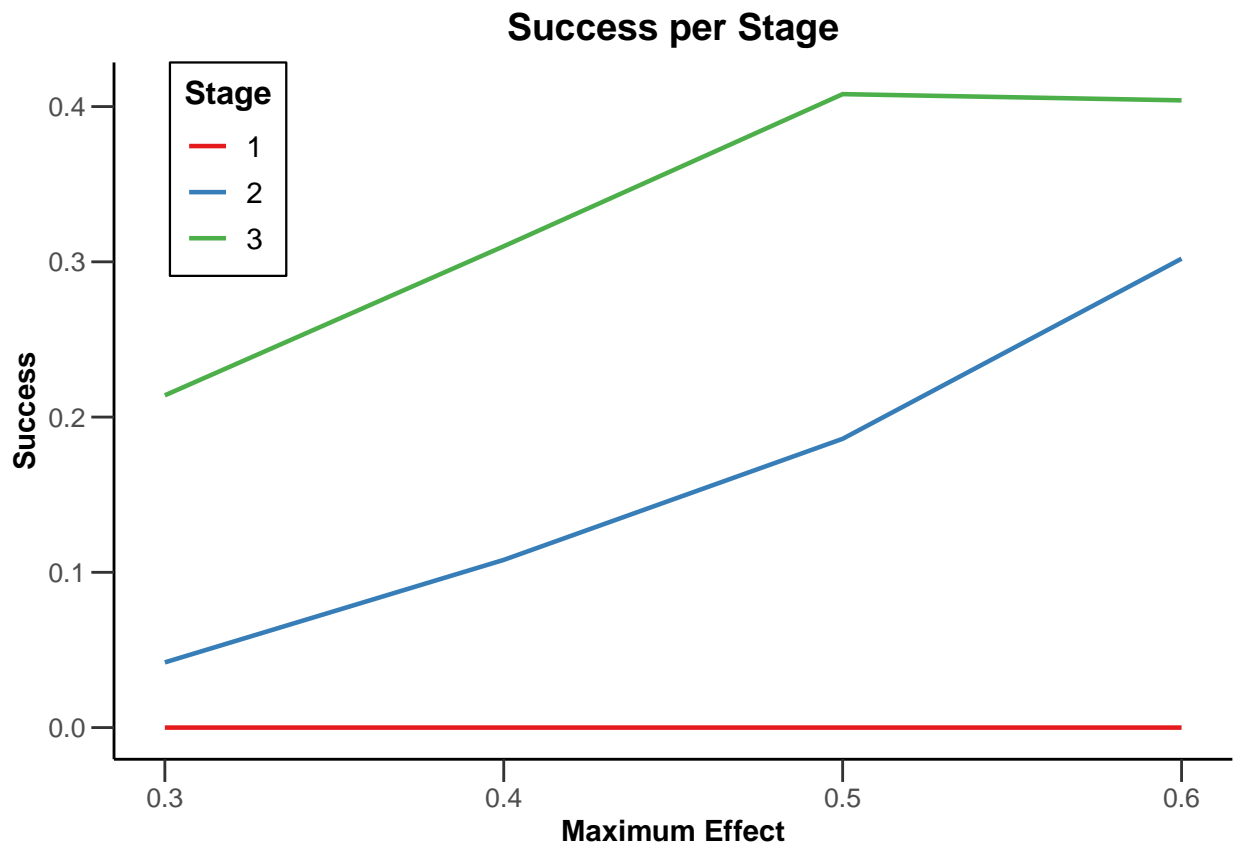


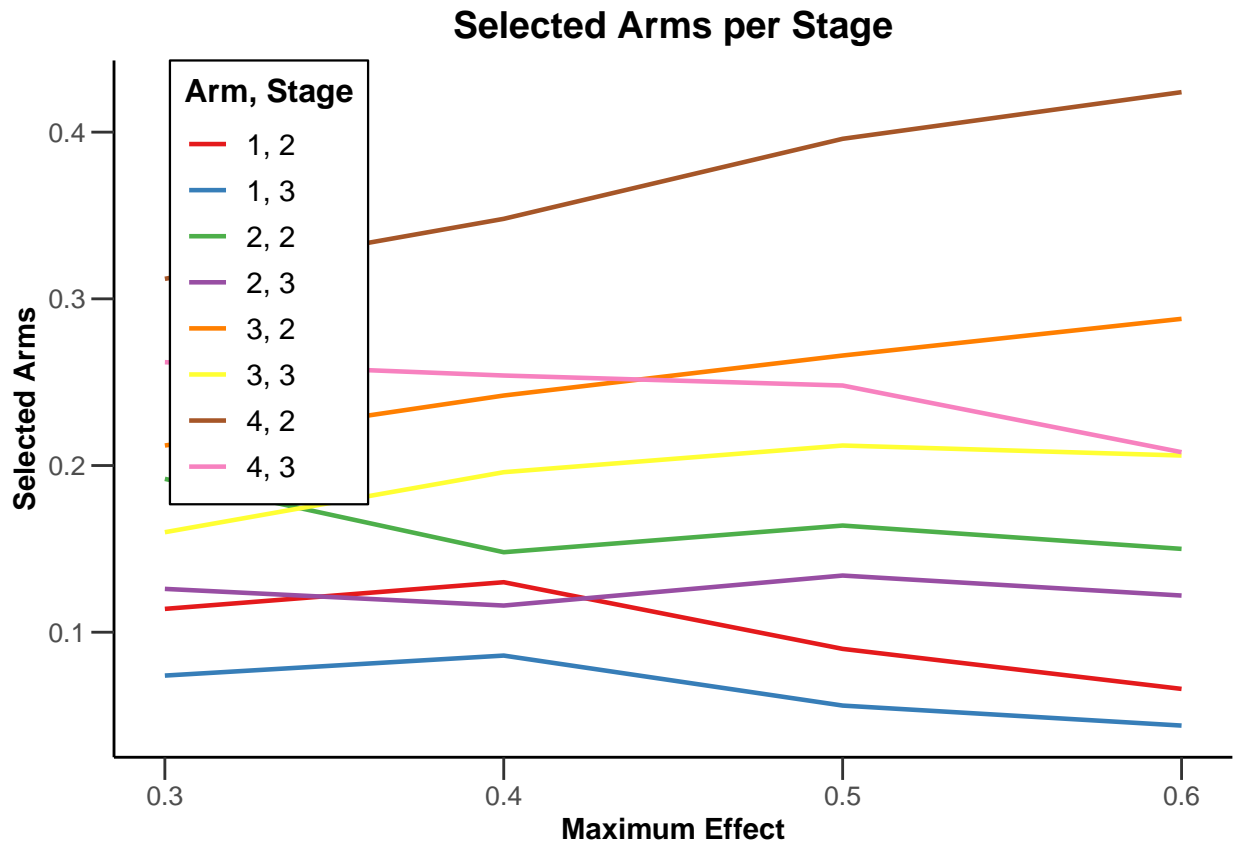
### 3 Simulation results multi-arm

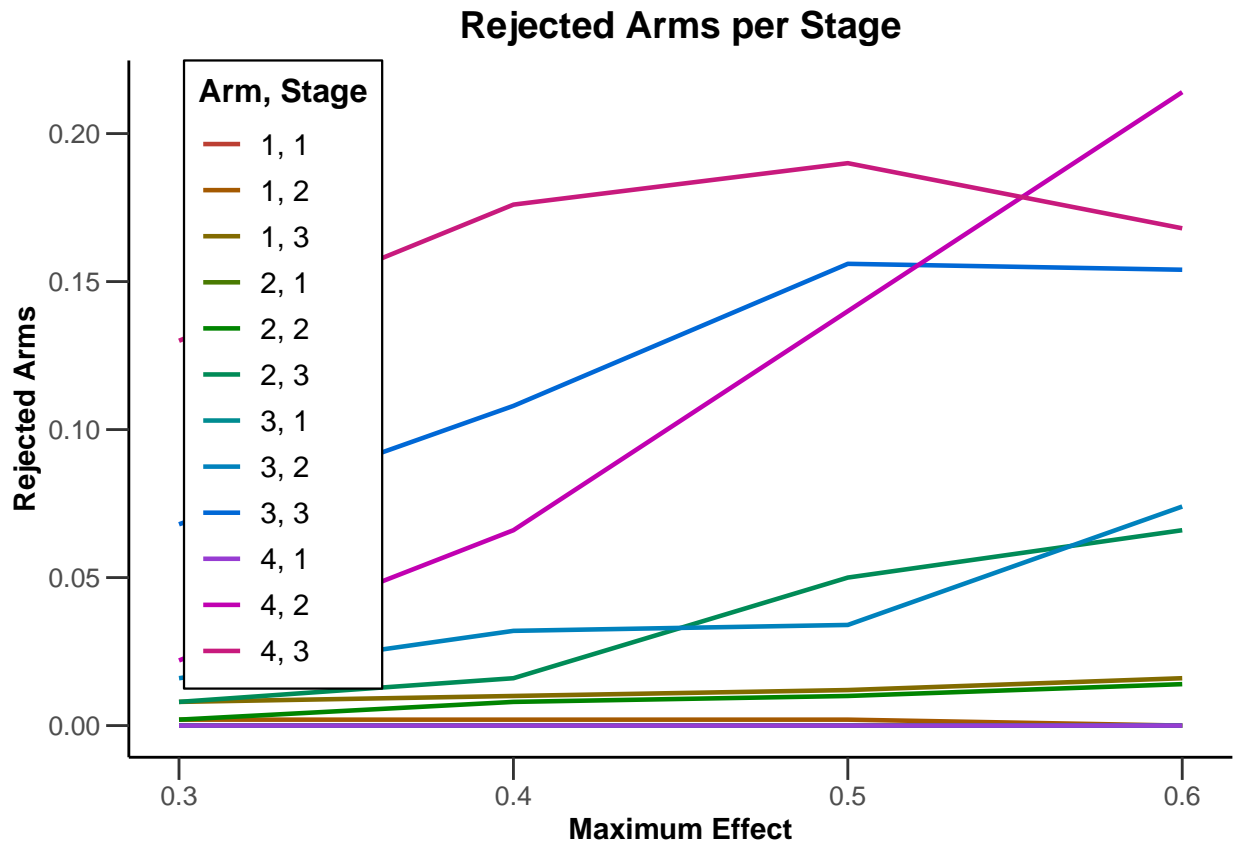
#### 3.1 Simulation results multi-arm - means

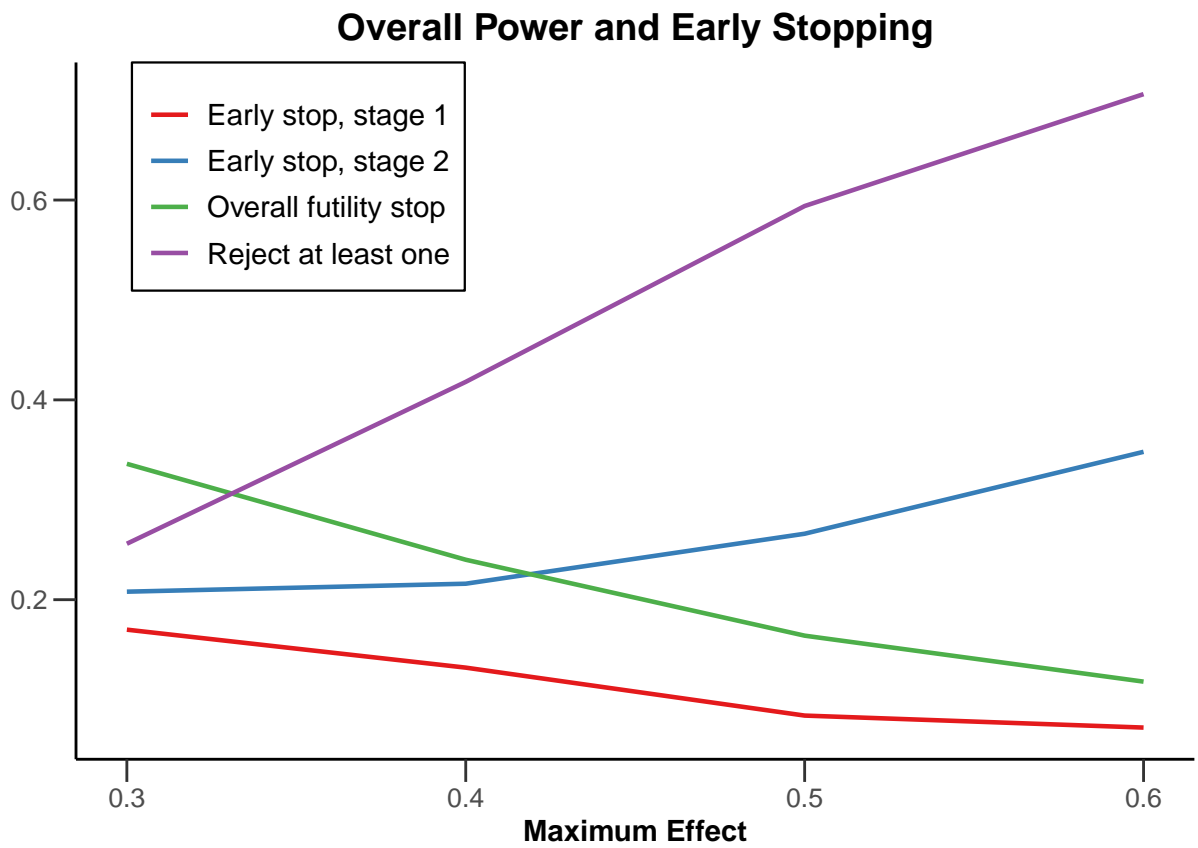
```
design <- getDesignInverseNormal(
  informationRates = c(0.2, 0.6, 1),
  futilityBounds = c(-0.5, 0.5)
)
x <- getSimulationMultiArmMeans(
  design = design, typeOfShape = "linear",
  activeArms = 4, plannedSubjects = c(10, 30, 50), stDev = 1.2,
  muMaxVector = seq(0.3, 0.6, 0.1), adaptations = rep(TRUE, 2),
  conditionalPower = 0.8, minNumberOfSubjectsPerStage = c(10, 4, 4),
  maxNumberOfSubjectsPerStage = c(10, 100, 100),
  maxNumberOfIterations = 500, seed = 1234567890
)
plot(x, type = "all", grid = 0)
```

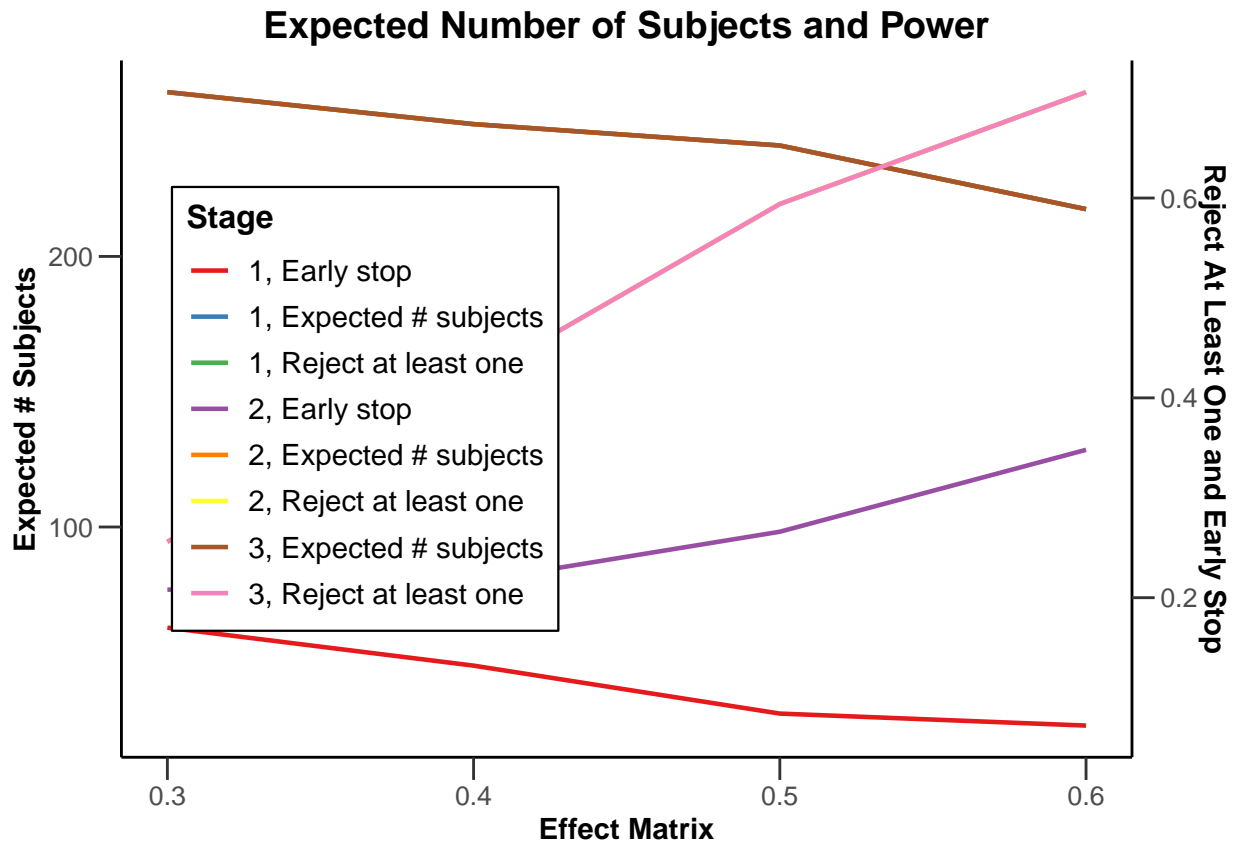




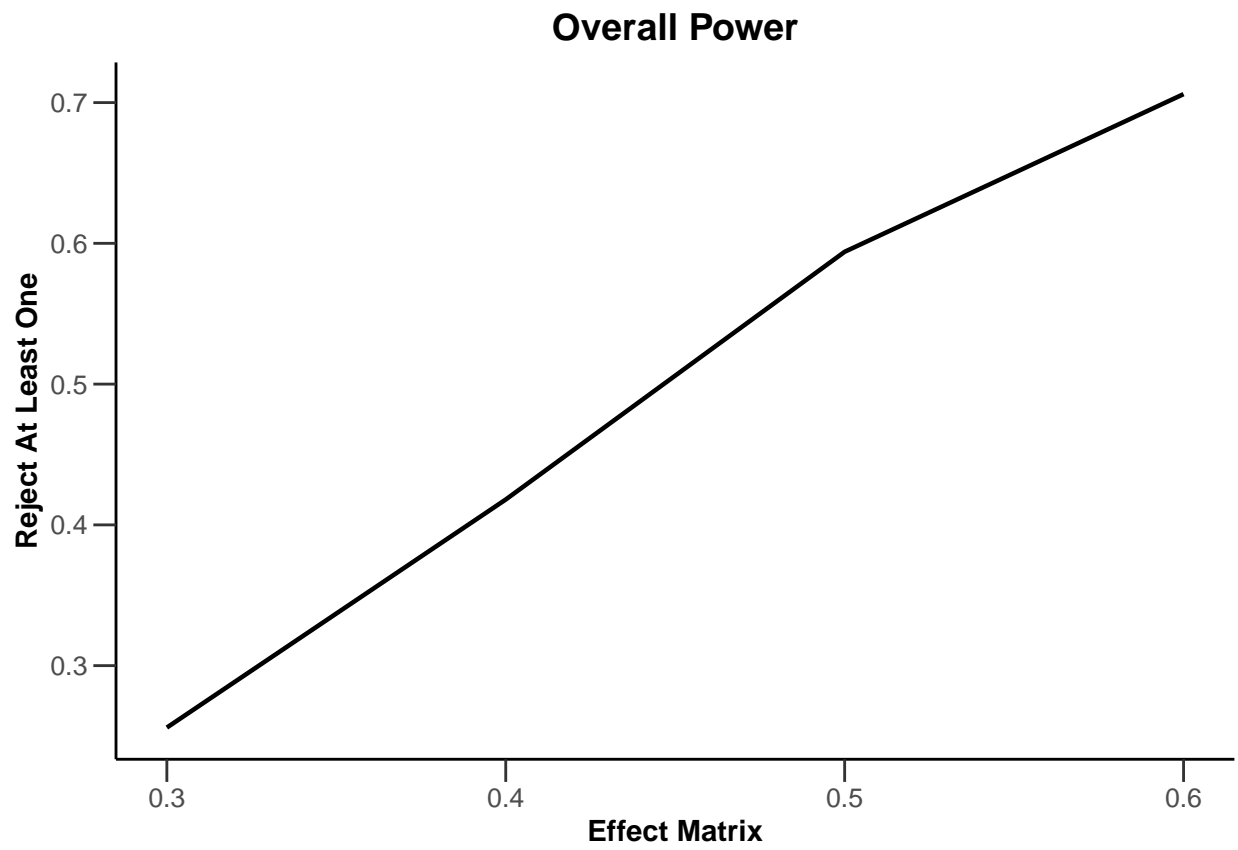


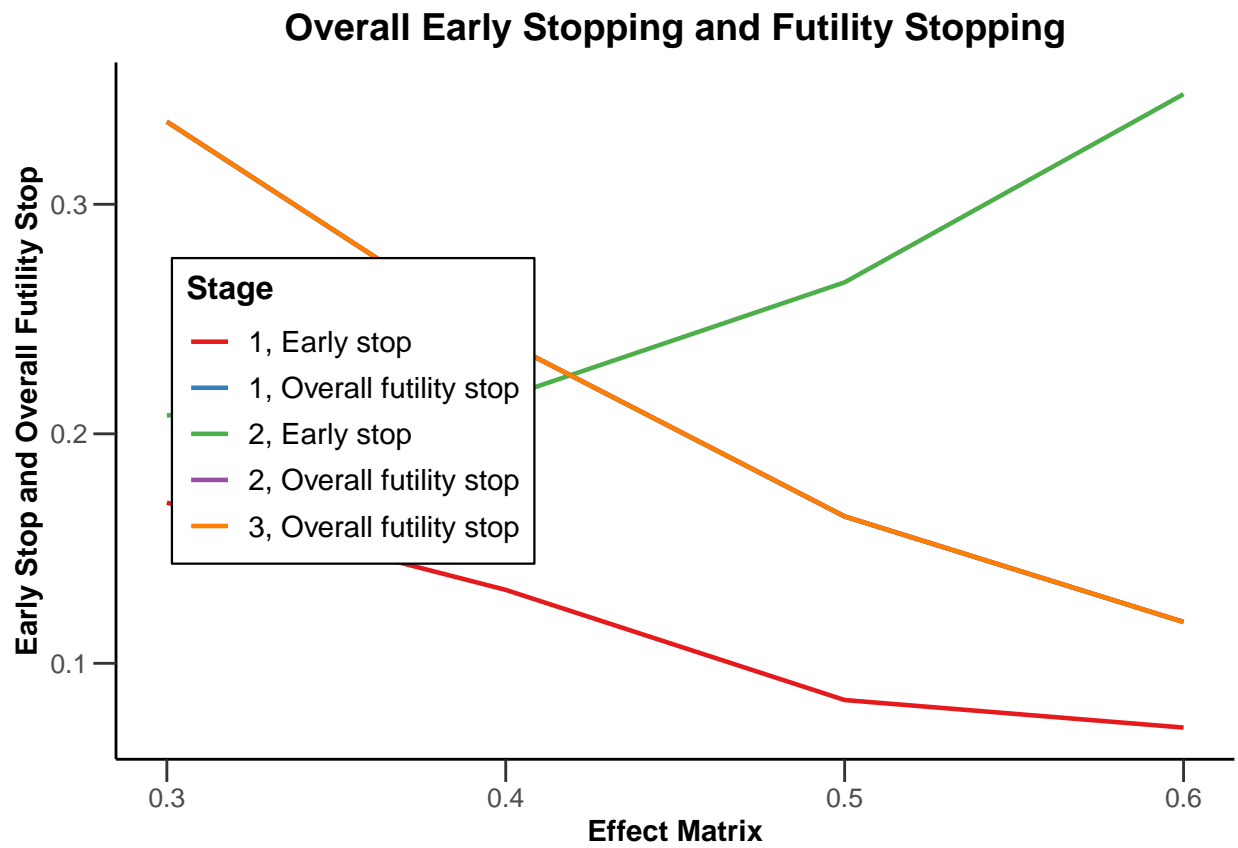


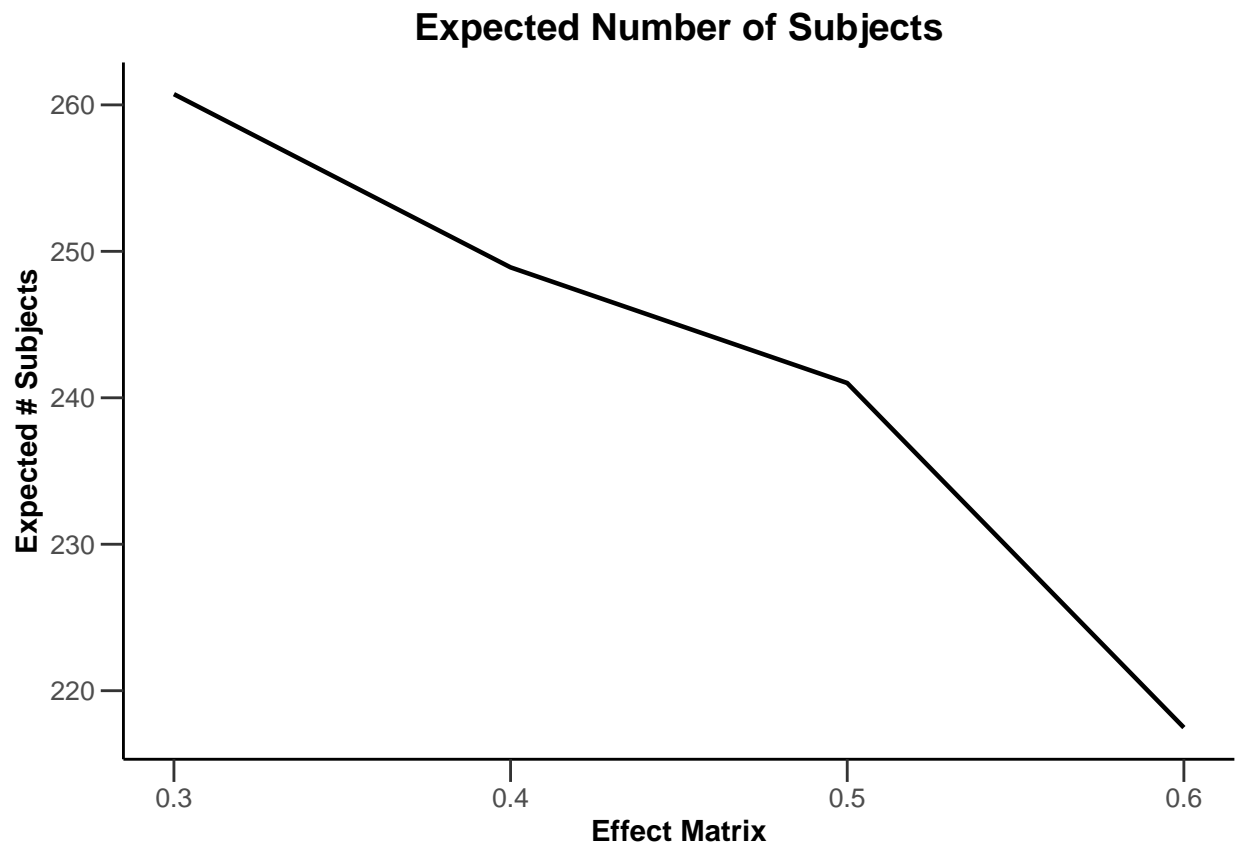






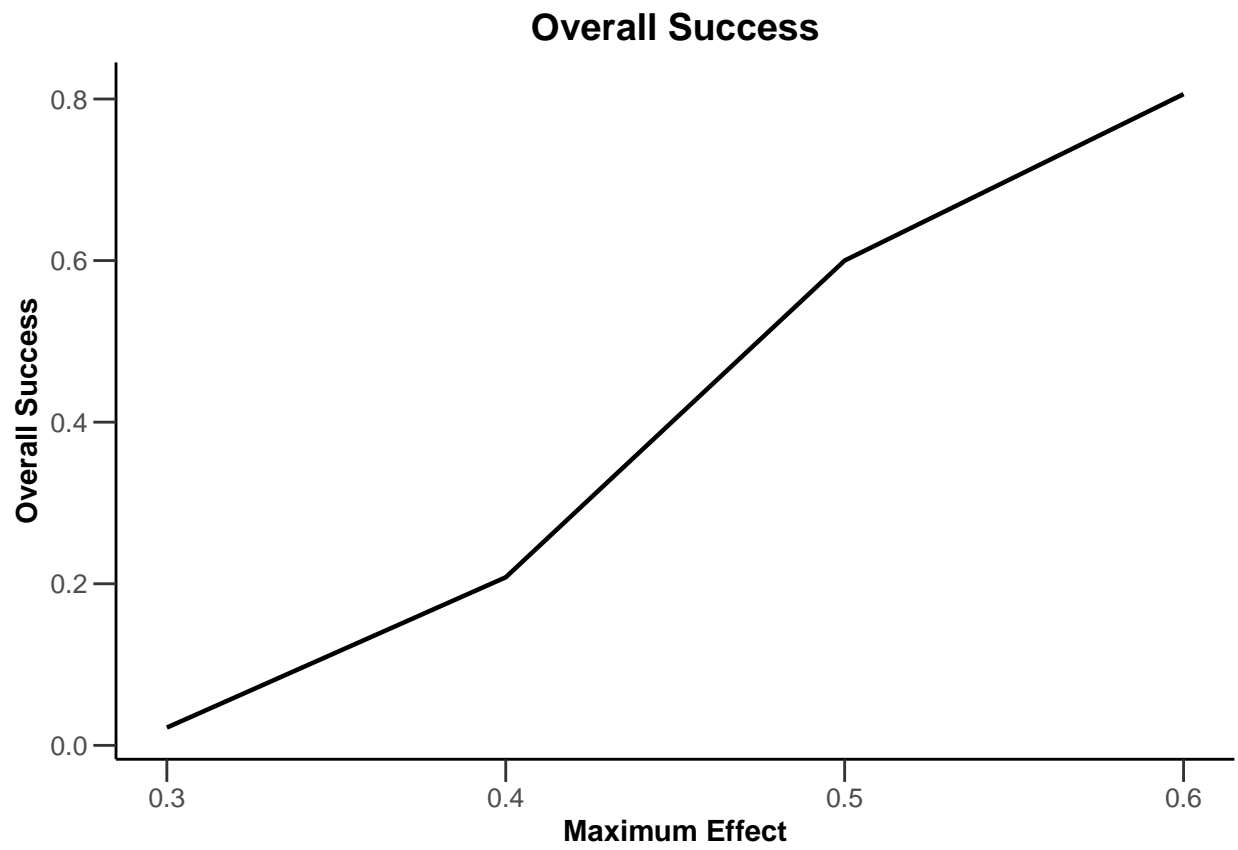


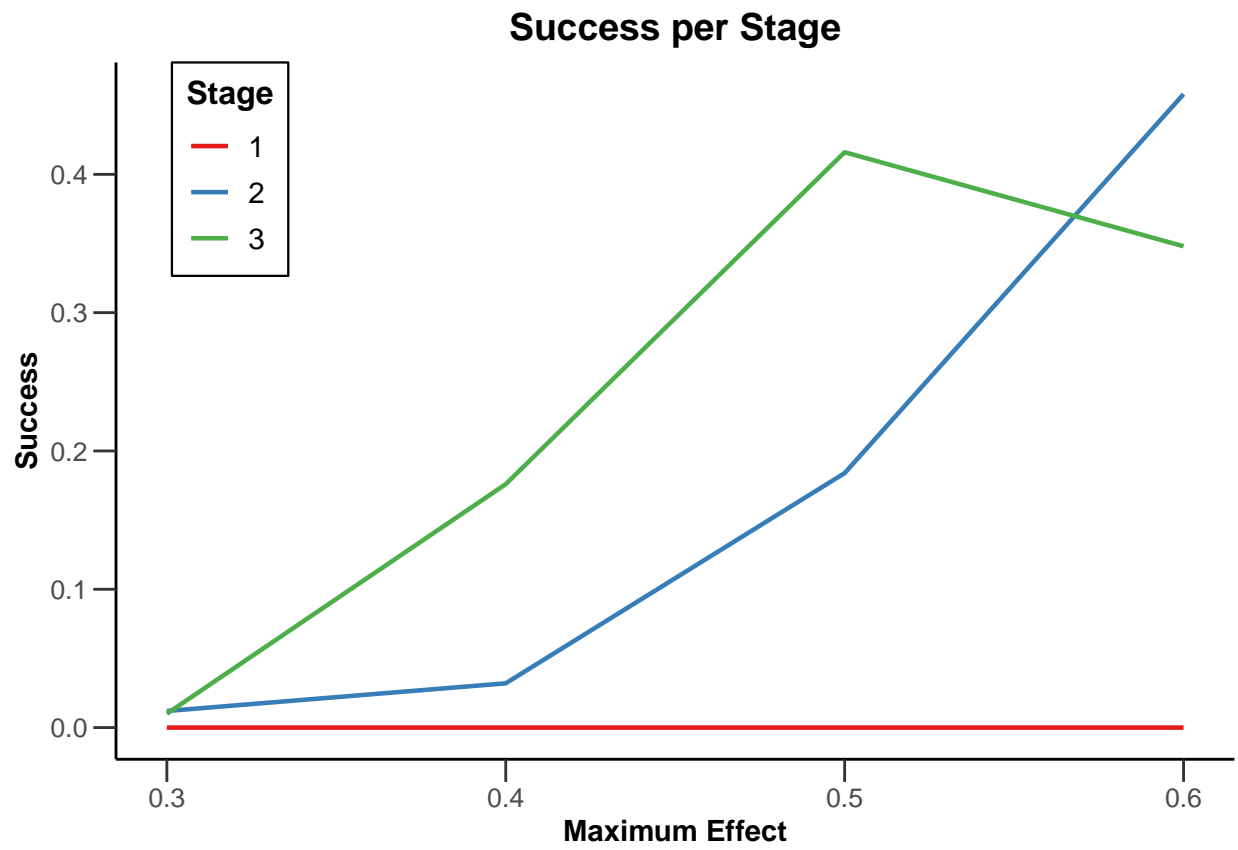


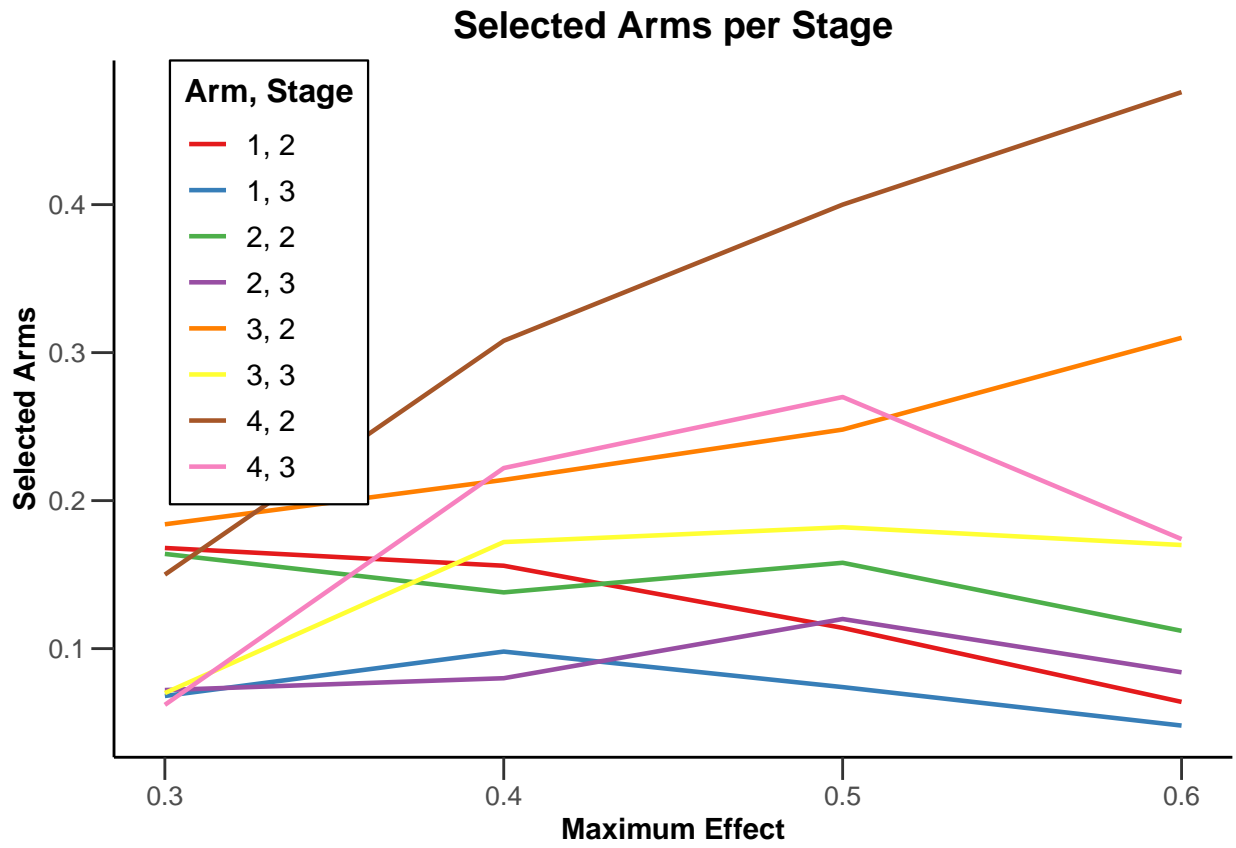


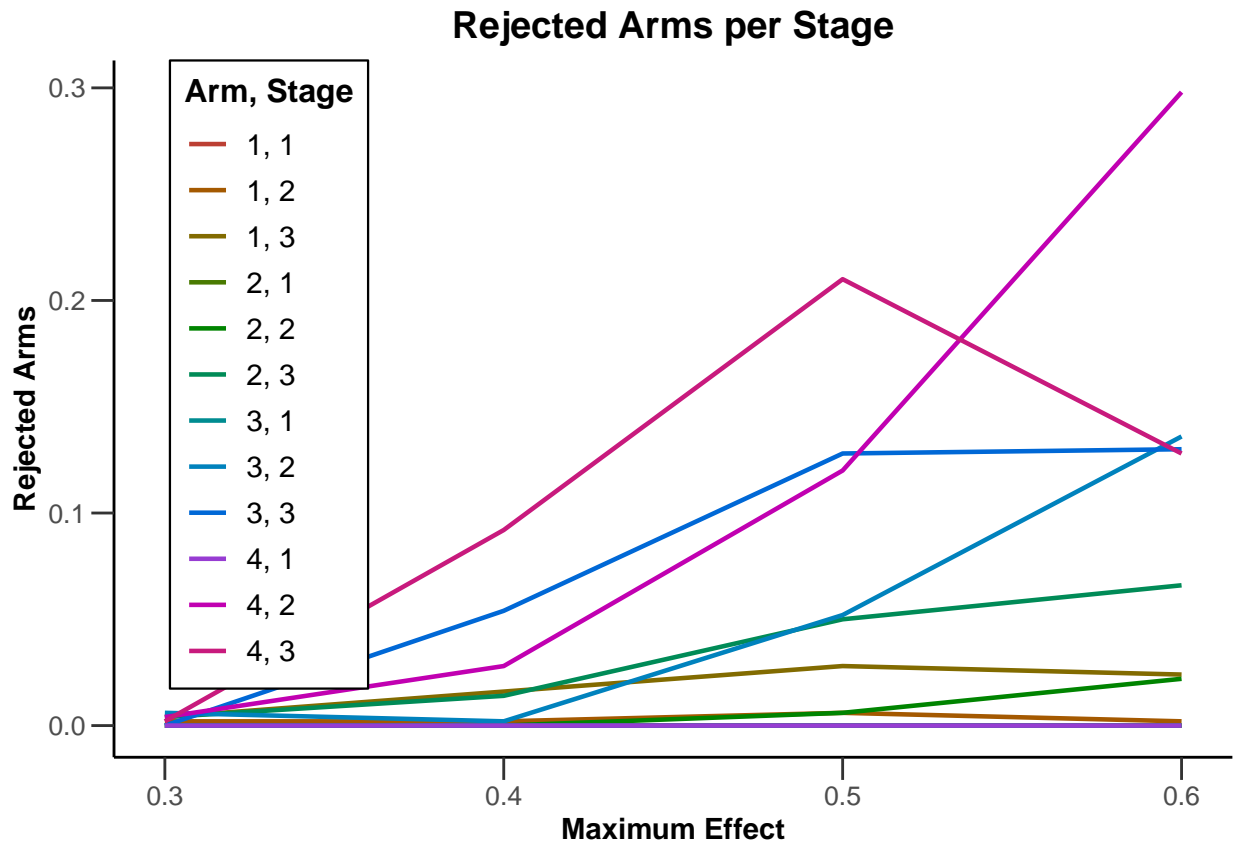
### 3.2 Simulation results multi-arm - rates

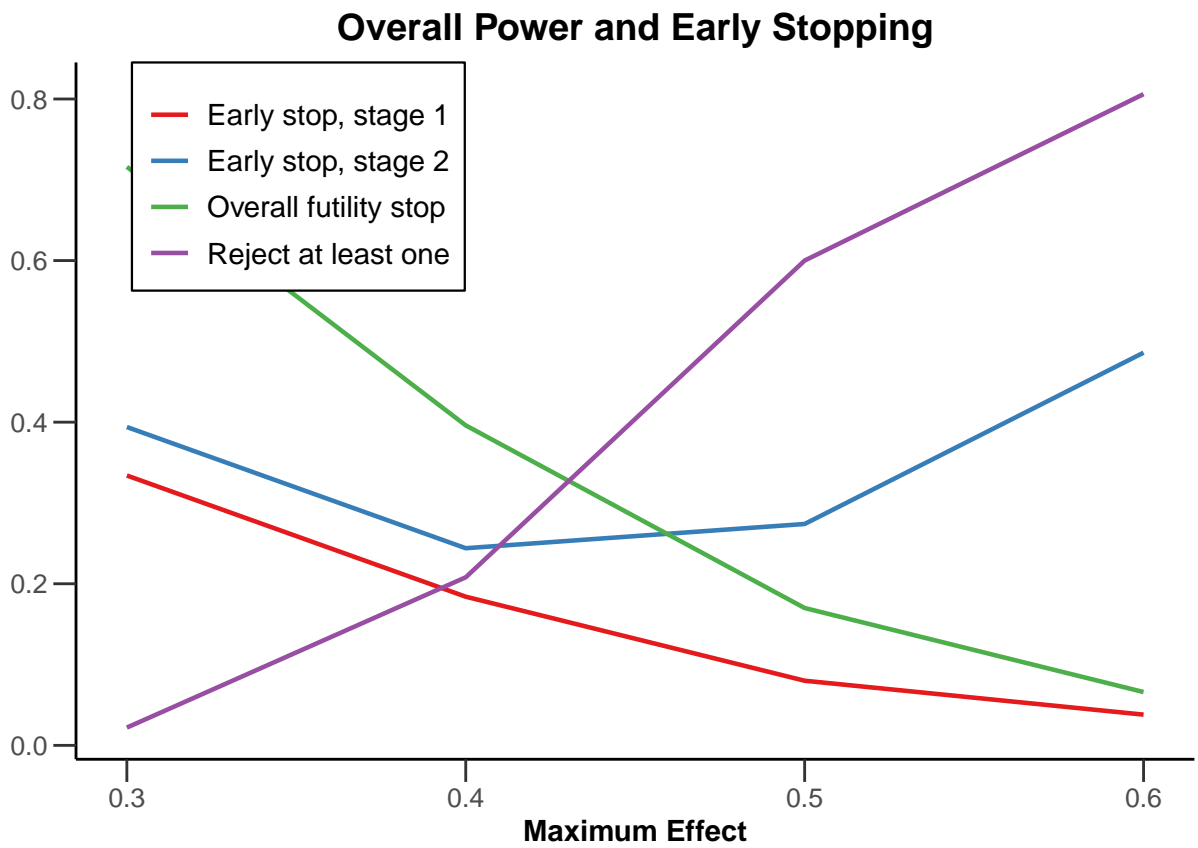
```
design <- getDesignInverseNormal(  
  informationRates = c(0.2, 0.6, 1),  
  futilityBounds = c(-0.5, 0.5)  
)  
x <- getSimulationMultiArmRates(  
  design = design, typeOfShape = "linear",  
  activeArms = 4, plannedSubjects = c(10, 30, 50),  
  piControl = 0.3, piMaxVector = seq(0.3, 0.6, 0.1),  
  adaptations = rep(TRUE, 2), conditionalPower = 0.8,  
  minNumberOfSubjectsPerStage = c(10, 4, 4),  
  maxNumberOfSubjectsPerStage = c(10, 100, 100),  
  maxNumberOfIterations = 500, seed = 1234567890  
)  
plot(x, type = "all", grid = 0)
```



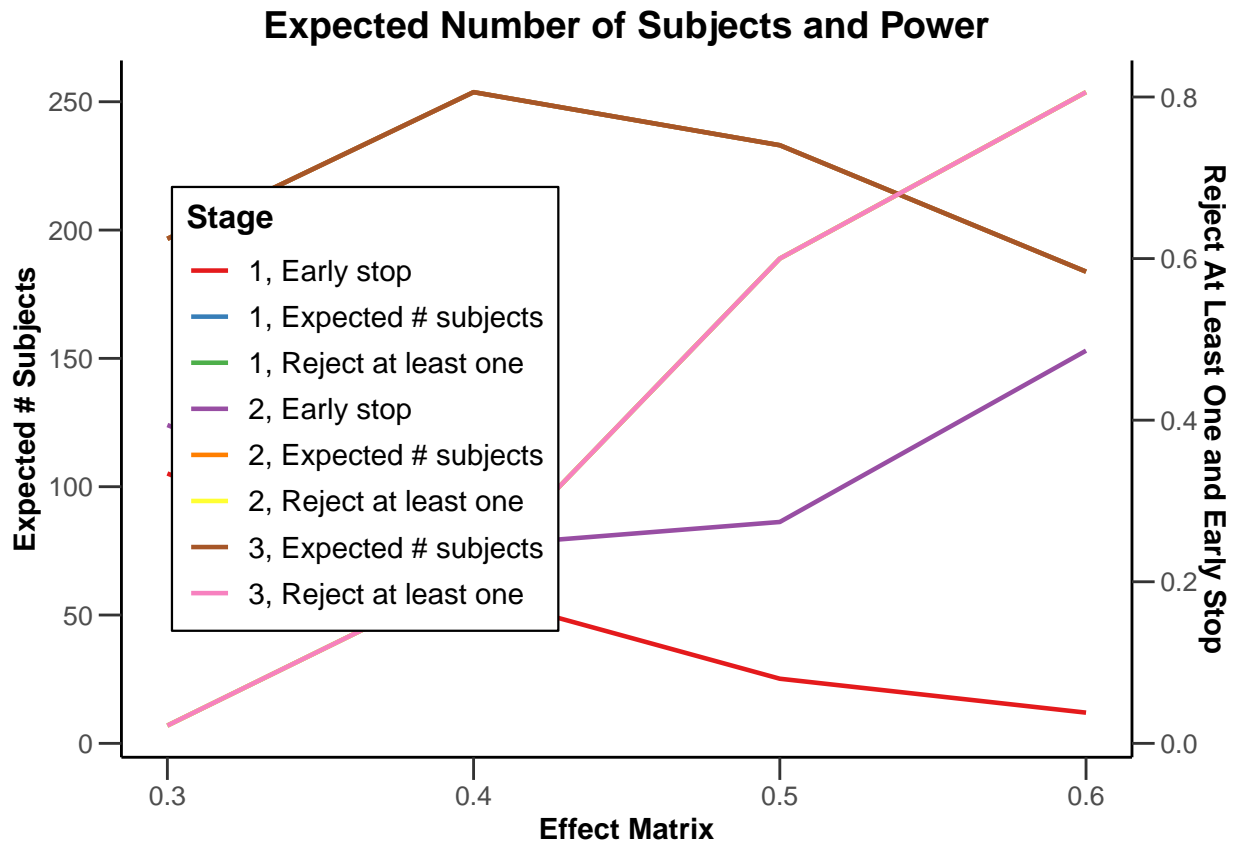


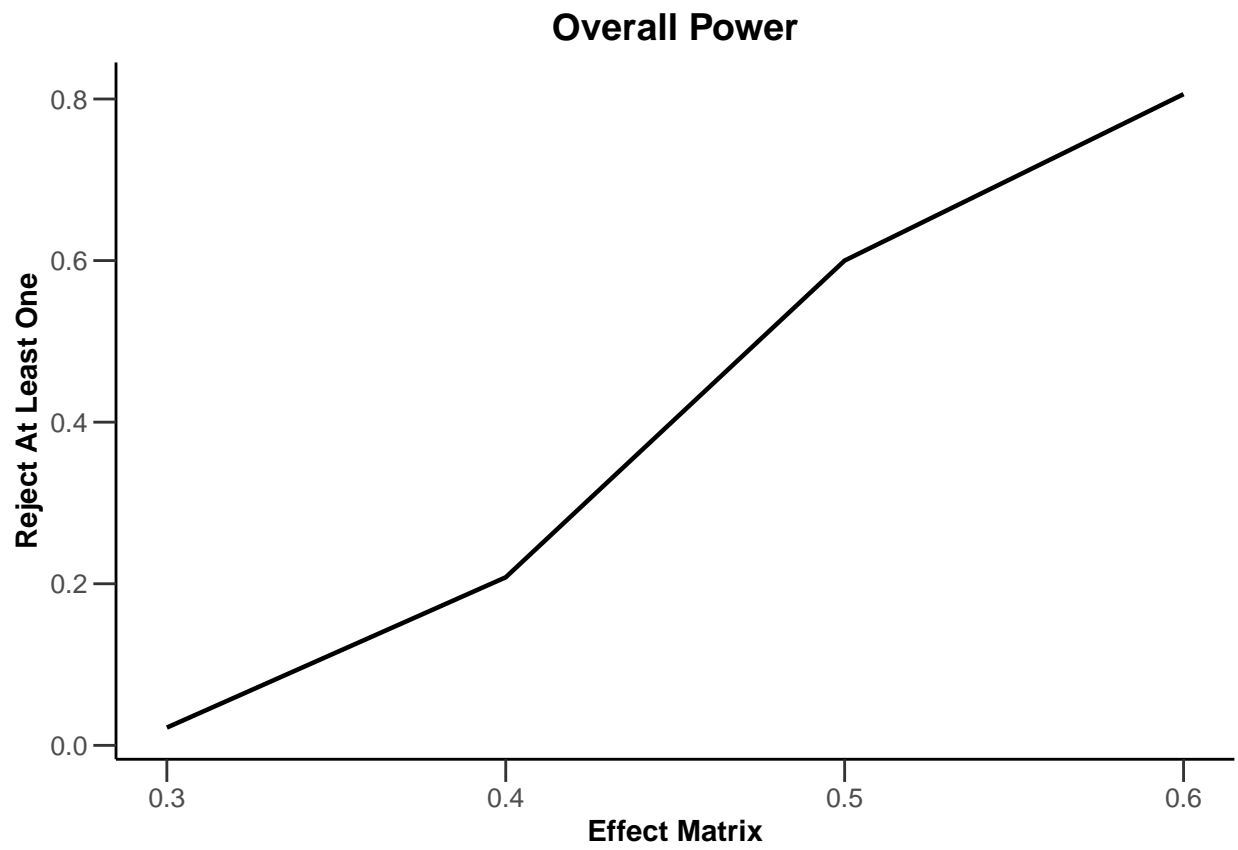


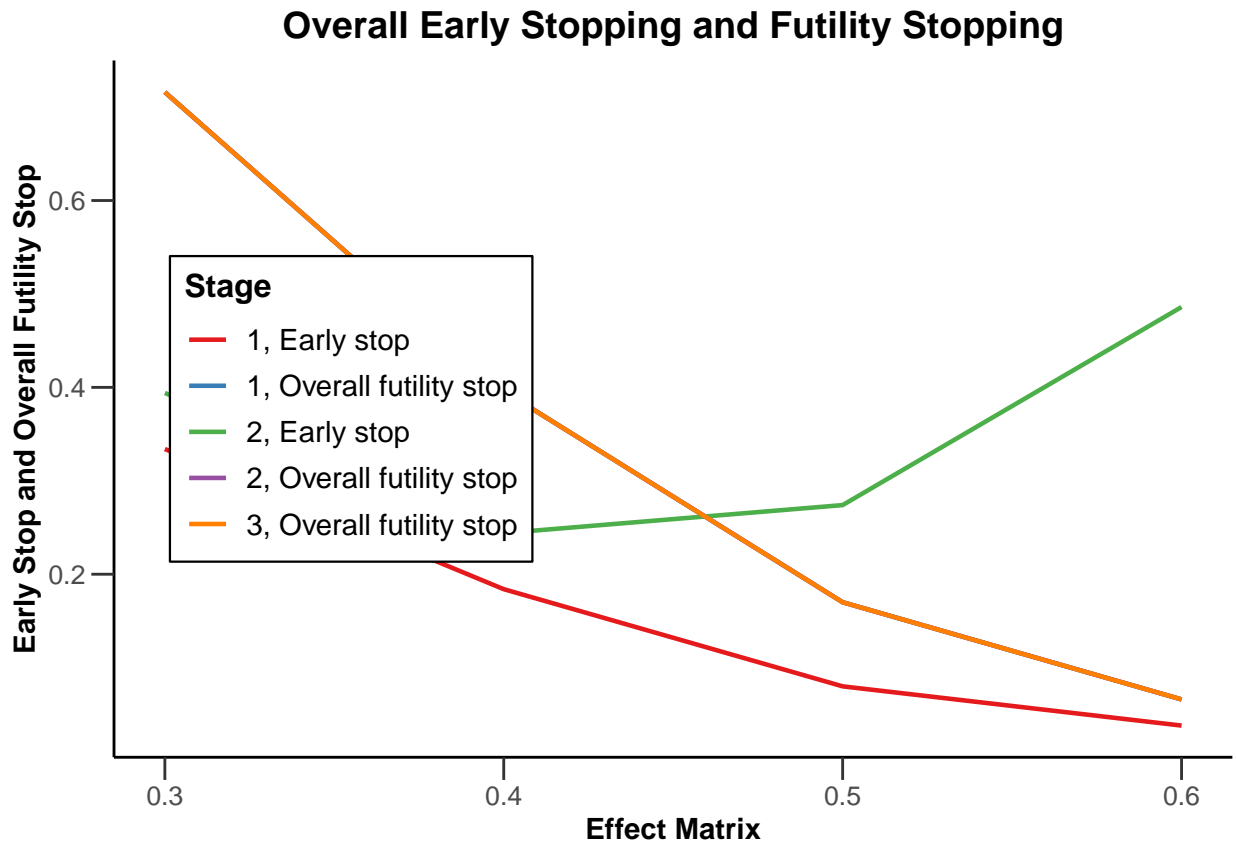


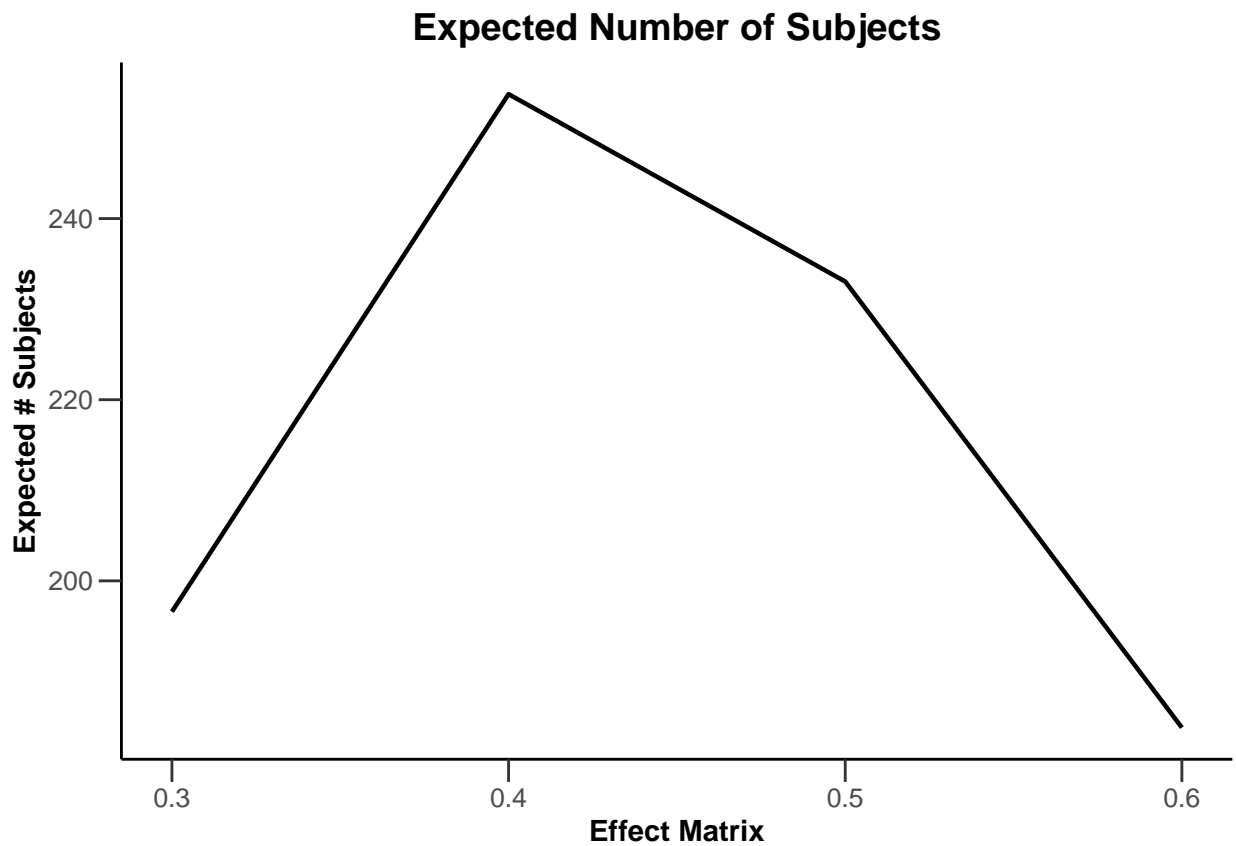






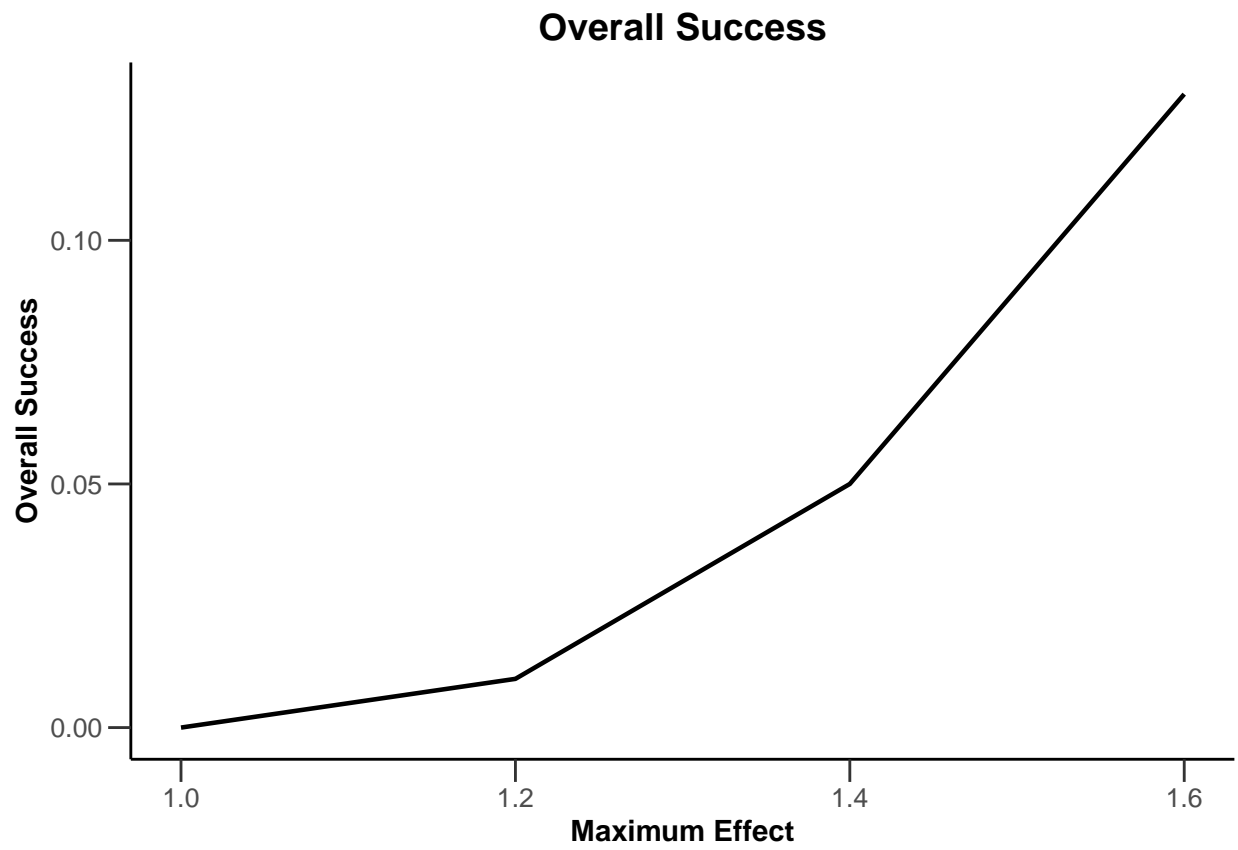


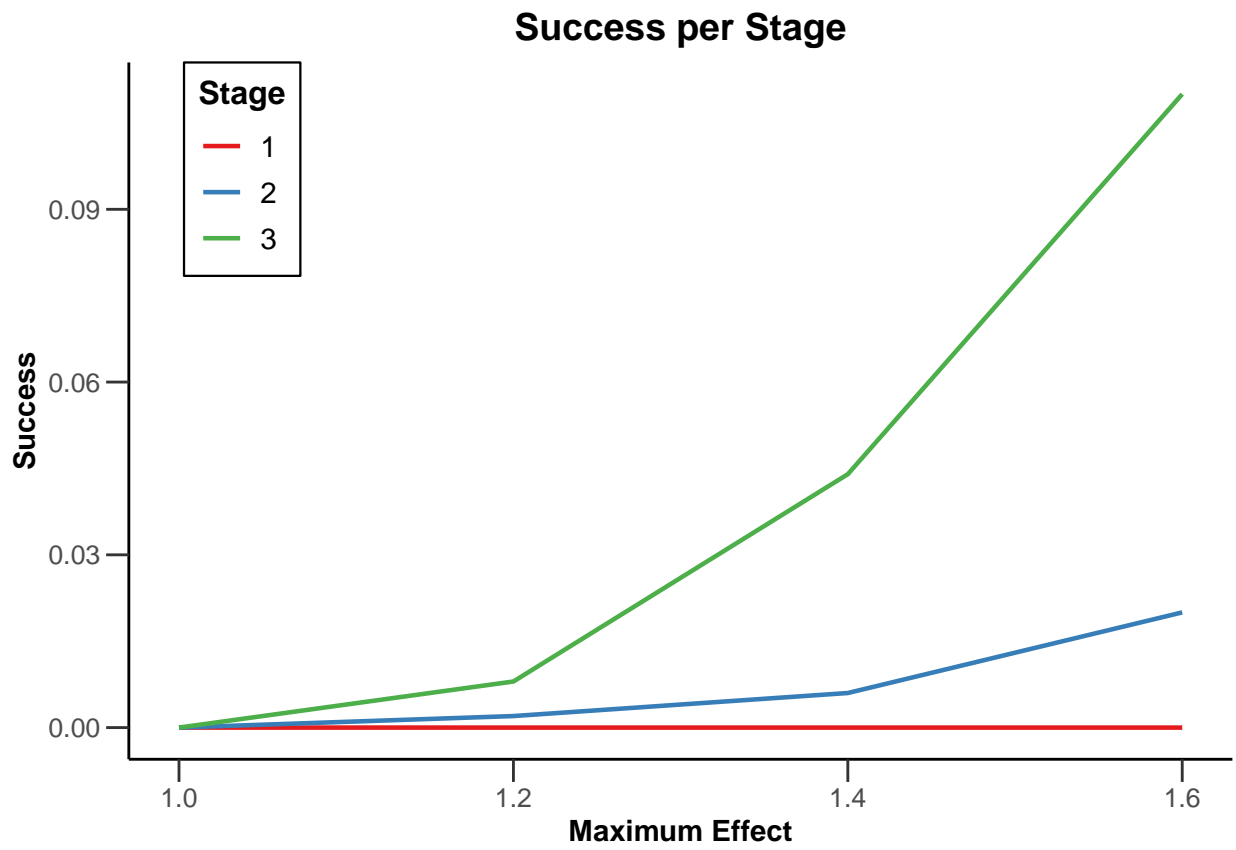


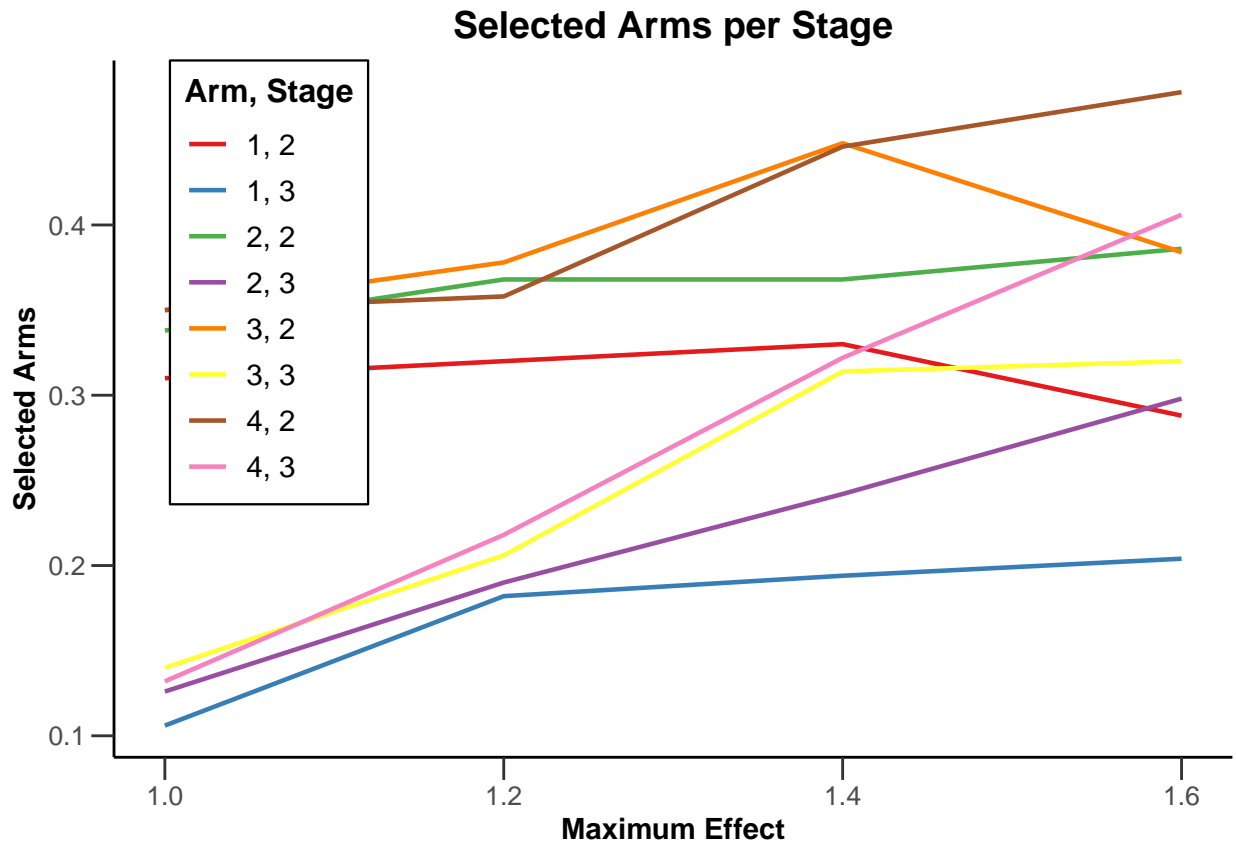


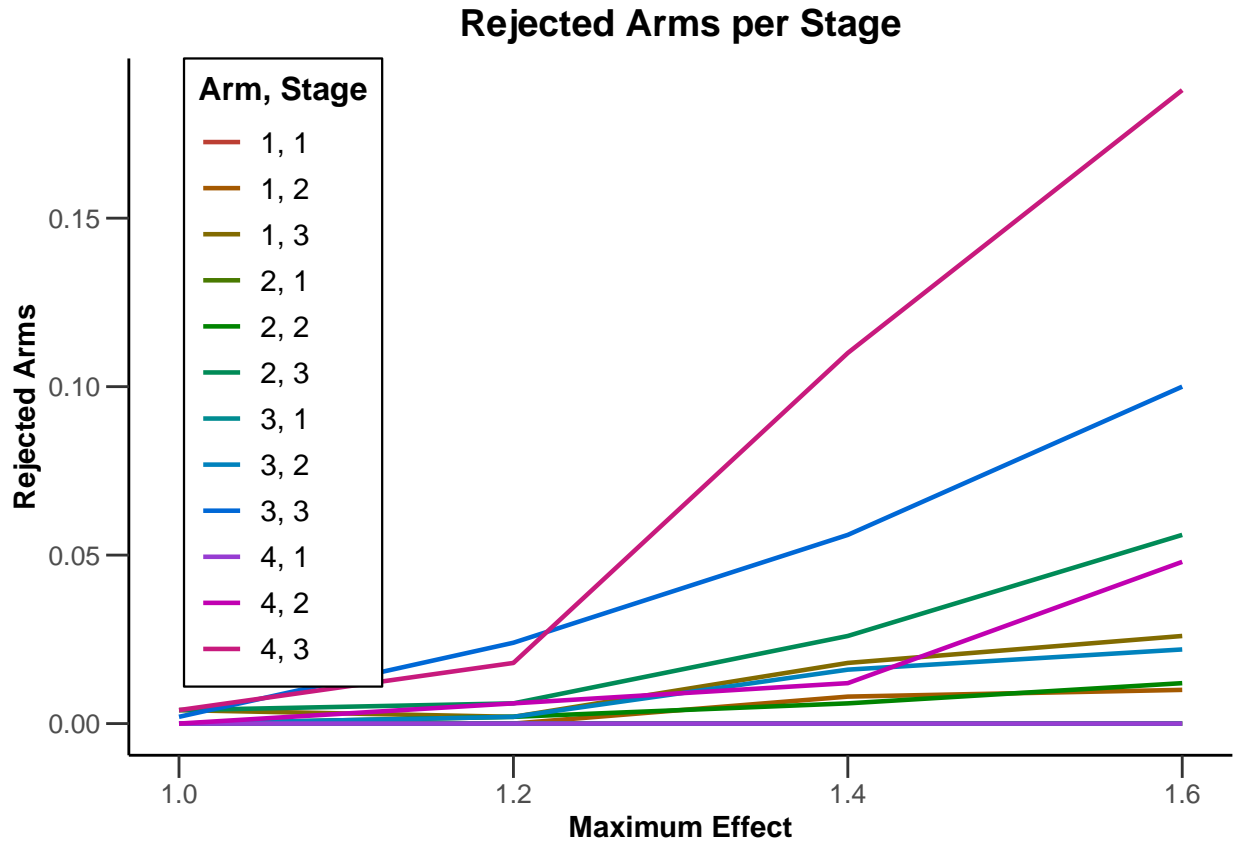
### 3.3 Simulation results multi-arm - survival

```
design <- getDesignInverseNormal(  
  informationRates = c(0.2, 0.6, 1),  
  futilityBounds = c(-0.5, 0.5)  
)  
x <- getSimulationMultiArmSurvival(  
  design = design, activeArms = 4,  
  typeOfSelection = "rBest", rValue = 2, plannedEvents = c(10, 30, 50),  
  omegaMaxVector = seq(1, 1.6, 0.2), adaptations = rep(TRUE, 2),  
  conditionalPower = 0.8, minNumberOfEventsPerStage = c(10, 4, 4),  
  maxNumberOfEventsPerStage = c(10, 100, 100),  
  maxNumberOfIterations = 500, seed = 1234567890  
)  
plot(x, type = "all", grid = 0)
```

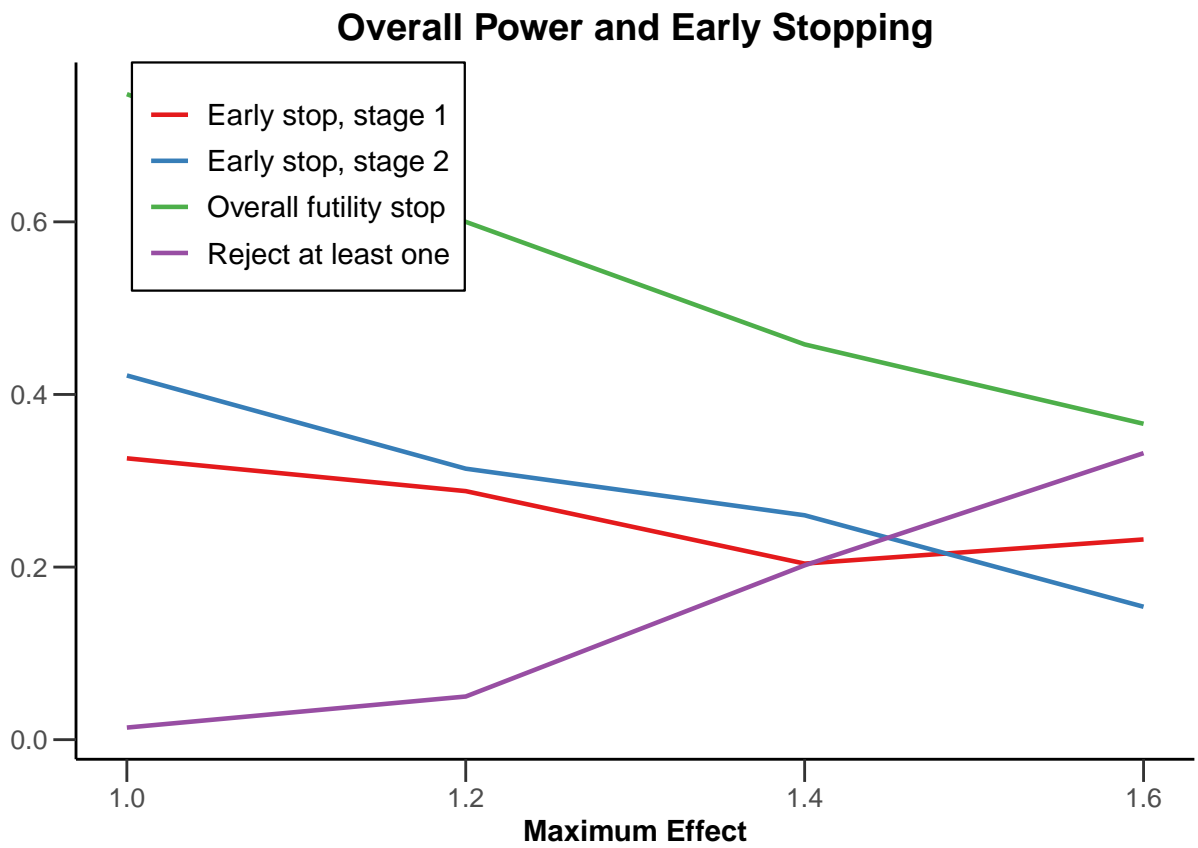


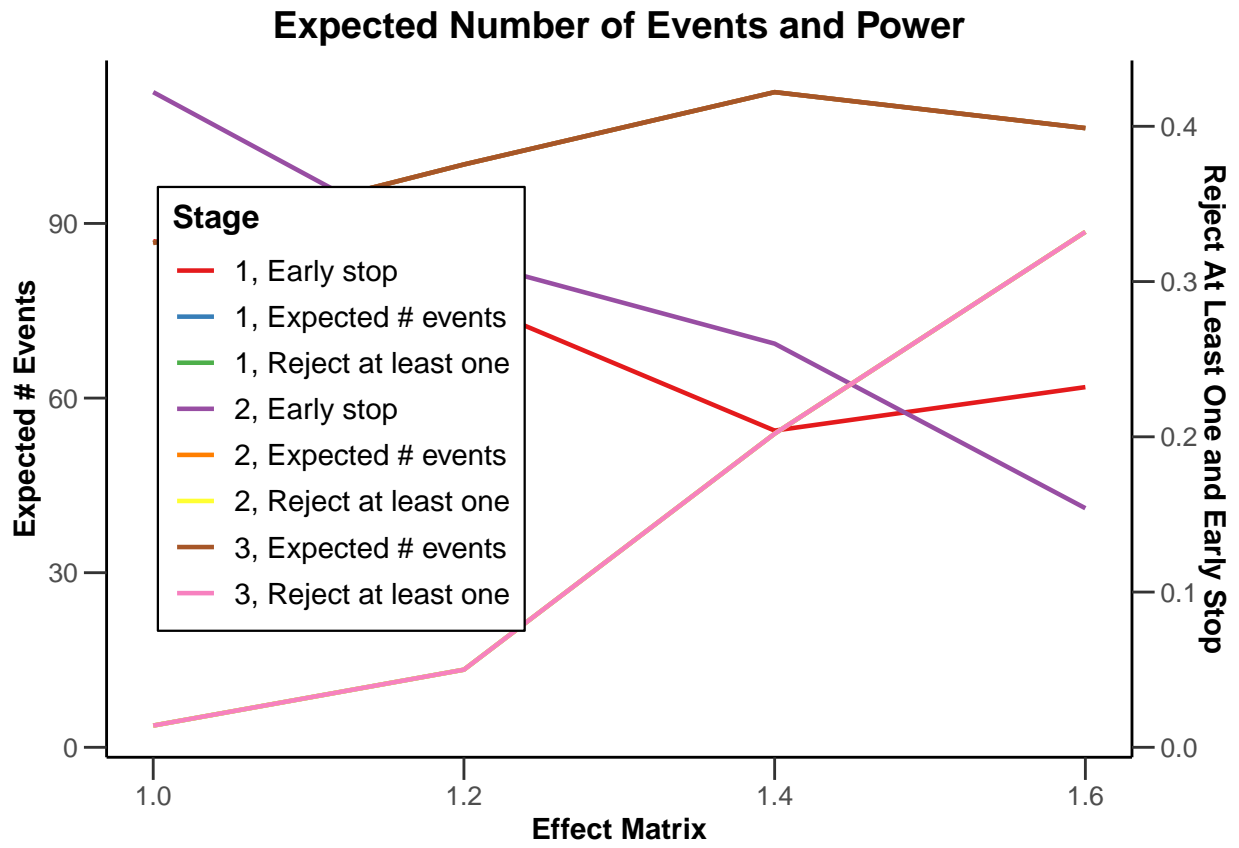


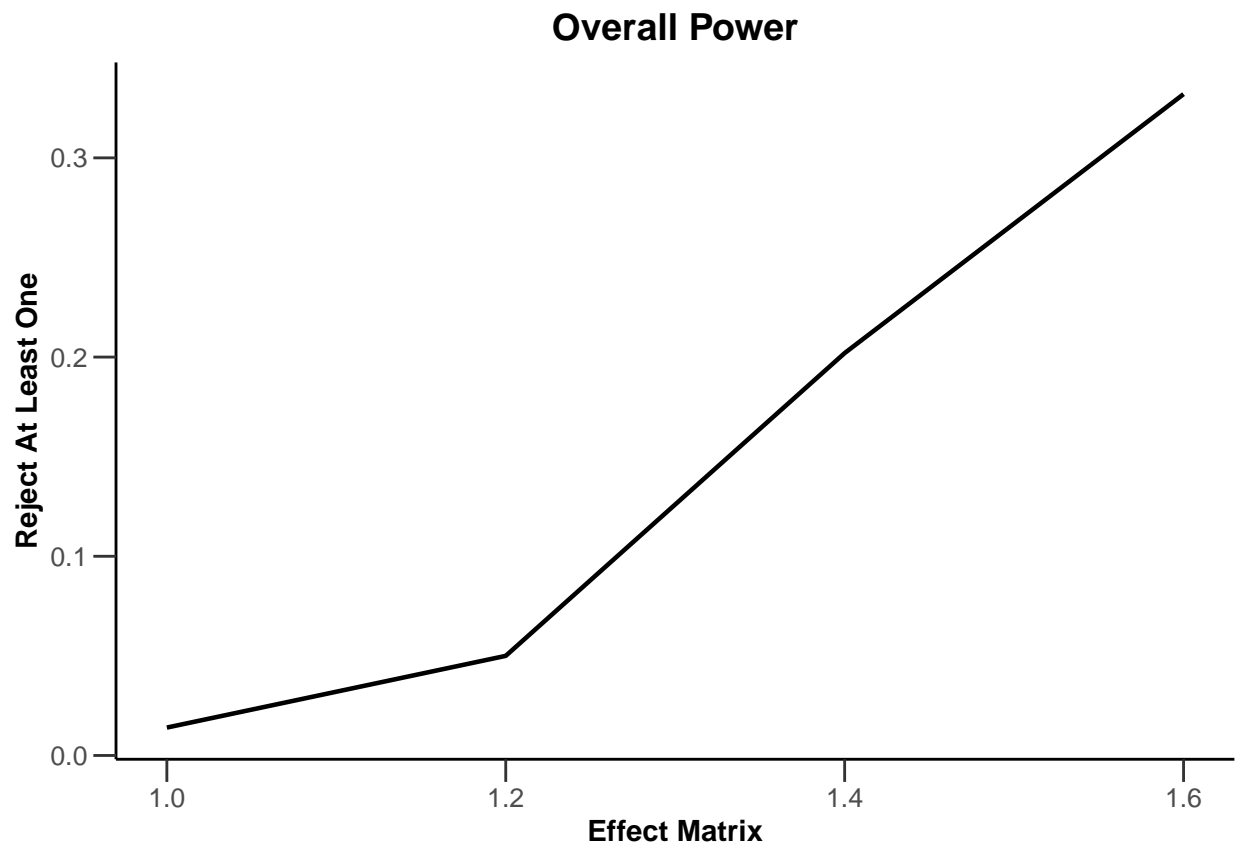


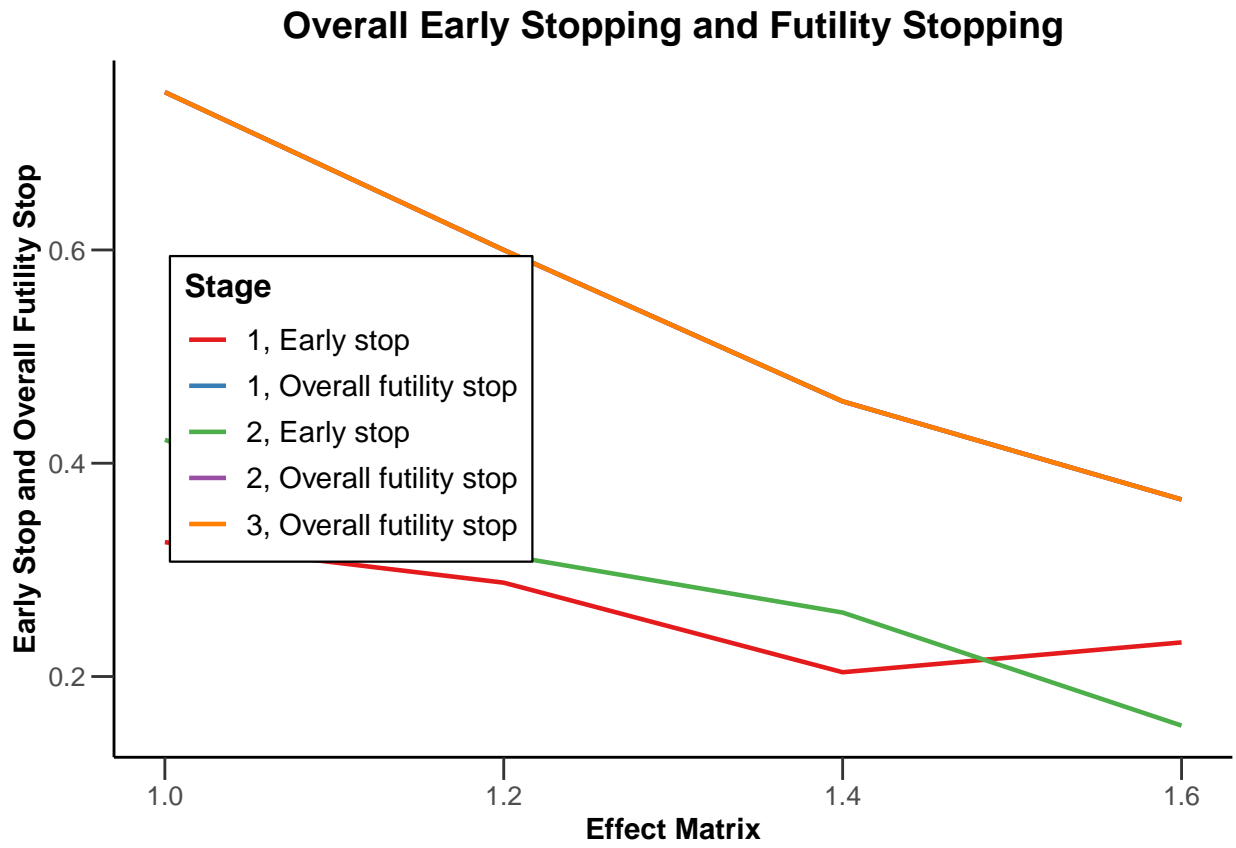


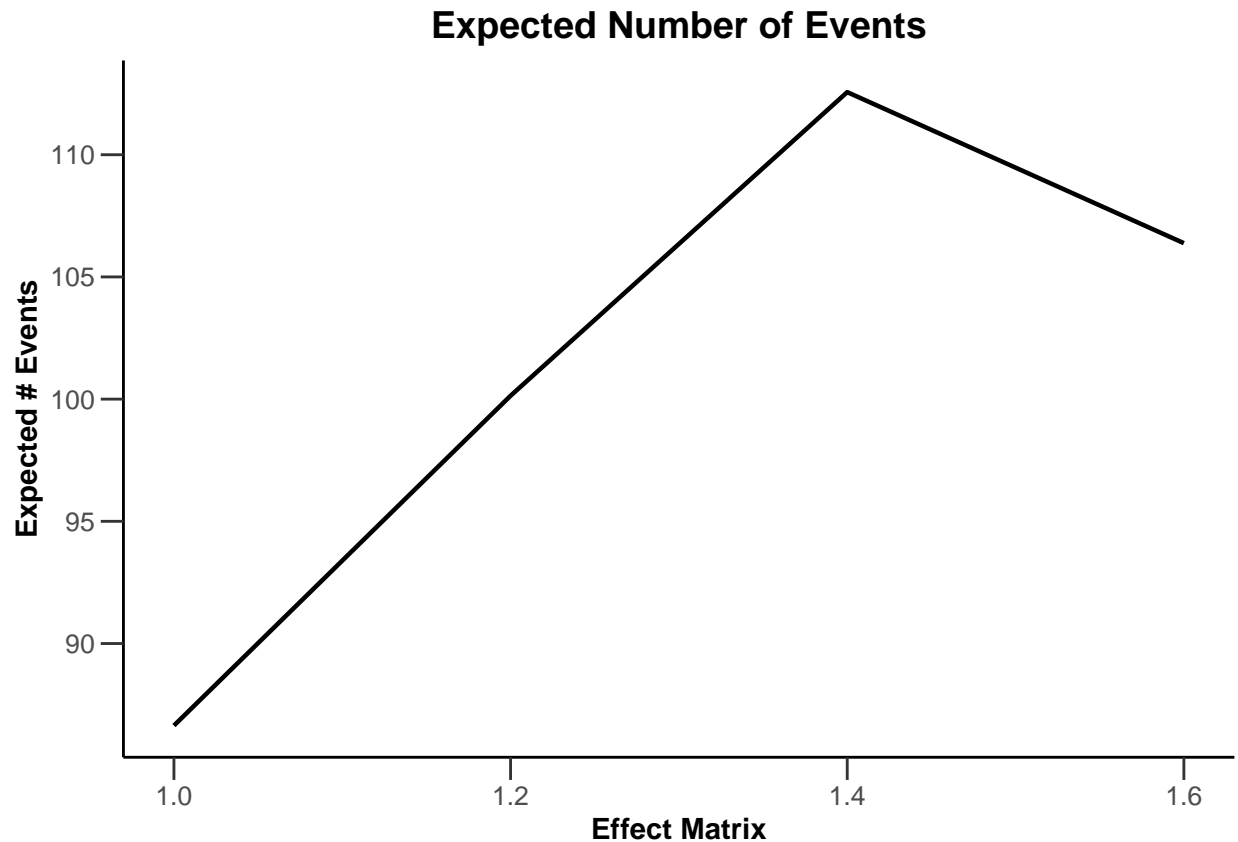












## 4 Simulation results enrichment

### 4.1 Simulation results enrichment - means

```

design <- getDesignInverseNormal(
  informationRates = c(0.2, 0.6, 1),
  futilityBounds = c(-0.5, 0.5)
)
# Define subgroups and their prevalences
subGroups <- c("S1", "S12", "S2", "R") # fixed names!
prevalences <- c(0.2, 0.3, 0.4, 0.1)

effectR <- 1.5
effectS12 <- 5
m <- c()
for (effectS1 in seq(0, 5, 5)) {
  for (effectS2 in seq(0, 5, 5)) {
    m <- c(m, effectS1, effectS12, effectS2, effectR)
  }
}
effects <- matrix(m, byrow = TRUE, ncol = 4)
stDev <- 10
# Define effect list
el <- list(
  subGroups = subGroups, prevalences = prevalences,

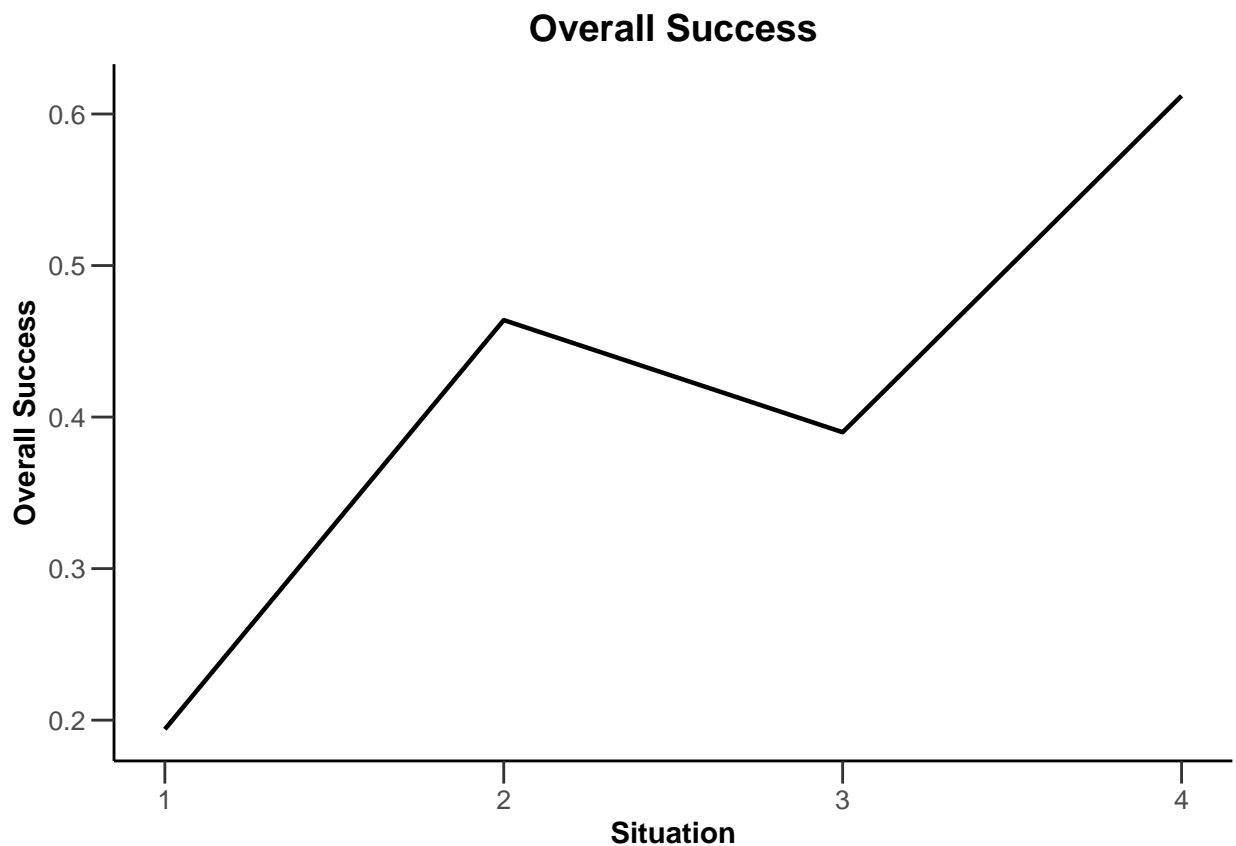
```

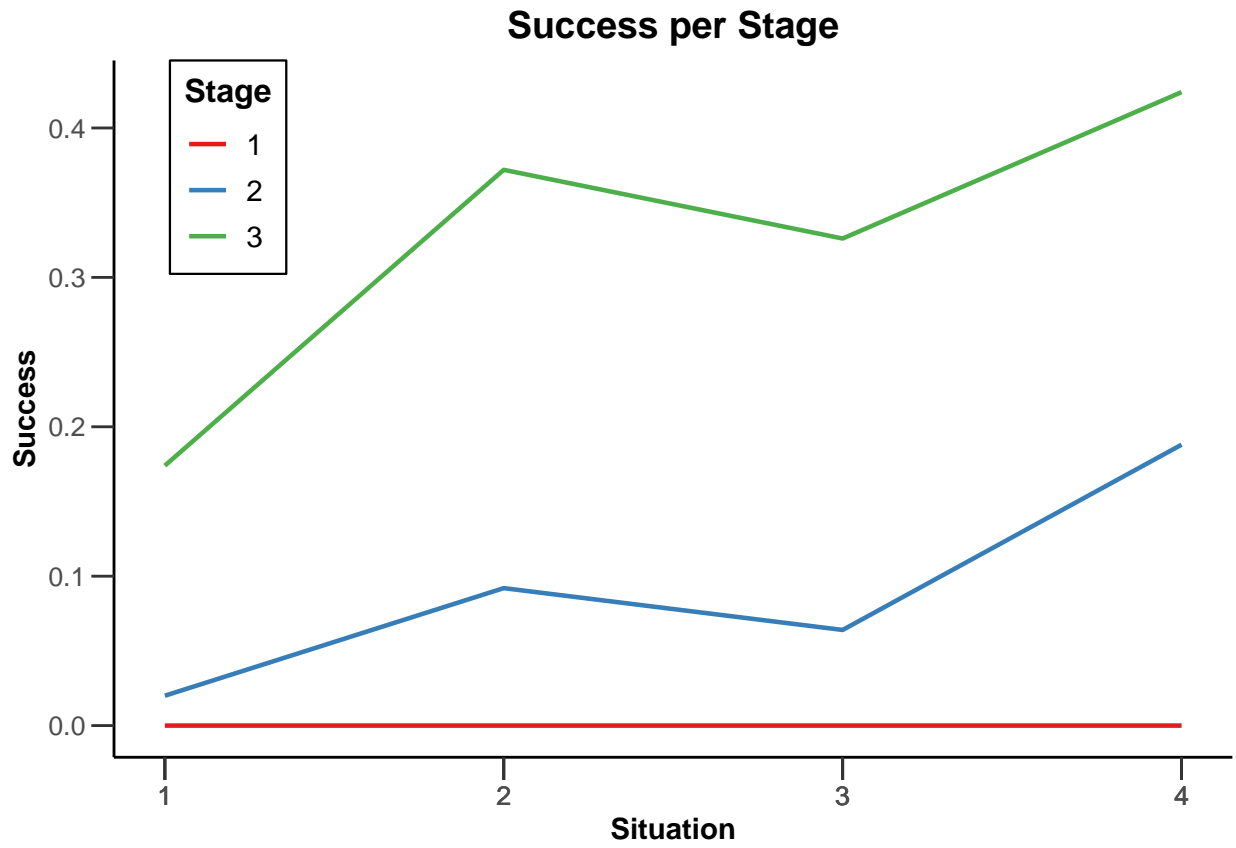
```
    stDevs = stDev, effects = effects
  )

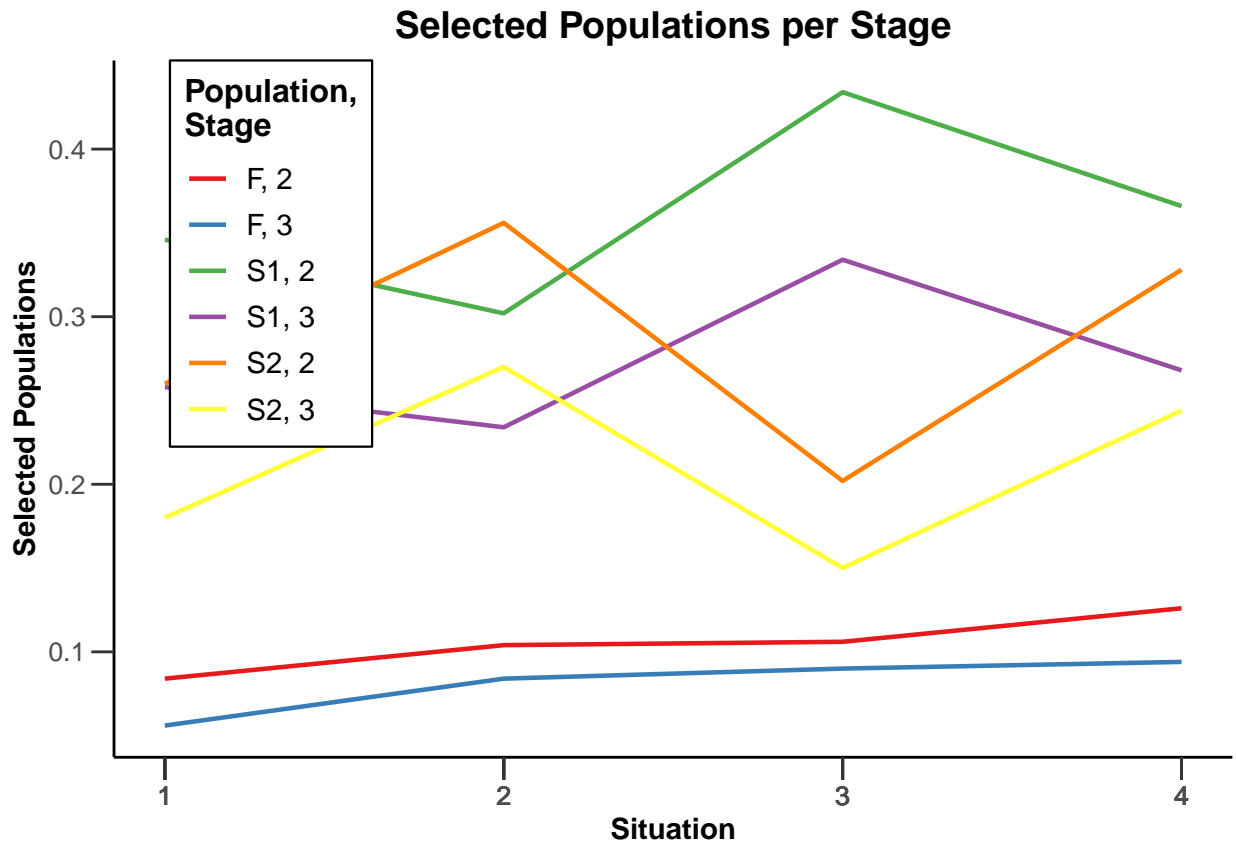
x <- getSimulationEnrichmentMeans(
  design = design,
  plannedSubjects = c(10, 30, 50),
  effectList = el,
  adaptations = rep(TRUE, 2),
  conditionalPower = 0.8,
  minNumberOfSubjectsPerStage = c(10, 4, 4),
  maxNumberOfSubjectsPerStage = c(10, 100, 100),
  maxNumberOfIterations = 500,
  seed = 1234567890
)
```

```
## Warning: Simulation of enrichment designs is experimental and hence not fully
## validated (see www.rpact.com/experimental)
```

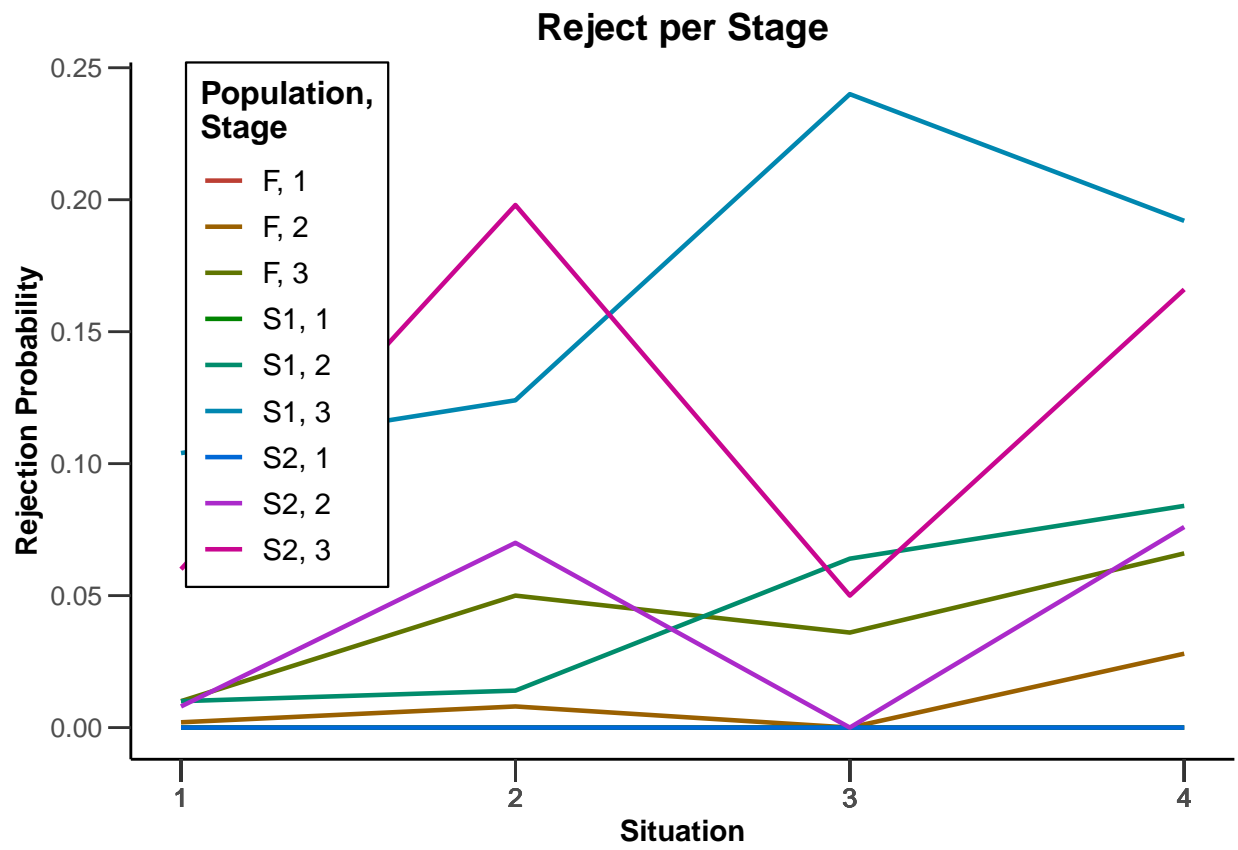
```
plot(x, type = "all", grid = 0)
```

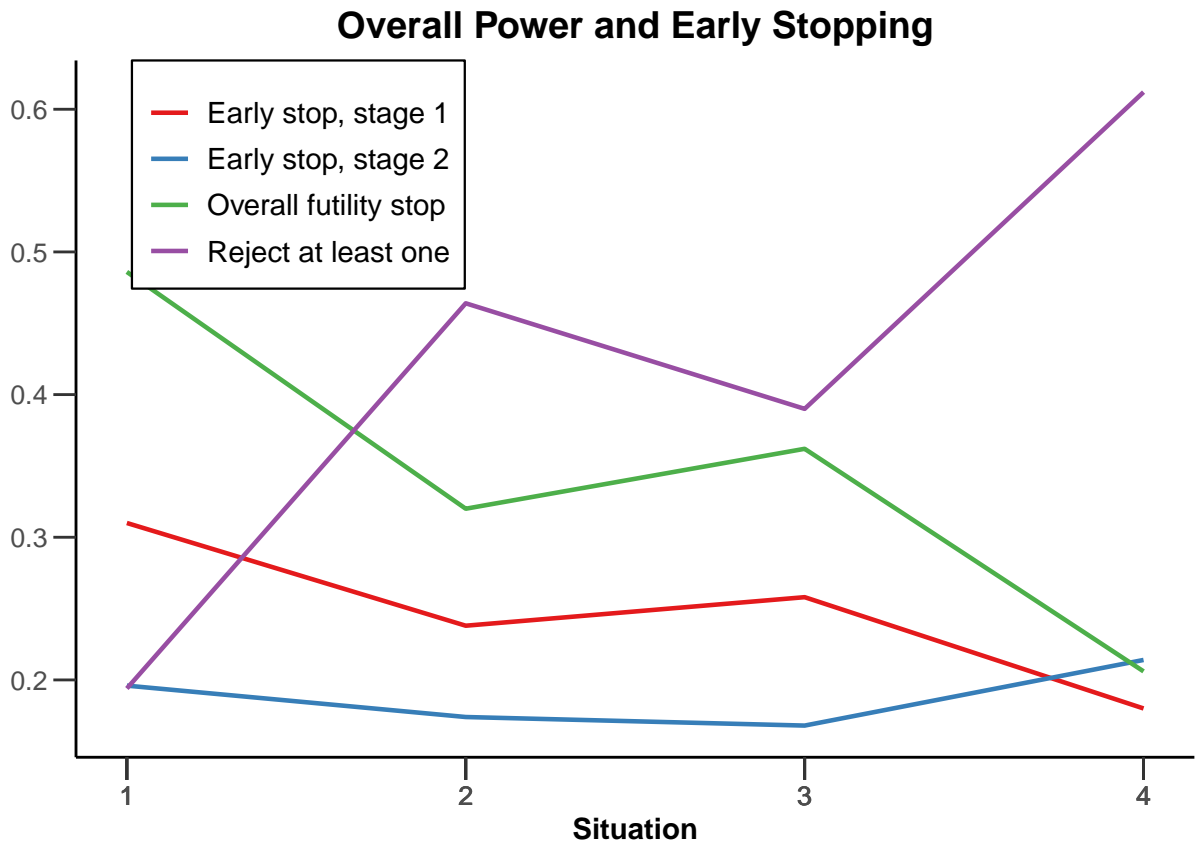


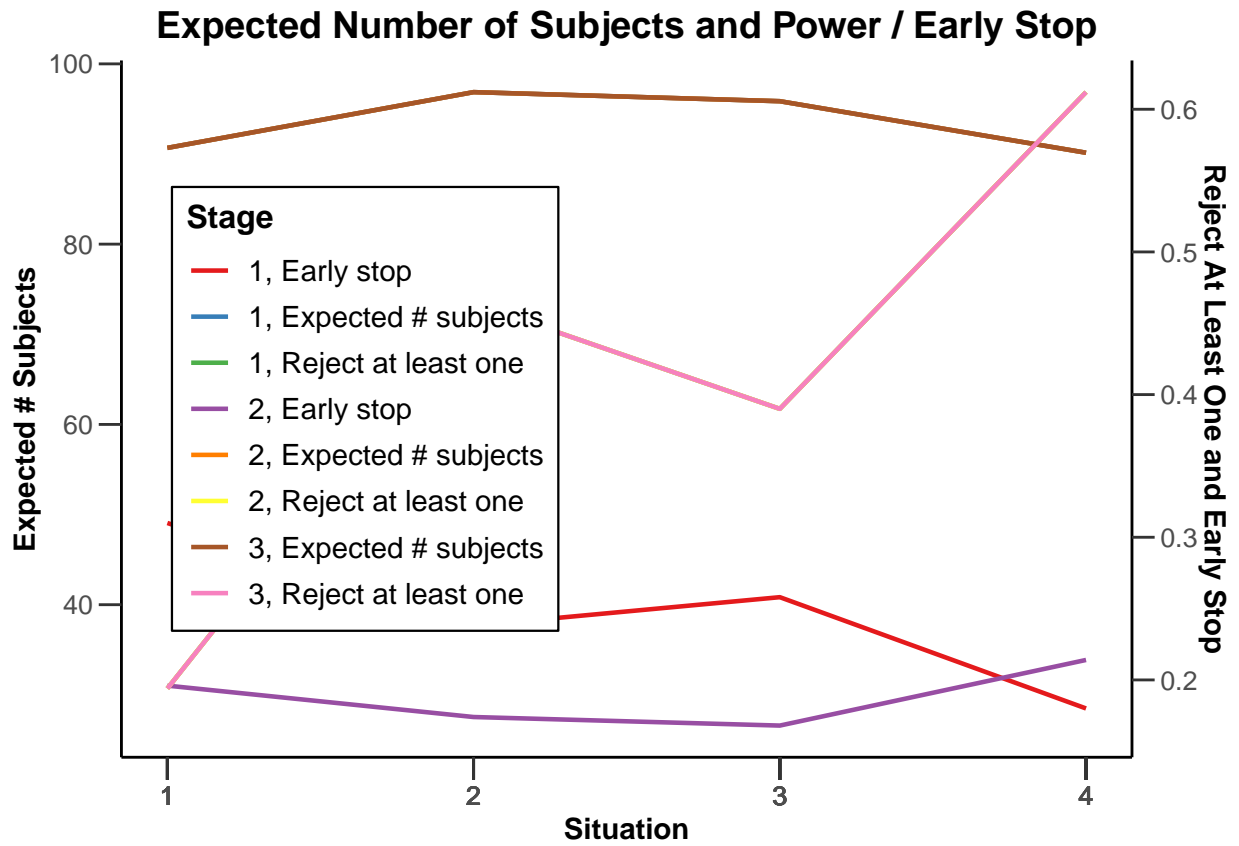


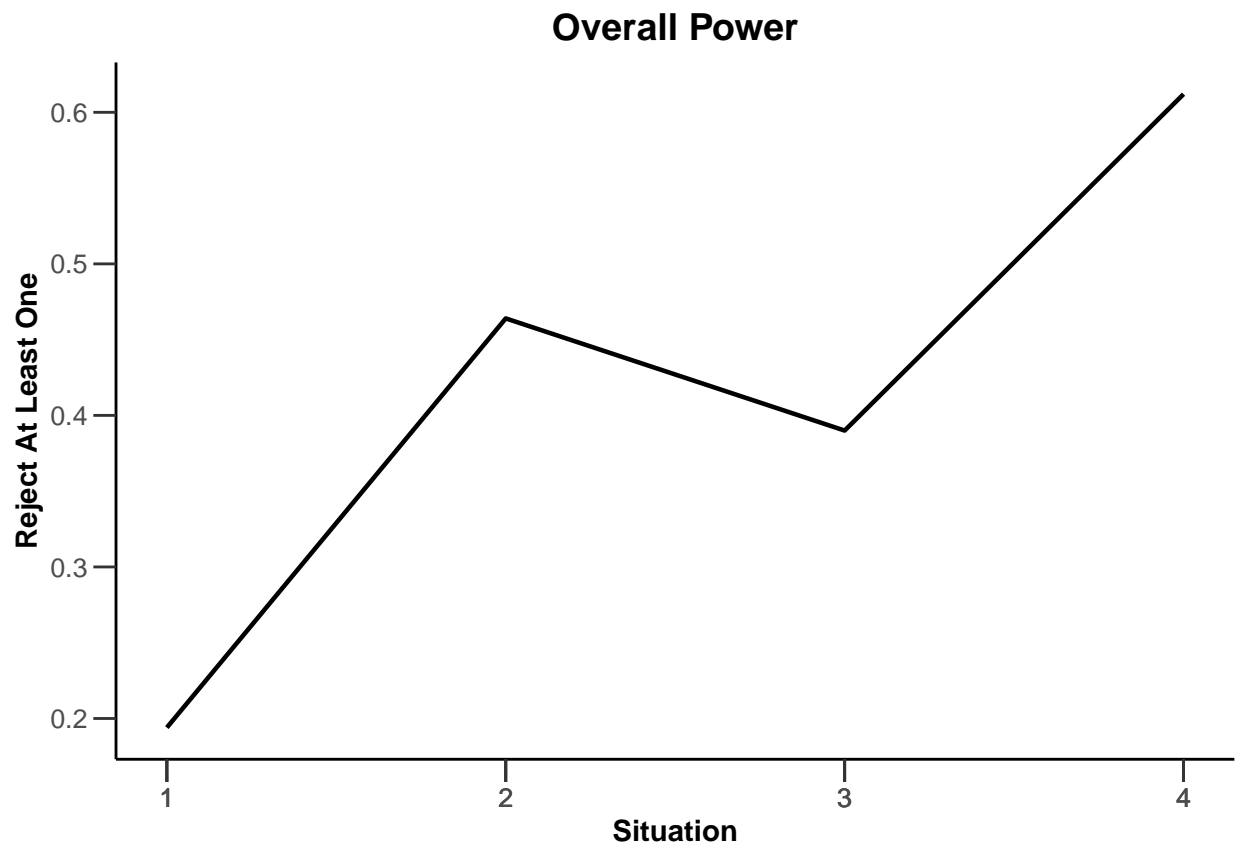


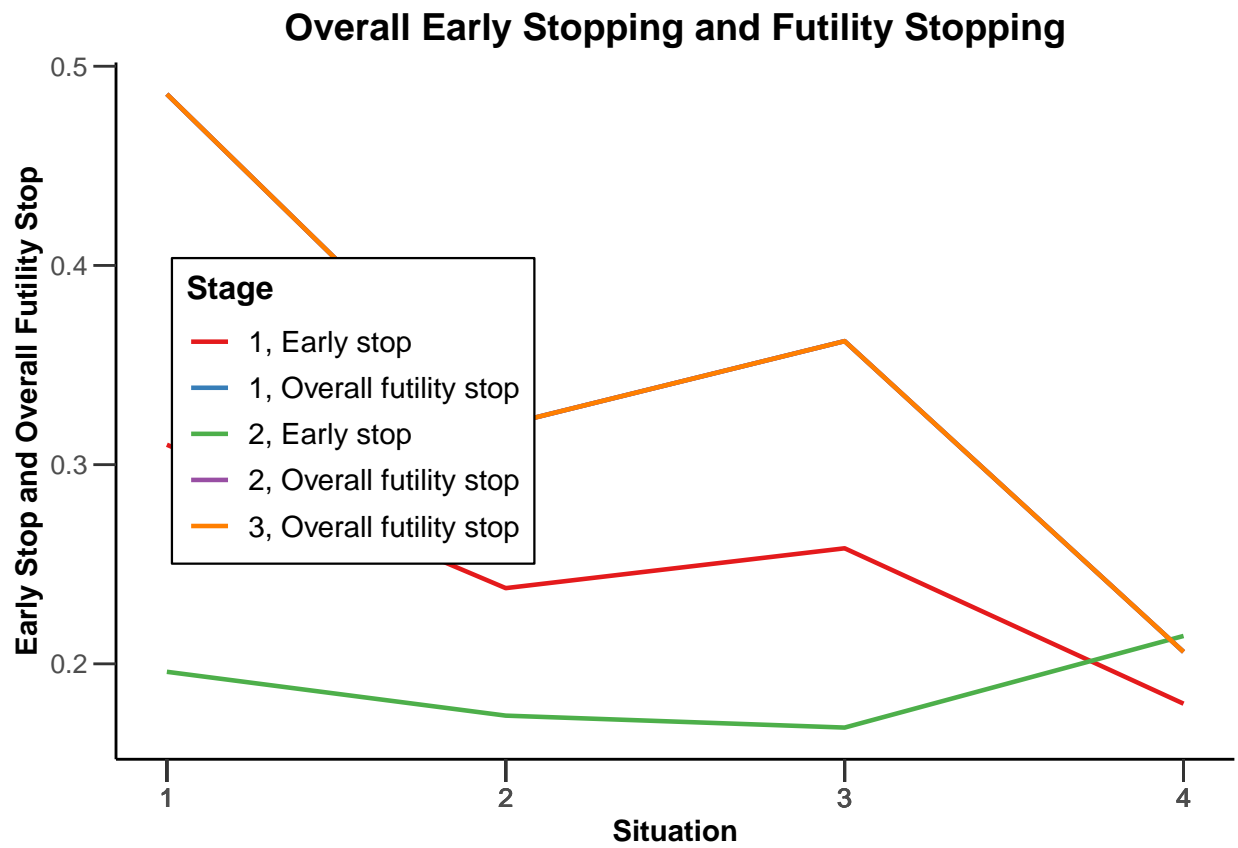


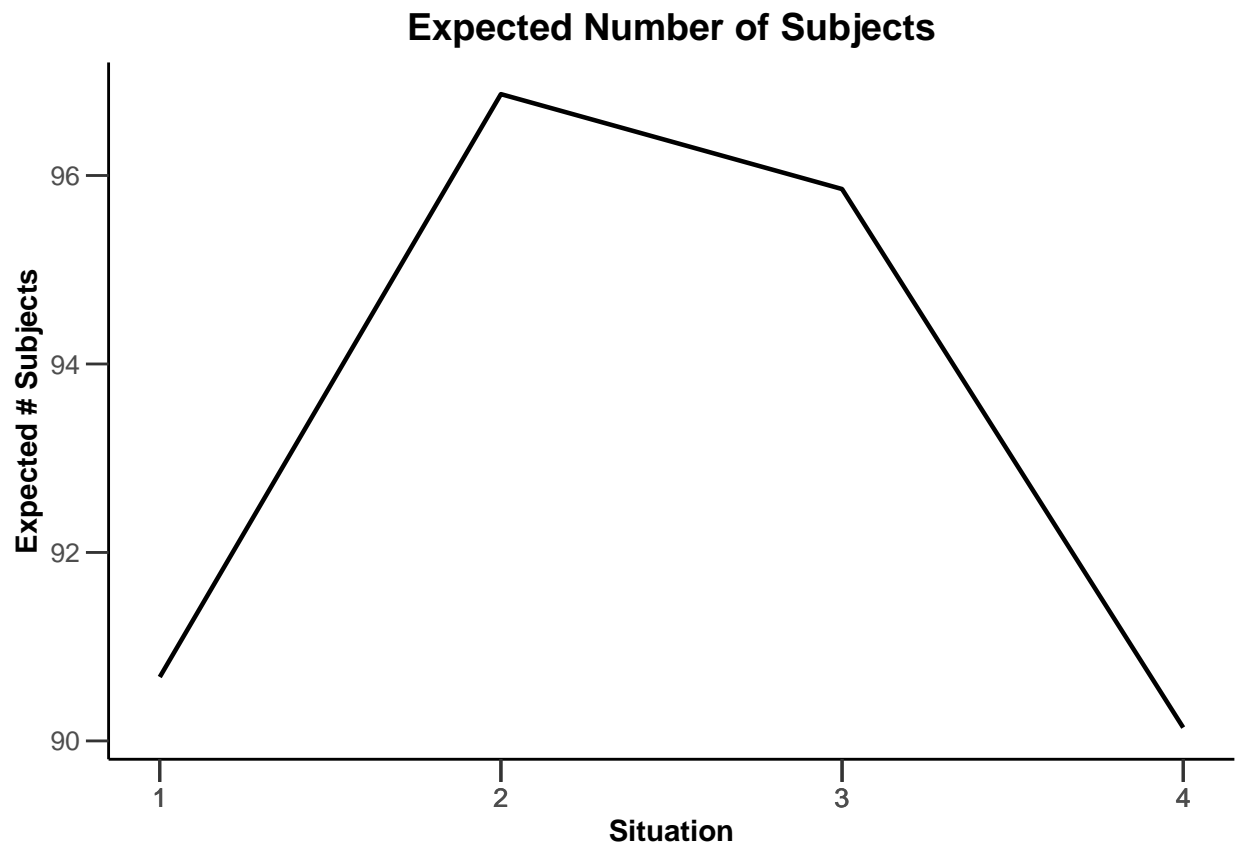












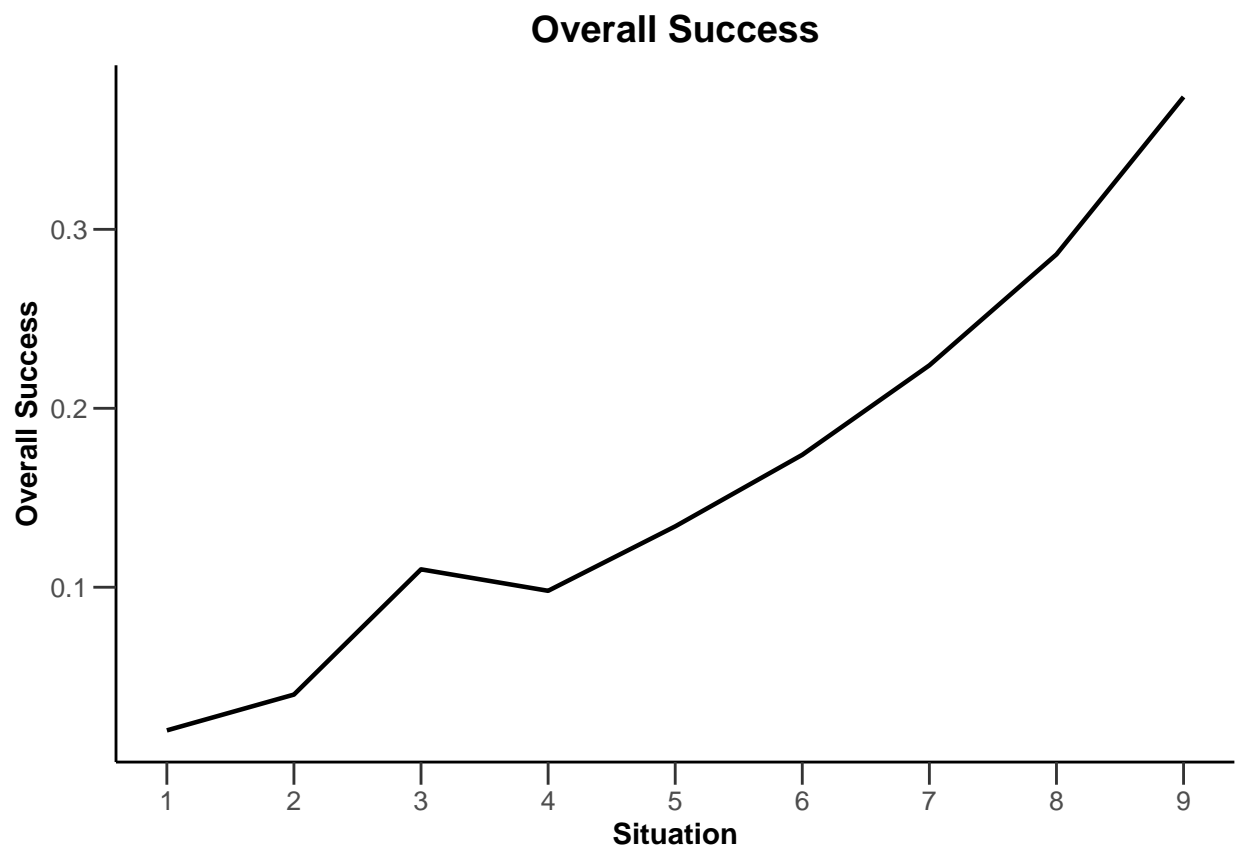
## 4.2 Simulation results enrichment - rates

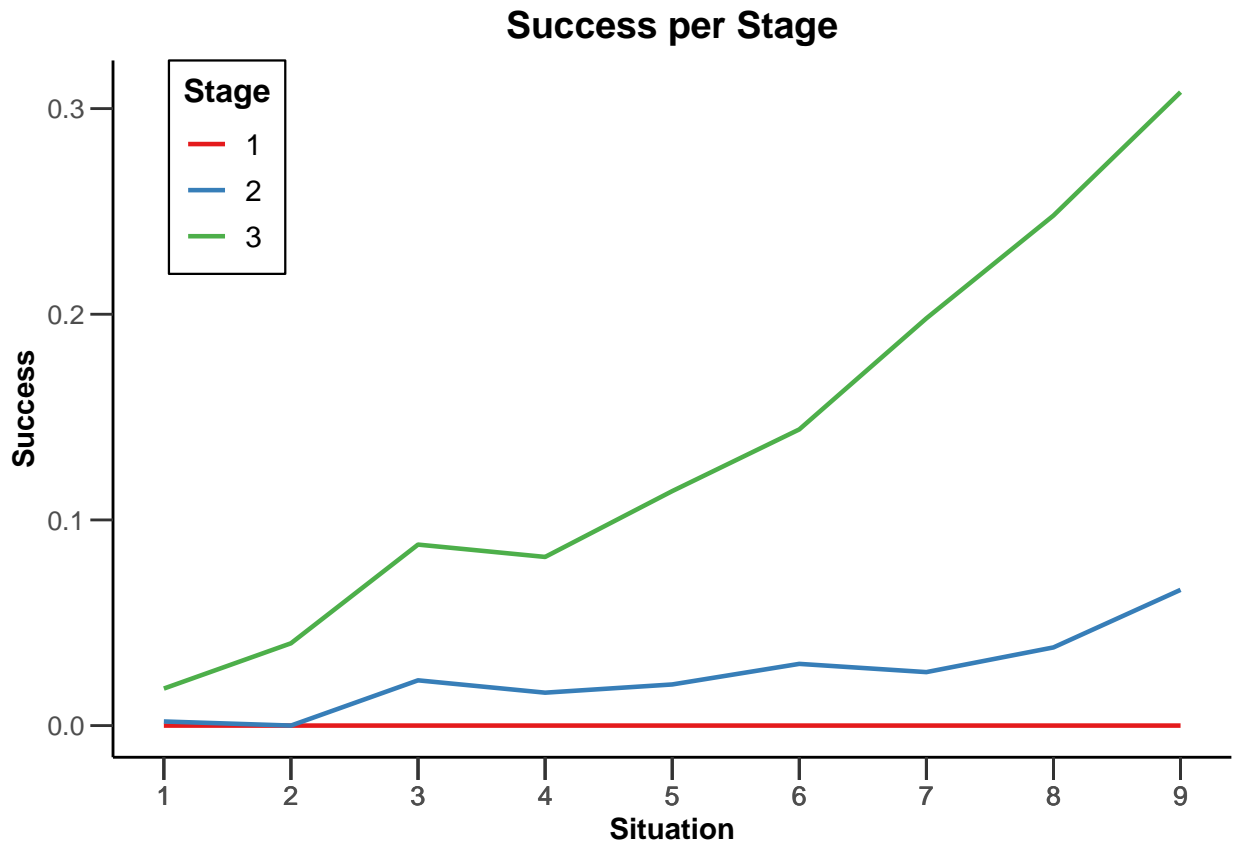
```

design <- getDesignInverseNormal(
  informationRates = c(0.2, 0.6, 1),
  futilityBounds = c(-0.5, 0.5)
)
# Define effect list
subGroups <- c("S", "R")
prevalences <- c(0.4, 0.6)
piControl <- c(0.1, 0.4)
range1 <- piControl[1] + seq(0.0, 0.2, 0.1)
range2 <- piControl[2] + seq(0.0, 0.2, 0.1)
piTreatments <- c()
for (x1 in range1) {
  for (x2 in range2) {
    piTreatments <- c(piTreatments, x1, x2)
  }
}
el <- list(
  subGroups = subGroups,
  prevalences = prevalences,
  piControl = piControl,
  piTreatments = matrix(piTreatments,
    byrow = TRUE, ncol = 2
  )
)

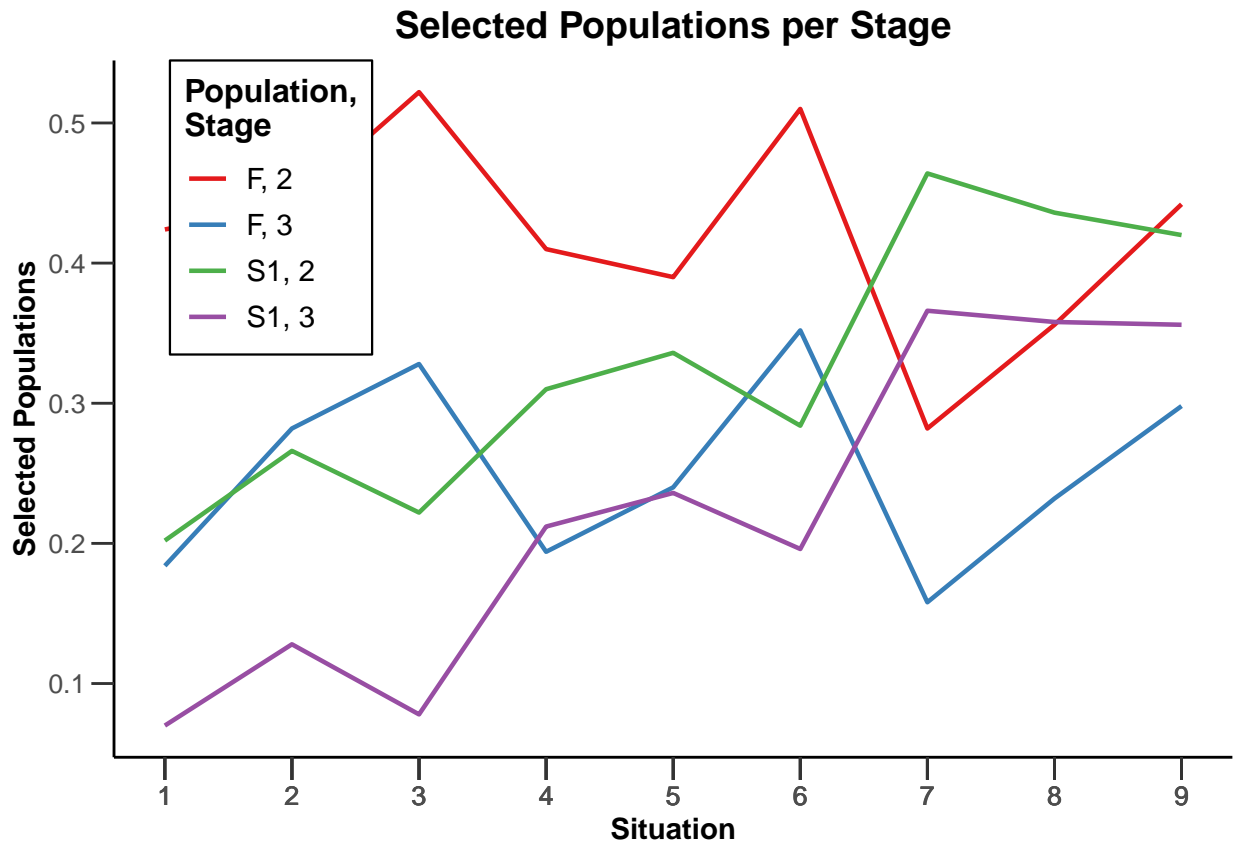
```

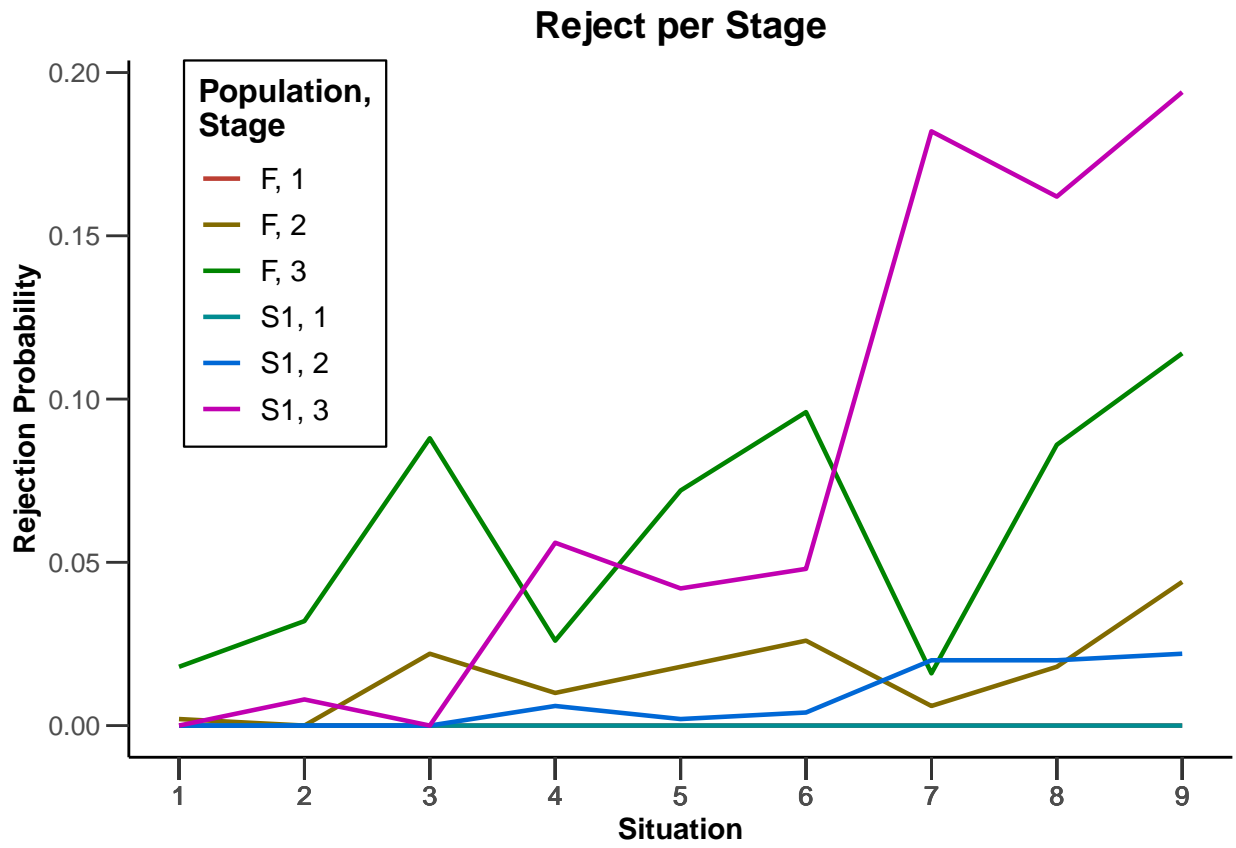
```
)  
x <- getSimulationEnrichmentRates(  
  design = design,  
  plannedSubjects = c(10, 30, 50),  
  effectList = el,  
  maxNumberOfIterations = 500,  
  seed = 1234567890  
)  
  
## Warning: Simulation of enrichment designs is experimental and hence not fully  
## validated (see www.rpact.com/experimental)  
plot(x, type = "all", grid = 0)
```

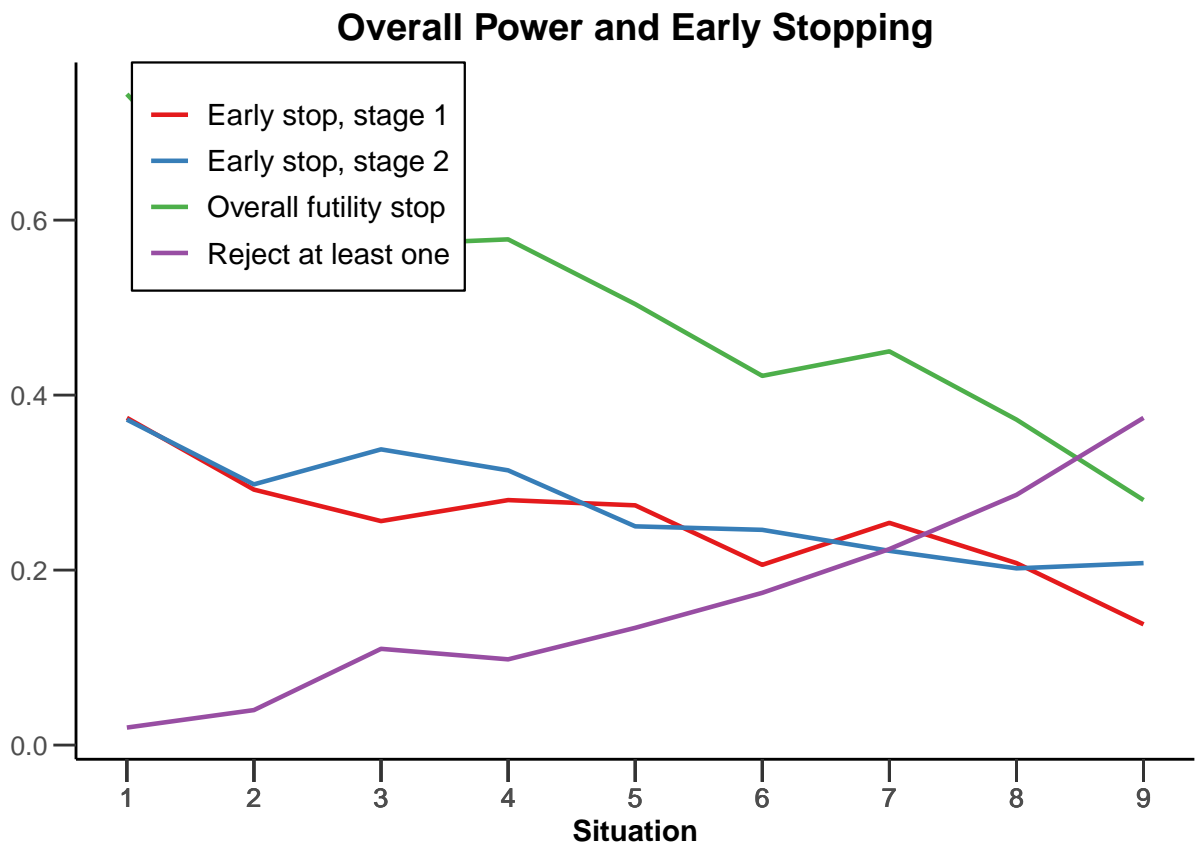


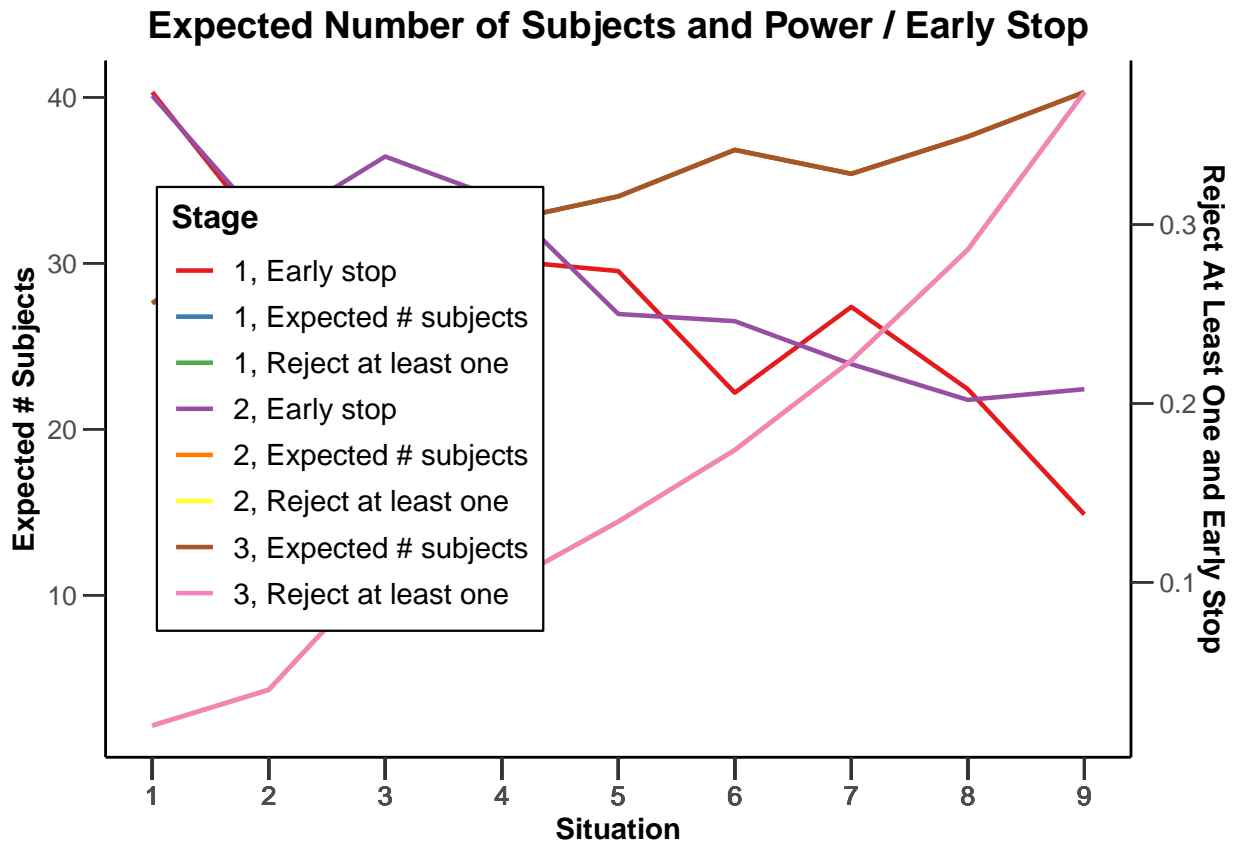


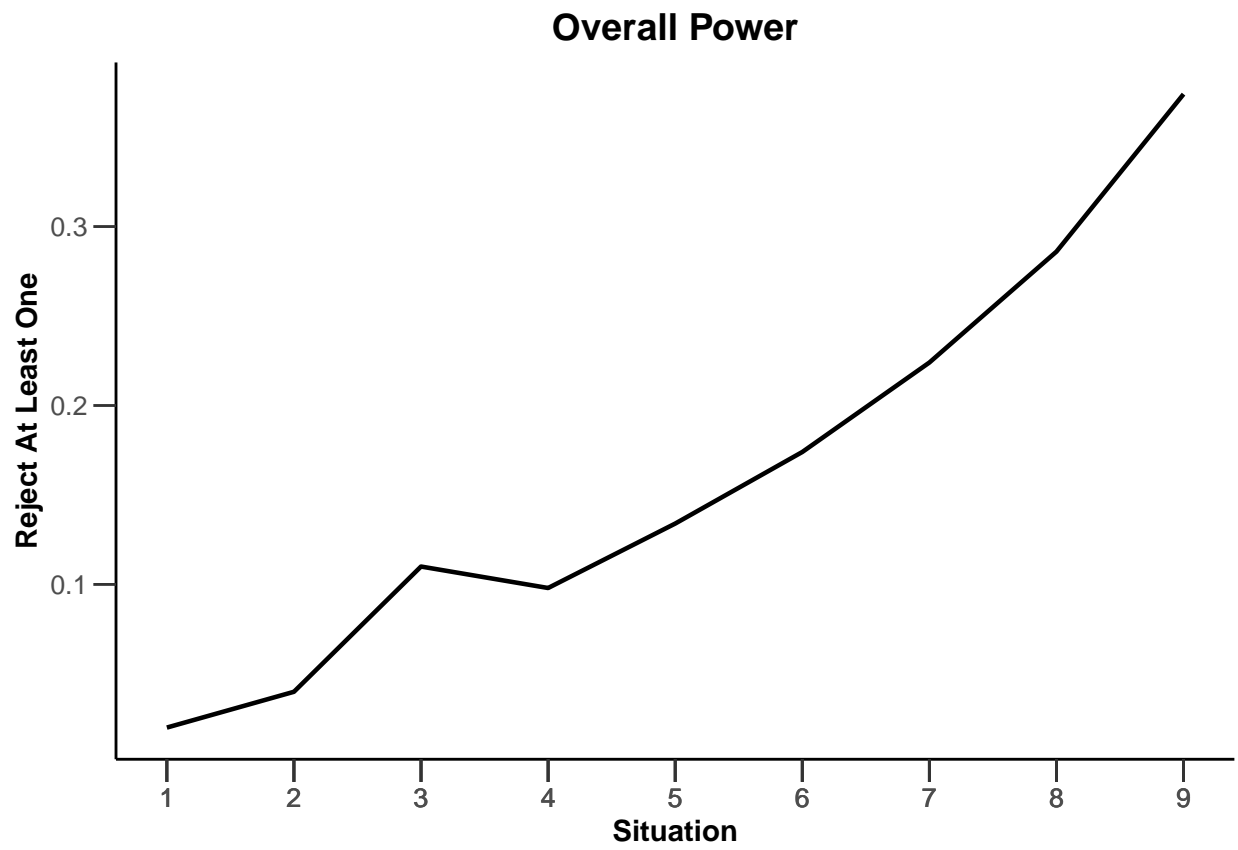


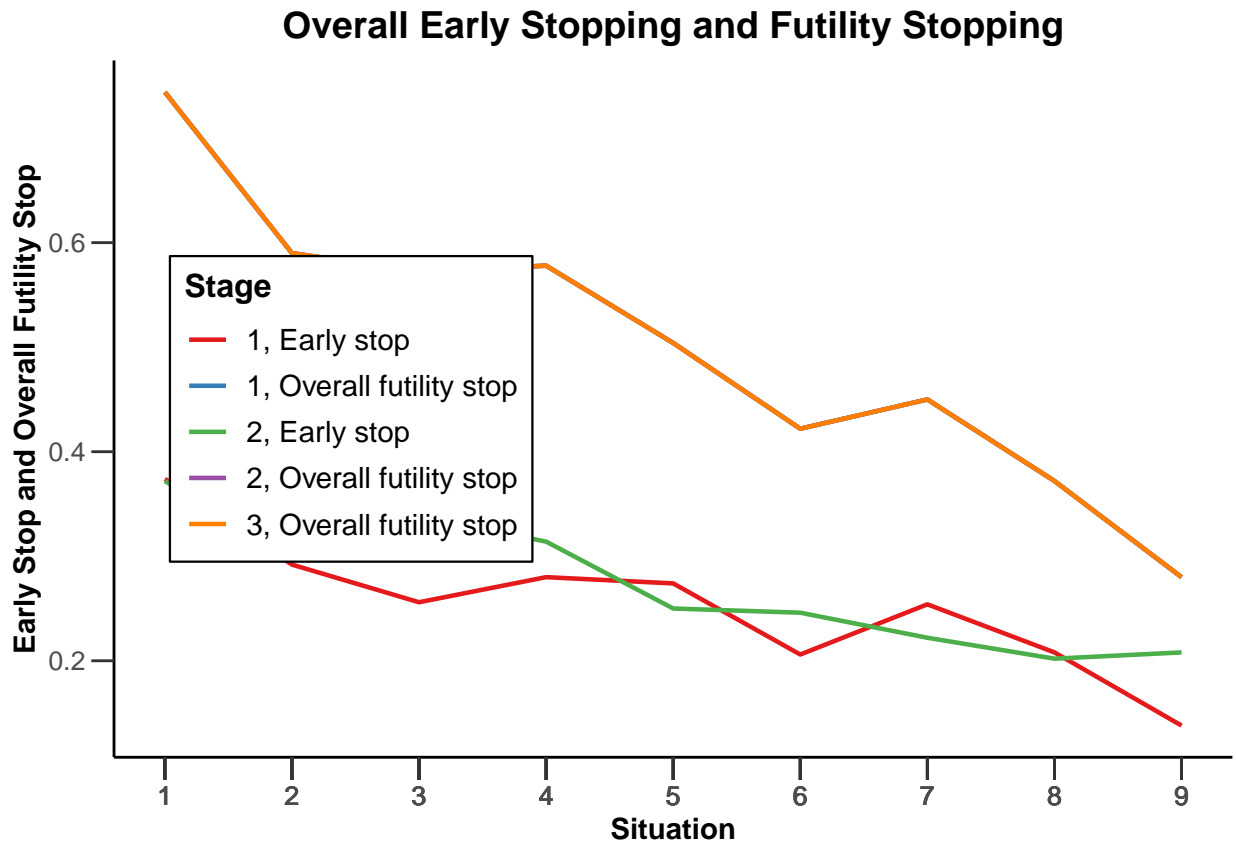


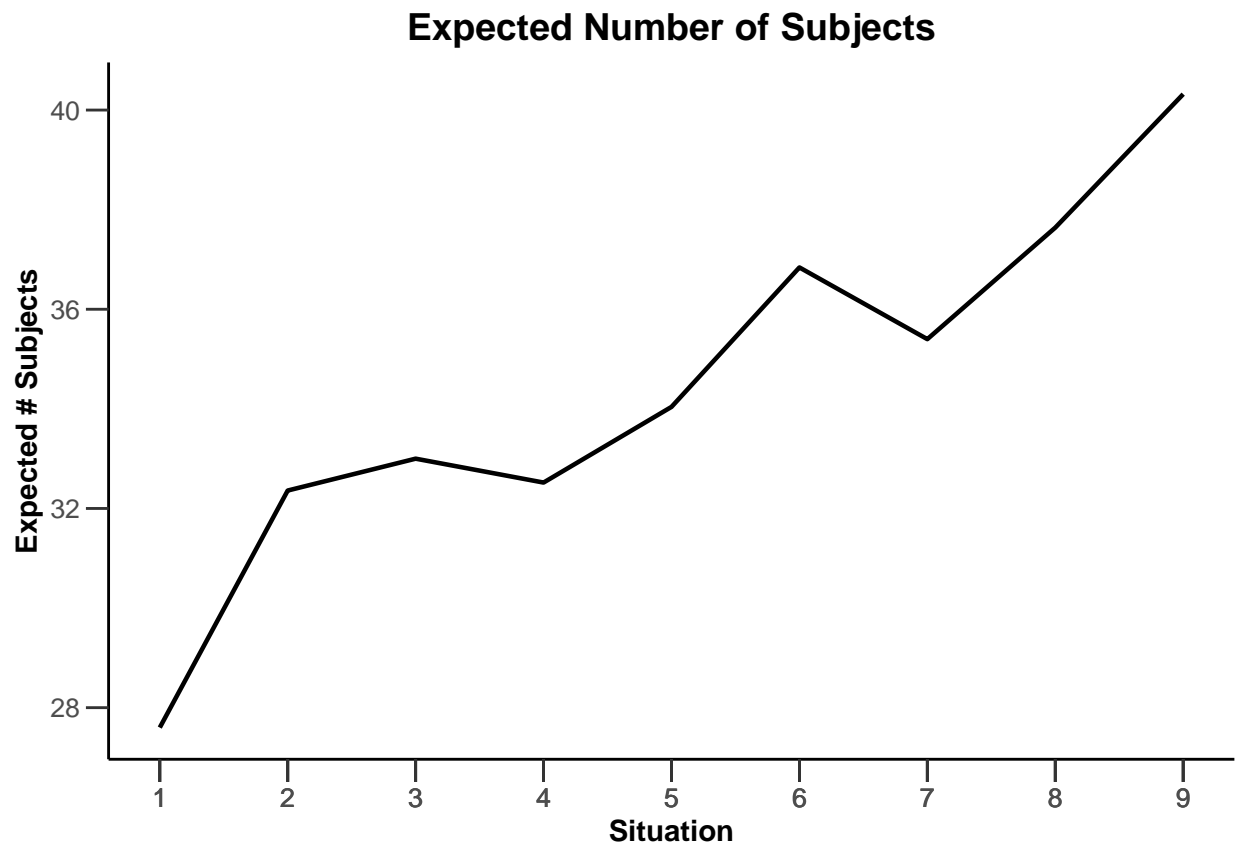












### 4.3 Simulation results enrichment - survival

```

# Define subgroups and their prevalences
subGroups <- c("S1", "S2", "S12", "R") # fixed names!
prevalences <- c(0.2, 0.3, 0.4, 0.1)

piControls <- c(0.2, 0.4, 0.15, 0.3)
effect <- c(-0.05, -0.02, -0.10, -0.10)
piTreatments <- piControls + effect

hr <- log(1 - piTreatments) / log(1 - piControls)

# Define effect list
el <- list(
  subGroups = subGroups, prevalences = prevalences,
  piControls = piControls, hazardRatios = matrix(rep(hr, 3), nrow = 3)
)

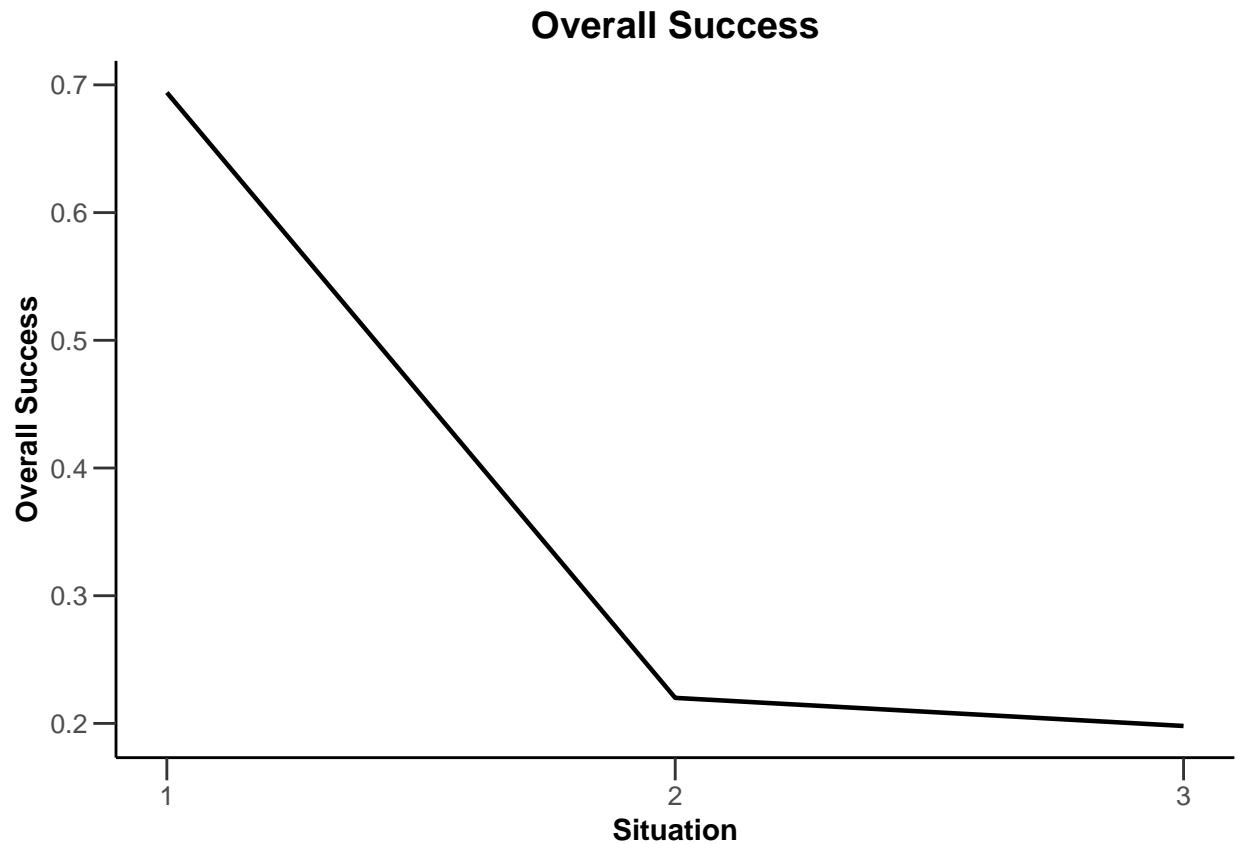
# Perform simulation
x <- getSimulationEnrichmentSurvival(
  design = getDesignInverseNormal(typeOfDesign = "noEarlyEfficacy"),
  effectList = el,
  typeOfSelection = "rbest",
  rValue = 2,
  intersectionTest = "Simes",

```

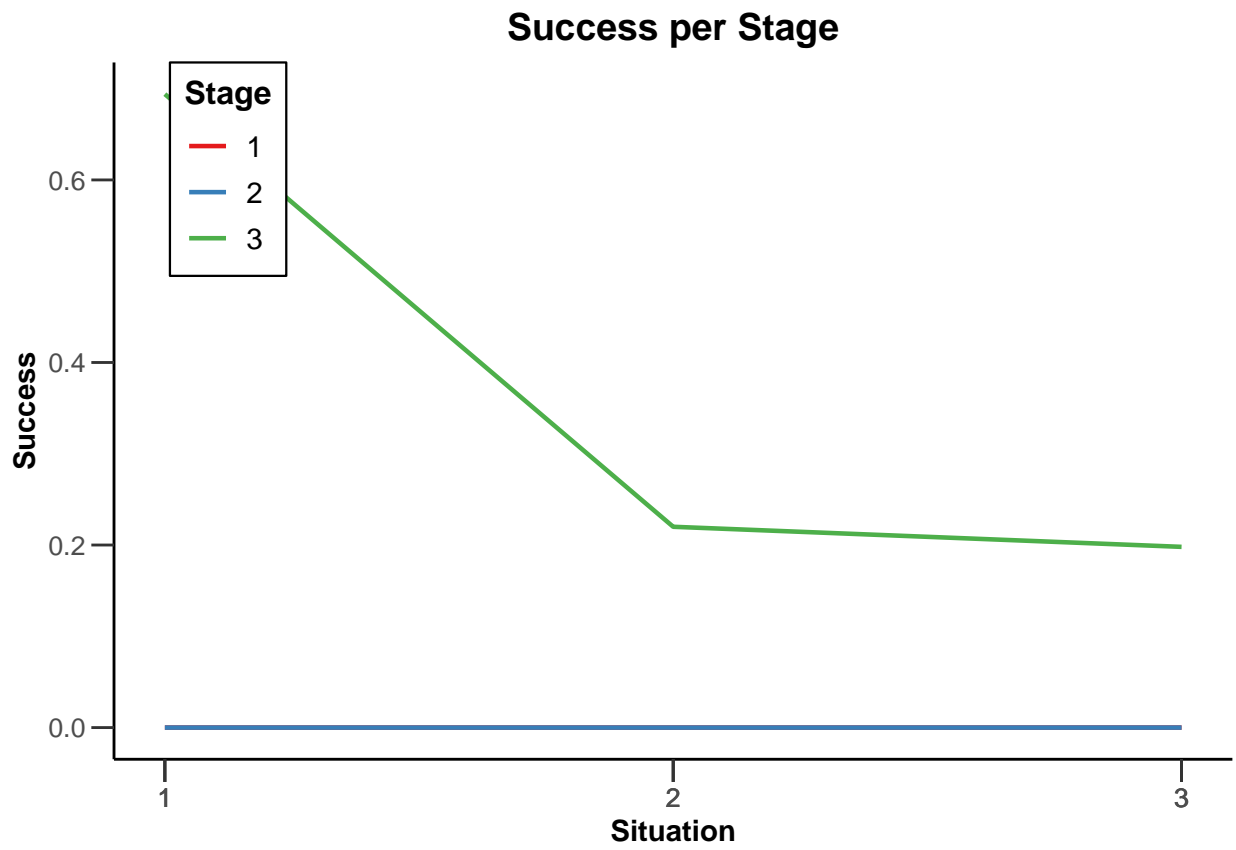
```
plannedEvents = c(30, 80, 120),  
maxNumberOfIterations = 500,  
directionUpper = FALSE  
)
```

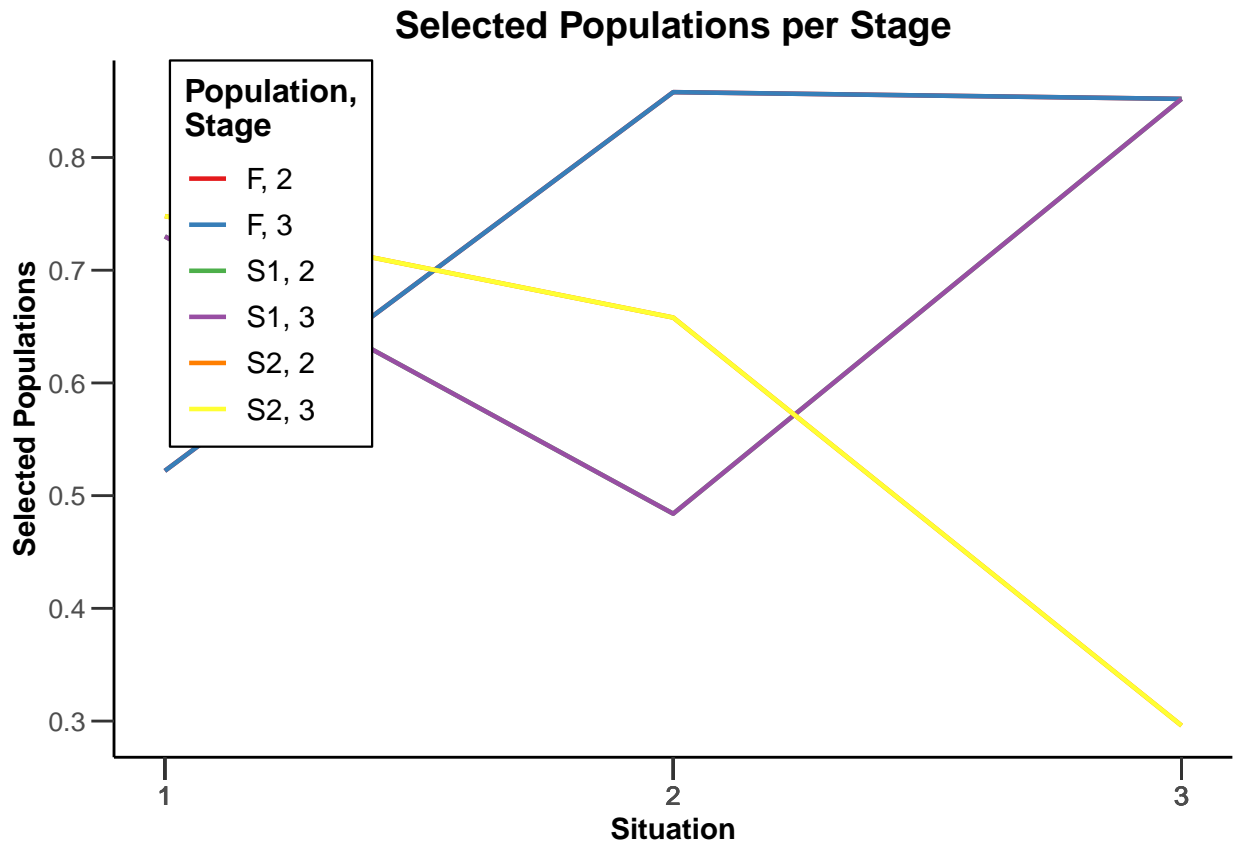
```
## Warning: Simulation of enrichment designs is experimental and hence not fully  
## validated (see www.rpact.com/experimental)
```

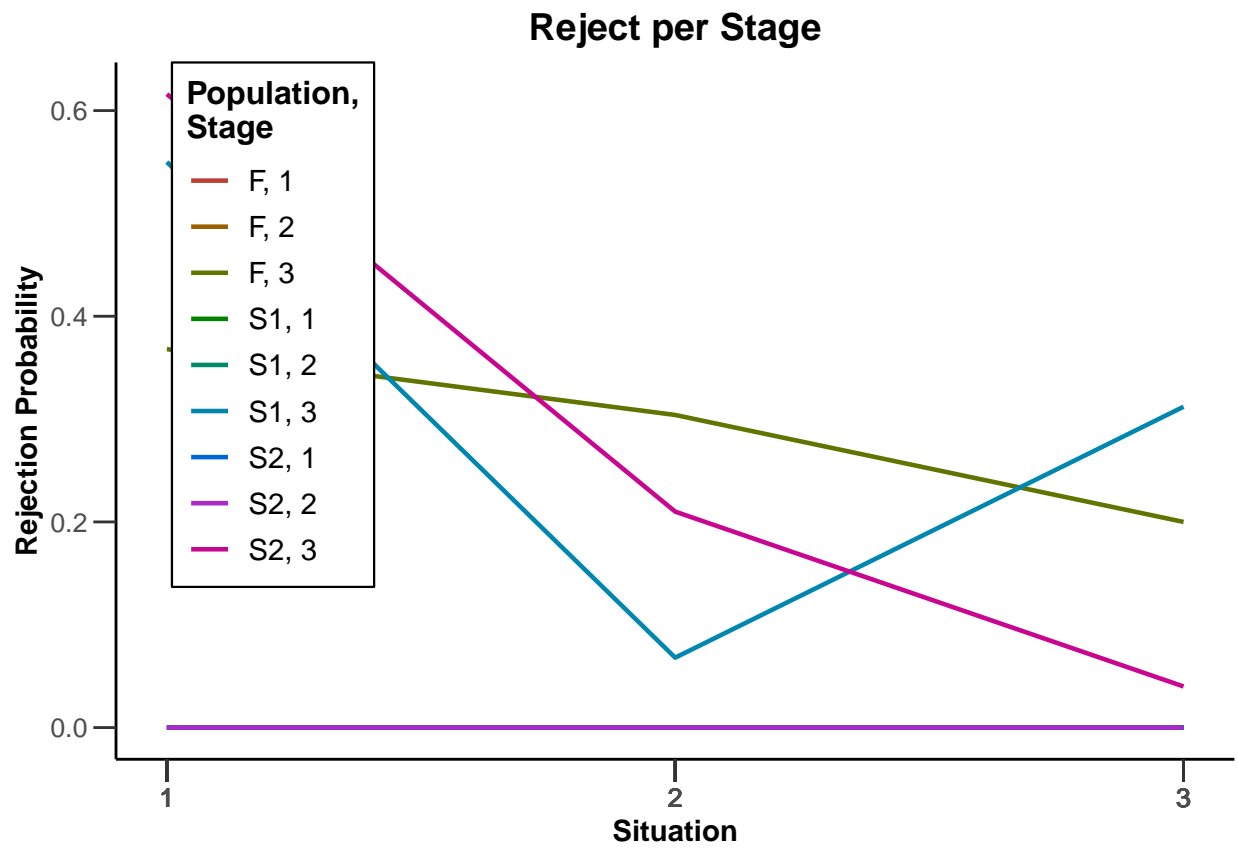
```
plot(x, type = "all", grid = 0)
```

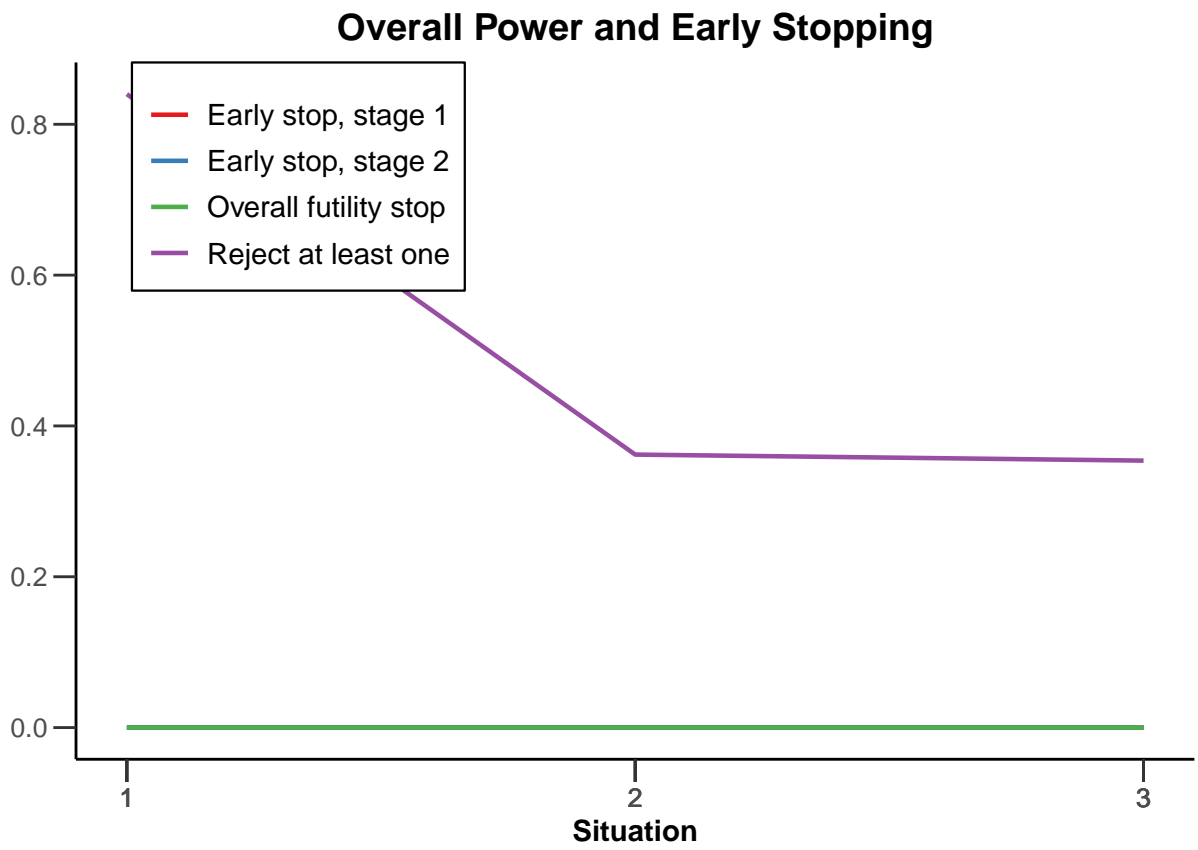


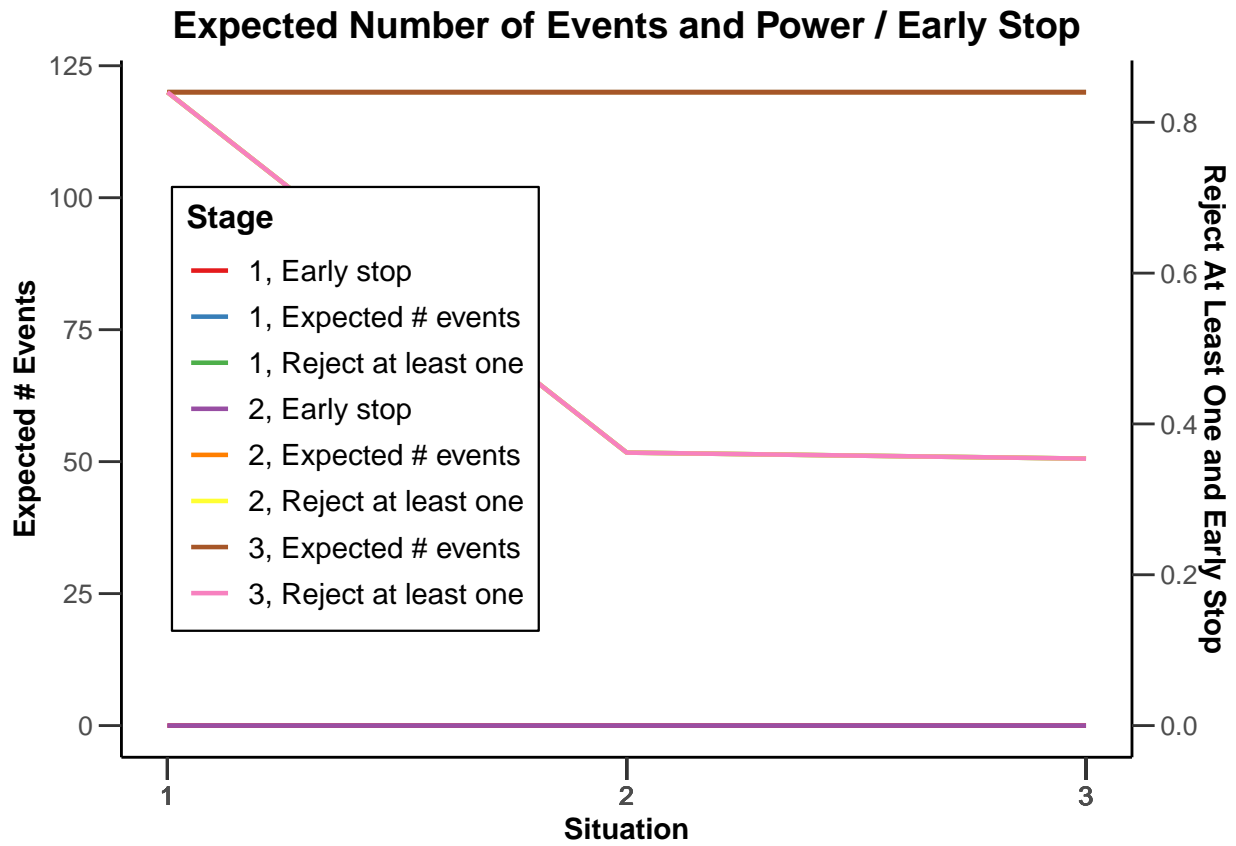


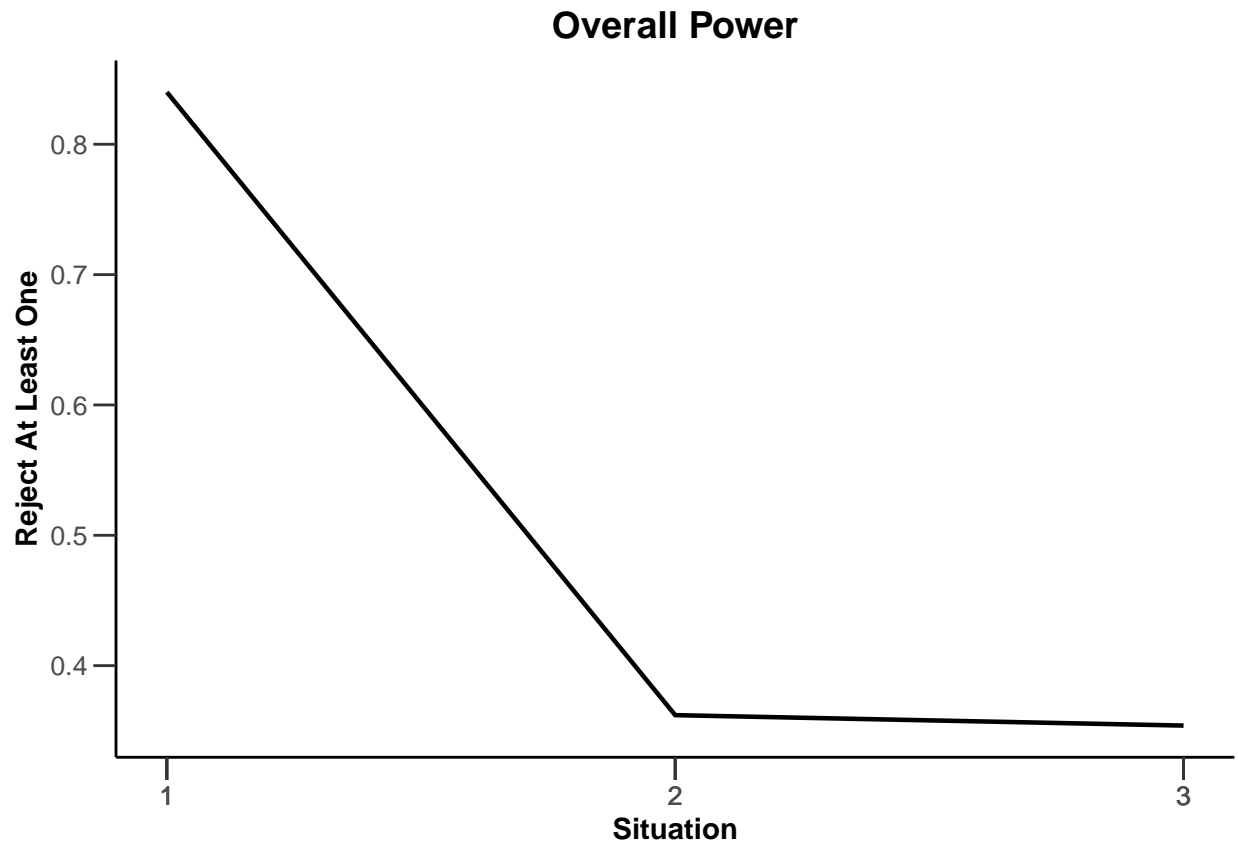


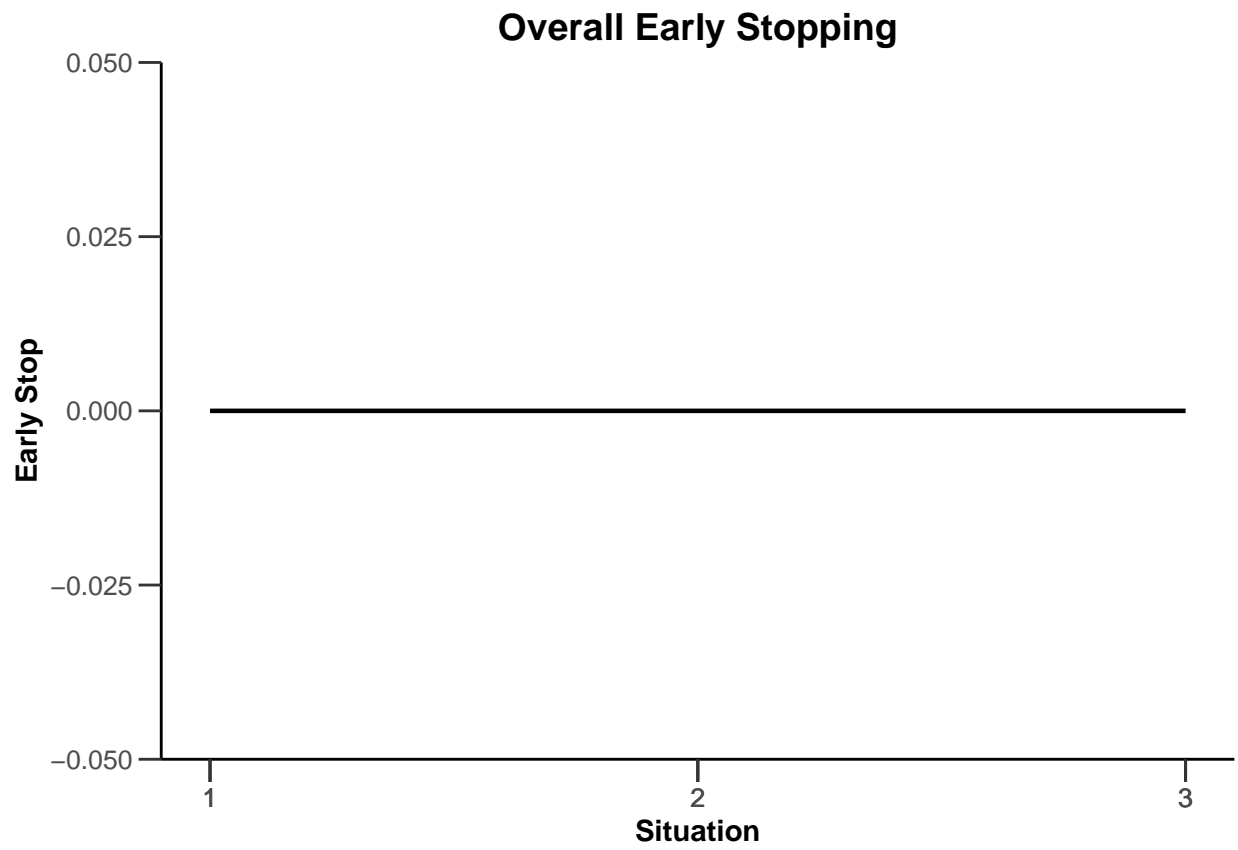


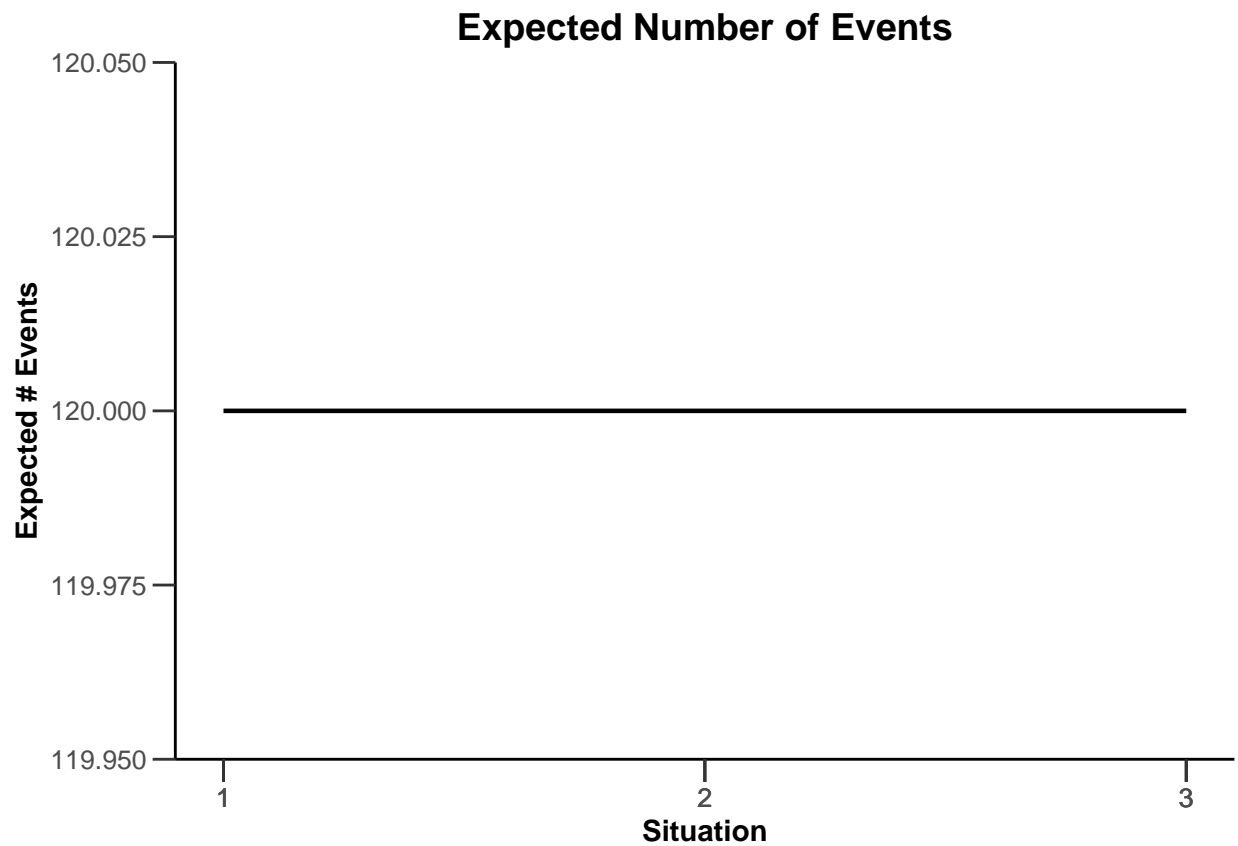












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System: rpact 3.3.2, R version 4.2.1 (2022-06-23 ucrt), platform: x86\_64-w64-mingw32

To cite R in publications use:

R Core Team (2022). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL <https://www.R-project.org/>.

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Wassmer G, Pahlke F (2022). *rpact: Confirmatory Adaptive Clinical Trial Design and Analysis*. <https://www.rpact.org>, <https://www.rpact.com>, <https://github.com/rpact-com/rpact>.

