01-B3-BHM-Simstudy-ORR-report

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Table of Contents

# Introduction

**Table** 95% and 50% ranges of tissue specific event rates for selected levels of heterogeneity (random effects SD) as well as probability of being below 0.3

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| re.sd | PrIlo | Q1 | Q3 | PrIup | ProbBelow0.3 |
| 0.3 | 0.36 | 0.45 | 0.55 | 0.64 | 0 |
| 0.7 | 0.2 | 0.38 | 0.62 | 0.8 | 0.11 |

# Simulation settings

## Simulation scenarios

Simulations were run over the full grid of combinations below.

# True rate and heterogeneity  
bin\_grid

## p.pop re.sd  
## 1 0.5 0.3  
## 2 0.5 0.7

# Sample sizes (lead group and subsequent groups) and group numbers  
sample\_grid

## lead.grp lead.grp.size subseq.grp.size n.grp  
## 1 yes 5 2 8  
## 2 yes 5 2 12  
## 3 yes 5 2 16  
## 4 yes 5 2 19  
## 5 yes 5 3 6  
## 6 yes 5 3 10  
## 7 yes 5 3 13  
## 8 yes 5 4 5  
## 9 yes 5 4 7  
## 10 yes 5 4 10  
## 11 no 5 5 4  
## 12 no 5 5 6  
## 13 no 5 5 8

# Analysis priors (RE SD)  
prior\_grid

## dist  
## 1 U(0,5)  
## 2 HN(0.5)  
## 3 HN(1)

# Resulting full scenario grid  
dim(full\_grid)

## [1] 78 7

head(full\_grid)

## p.pop re.sd lead.grp lead.grp.size subseq.grp.size n.grp dist  
## 1 0.5 0.3 yes 5 2 8 U(0,5)  
## 2 0.5 0.3 yes 5 2 8 HN(0.5)  
## 3 0.5 0.3 yes 5 2 8 HN(1)  
## 4 0.5 0.3 yes 5 2 12 U(0,5)  
## 5 0.5 0.3 yes 5 2 12 HN(0.5)  
## 6 0.5 0.3 yes 5 2 12 HN(1)

tail(full\_grid)

## p.pop re.sd lead.grp lead.grp.size subseq.grp.size n.grp dist  
## 73 0.5 0.7 no 5 5 6 U(0,5)  
## 74 0.5 0.7 no 5 5 6 HN(0.5)  
## 75 0.5 0.7 no 5 5 6 HN(1)  
## 76 0.5 0.7 no 5 5 8 U(0,5)  
## 77 0.5 0.7 no 5 5 8 HN(0.5)  
## 78 0.5 0.7 no 5 5 8 HN(1)

## Global parameters

global\_par

## $n\_sim  
## [1] 500  
##   
## $n\_chains  
## [1] 3  
##   
## $n\_iter  
## [1] 11000  
##   
## $n\_burnin  
## [1] 1000  
##   
## $n\_thin  
## [1] 1  
##   
## $p.threshold  
## [1] 0.3

# Simulation results

Dimension, first and last few lines of results data frame.

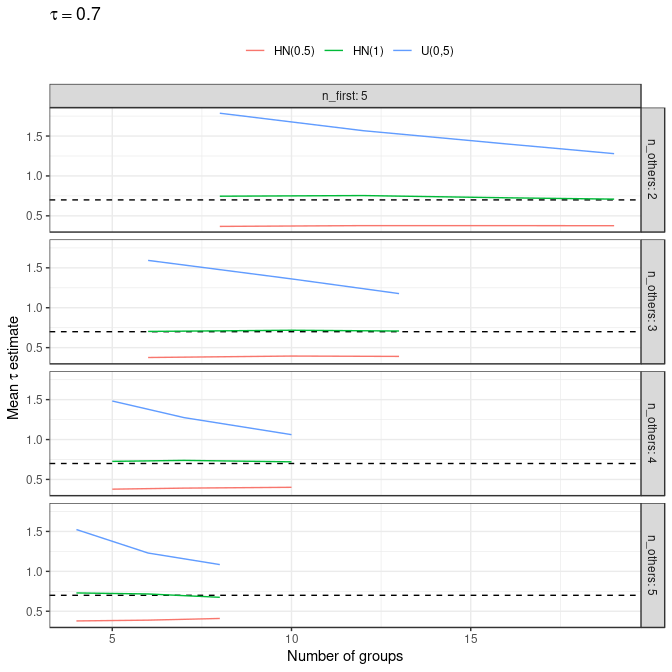
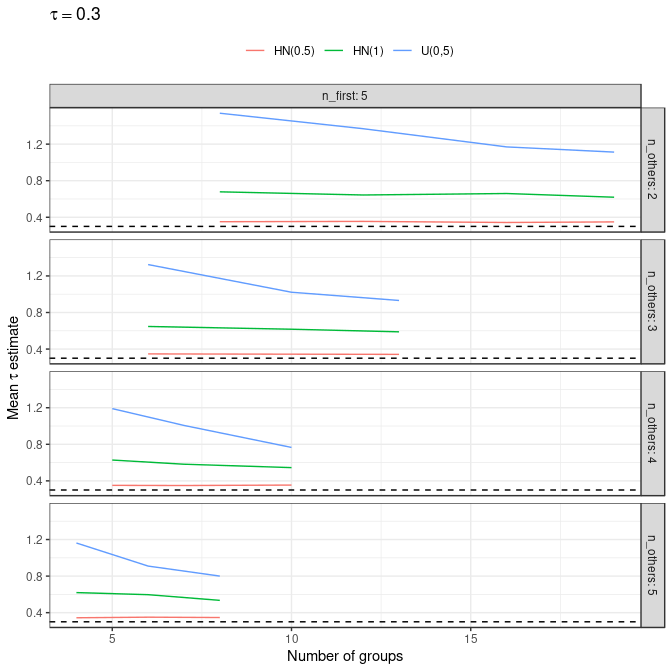
## [1] 624 15

## scenario node var1 var2 value p.pop re.sd lead.grp  
## 1 1 p.new CrIR mean 0.94957401 0.5 0.3 yes  
## 2 1 p.new IQR mean 0.42700195 0.5 0.3 yes  
## 3 1 p.new ProbAbove0.3 mean 0.69292473 0.5 0.3 yes  
## 4 1 re.sd 50% mean 1.53801781 0.5 0.3 yes  
## 5 1 p.new CrIR sd 0.05775532 0.5 0.3 yes  
## 6 1 p.new IQR sd 0.14986284 0.5 0.3 yes  
## lead.grp.size subseq.grp.size n.grp dist n.tot n\_first n\_others  
## 1 5 2 8 U(0,5) 19 5 2  
## 2 5 2 8 U(0,5) 19 5 2  
## 3 5 2 8 U(0,5) 19 5 2  
## 4 5 2 8 U(0,5) 19 5 2  
## 5 5 2 8 U(0,5) 19 5 2  
## 6 5 2 8 U(0,5) 19 5 2

## scenario node var1 var2 value p.pop re.sd lead.grp  
## 619 78 p.new ProbAbove0.3 mean 0.82597453 0.5 0.7 no  
## 620 78 re.sd 50% mean 0.67447909 0.5 0.7 no  
## 621 78 p.new CrIR sd 0.10533791 0.5 0.7 no  
## 622 78 p.new IQR sd 0.06838547 0.5 0.7 no  
## 623 78 p.new ProbAbove0.3 sd 0.12315668 0.5 0.7 no  
## 624 78 re.sd 50% sd 0.28382175 0.5 0.7 no  
## lead.grp.size subseq.grp.size n.grp dist n.tot n\_first n\_others  
## 619 5 5 8 HN(1) 40 5 5  
## 620 5 5 8 HN(1) 40 5 5  
## 621 5 5 8 HN(1) 40 5 5  
## 622 5 5 8 HN(1) 40 5 5  
## 623 5 5 8 HN(1) 40 5 5  
## 624 5 5 8 HN(1) 40 5 5

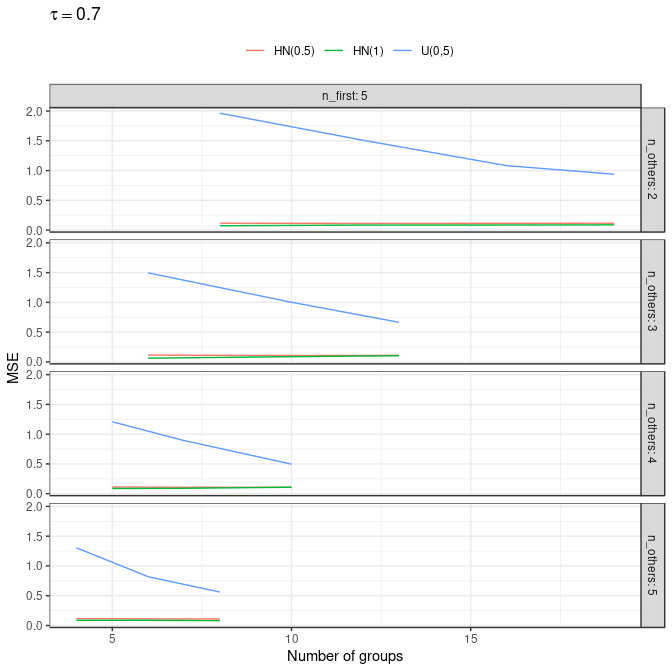
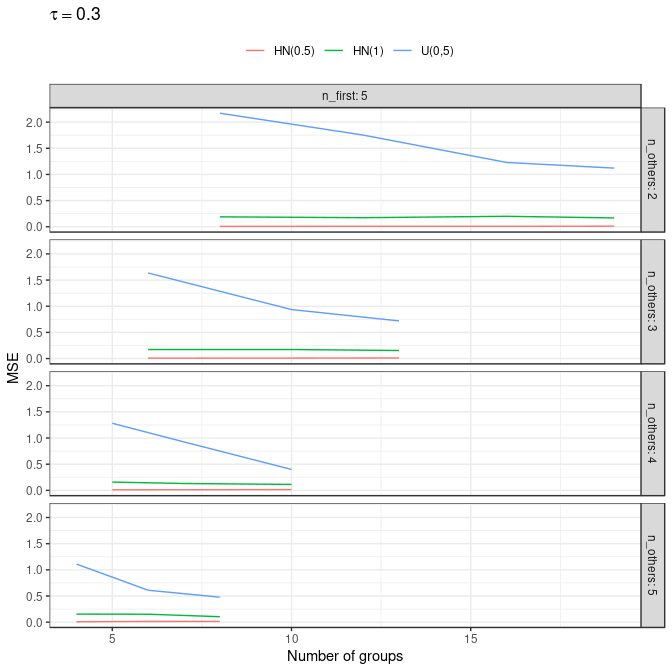
## Estimating between-study-heterogeneity (RE SD)

### Posterior median RE SD ()

**Figure** Posterior median of (mean over 500 simulations) 

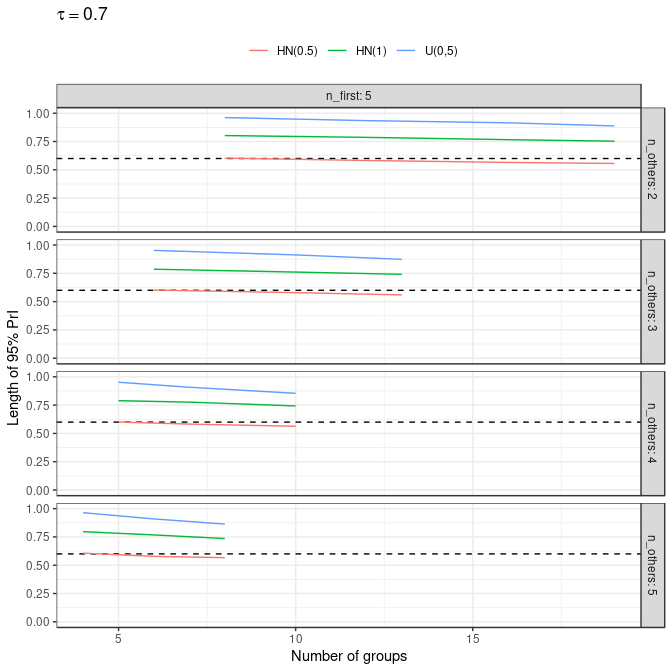
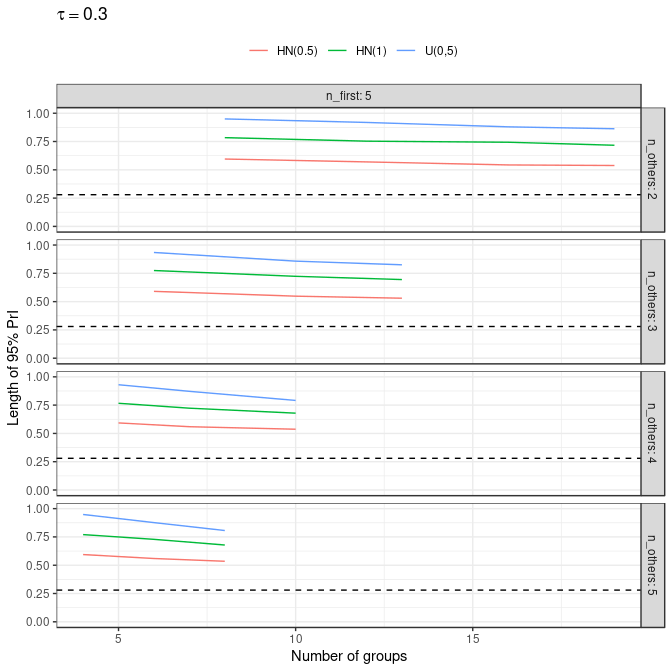
### Mean Squared Error

**Mean Squared Error (MSE)** of the posterior median as an estimator for ,

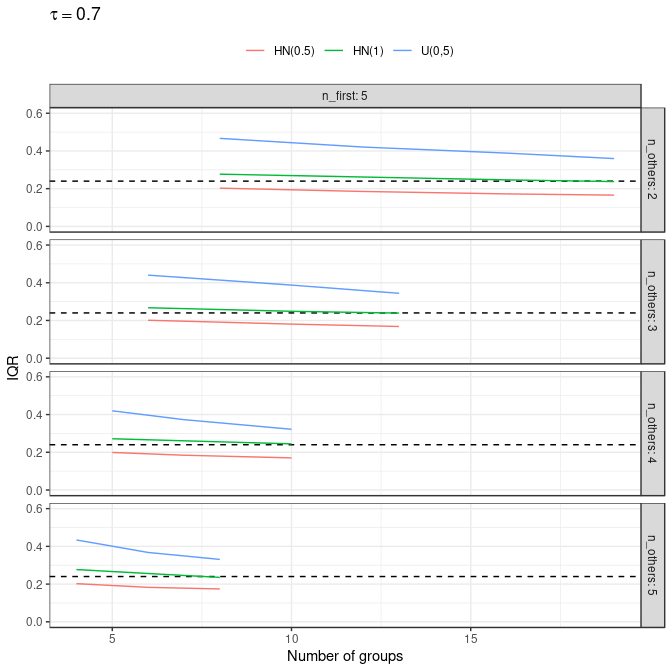
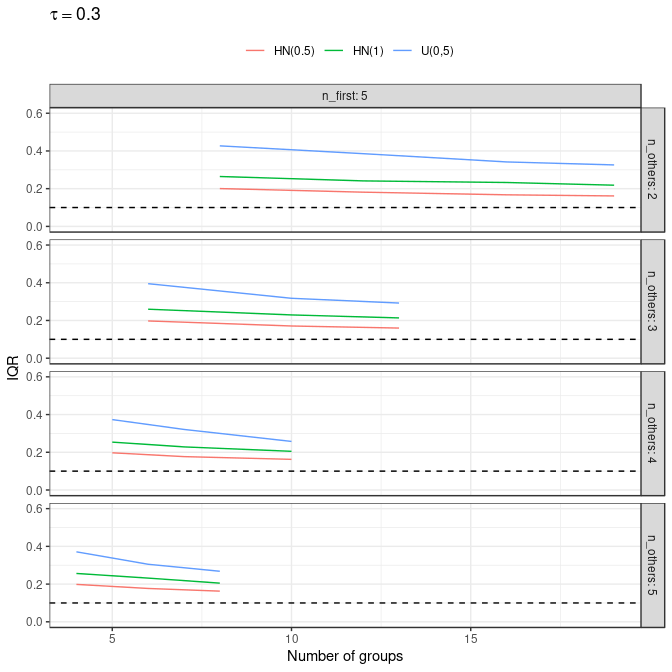
**Figure** MSE of the posterior median RE SD 

## Predictive uncertainty: new tissue response rate

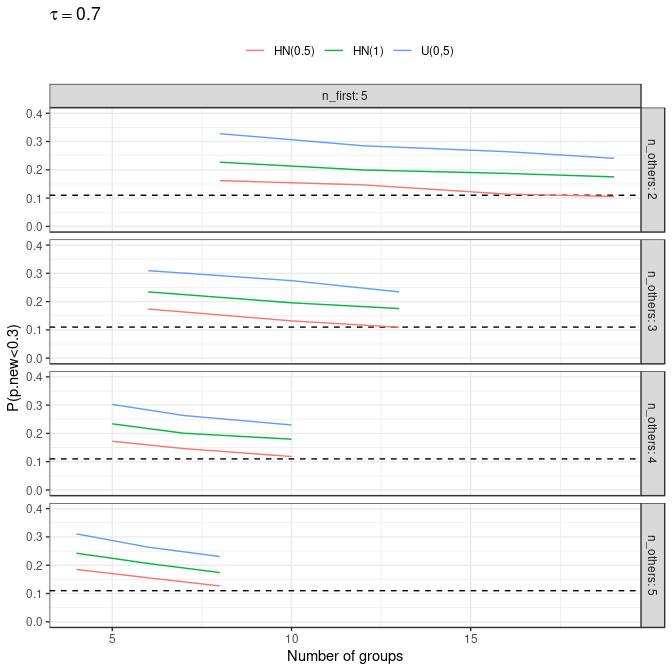
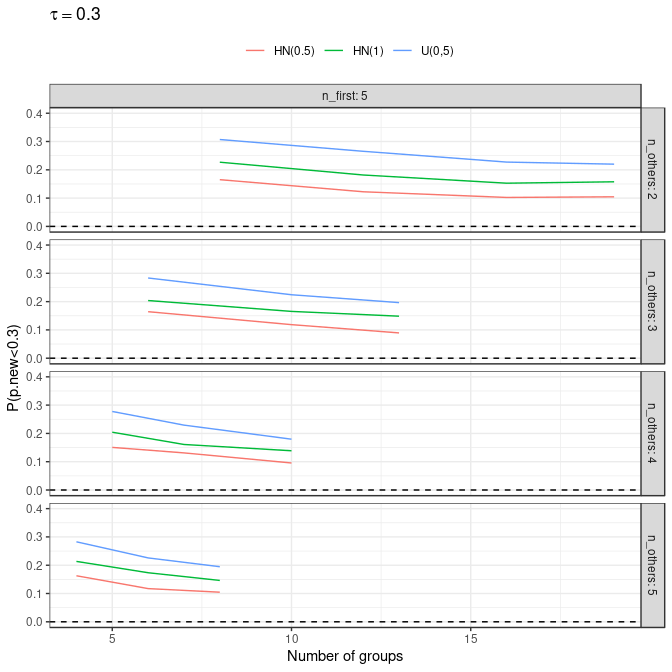
### 95% Prediction interval

**Figure** Length of 95% prediction interval of new group event probability (mean over 500 simulations) 

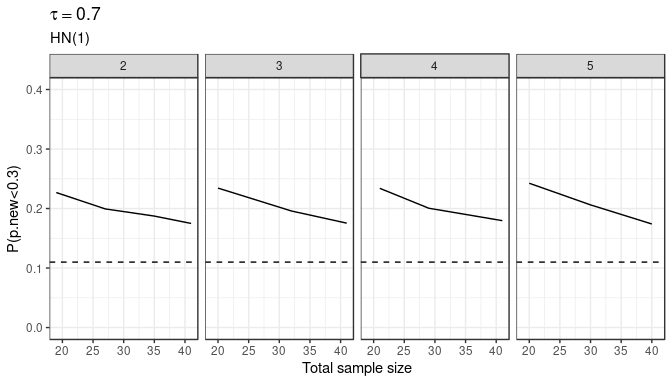
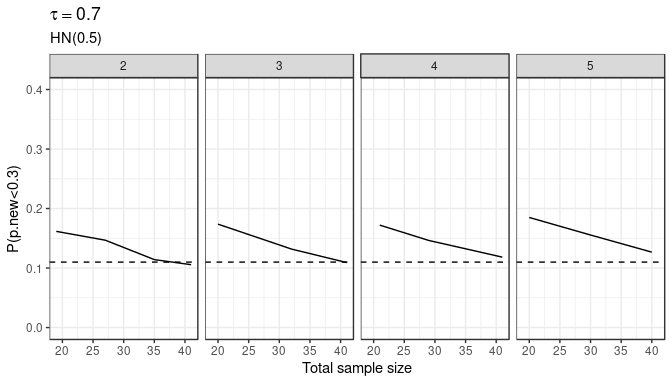
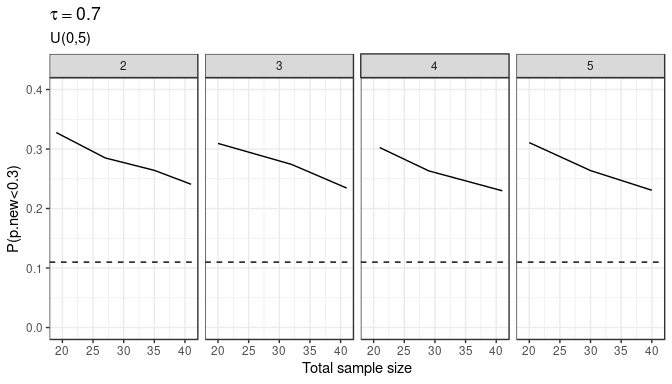
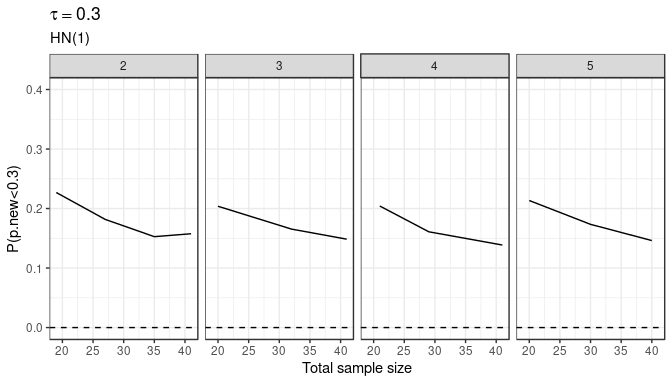
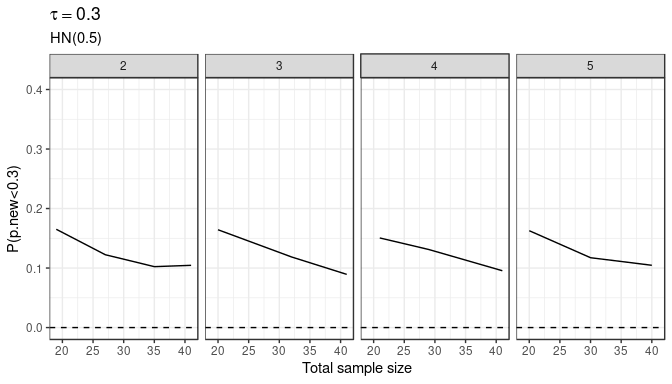
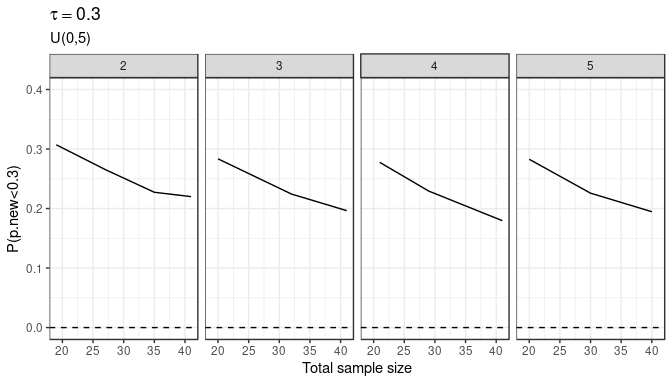
### Interquartile range

**Figure** Inter-quartile range of prediction interval of new group event probability (mean over 500 simulations) 

### Threshold probabilities

**Figure** Estimated posterior probability of new group event probability being lower than 0.3, P(p.new<0.3) (mean over 500 simulations) 

#### Compare impact of group size vs number of groups

**Figure** Threshold probability as a function of total sample size. The panels give the subsequent group size (the first group has always a size of 5). 

# Session info

## [1] "/home/bceuser/gsteigs1/GITHUB.COM/punta"

## R version 3.5.3 (2019-03-11)  
## Platform: x86\_64-pc-linux-gnu (64-bit)  
## Running under: Red Hat Enterprise Linux  
##   
## Matrix products: default  
## BLAS/LAPACK: /usr/lib64/libopenblas-r0.3.3.so  
##   
## locale:  
## [1] LC\_CTYPE=en\_US.UTF-8 LC\_NUMERIC=C   
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## [5] LC\_MONETARY=en\_US.UTF-8 LC\_MESSAGES=en\_US.UTF-8   
## [7] LC\_PAPER=en\_US.UTF-8 LC\_NAME=C   
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## [11] LC\_MEASUREMENT=en\_US.UTF-8 LC\_IDENTIFICATION=C   
##   
## attached base packages:  
## [1] stats graphics grDevices utils datasets methods base   
##   
## other attached packages:  
## [1] ggplot2\_3.2.1 tidyr\_0.8.3 dplyr\_0.8.3 rocheBCE\_2.4   
##   
## loaded via a namespace (and not attached):  
## [1] Rcpp\_1.0.2 knitr\_1.23 magrittr\_1.5 munsell\_0.5.0   
## [5] tidyselect\_0.2.5 colorspace\_1.4-1 R6\_2.4.0 rlang\_0.4.0   
## [9] plyr\_1.8.4 stringr\_1.4.0 tools\_3.5.3 grid\_3.5.3   
## [13] gtable\_0.3.0 xfun\_0.7 withr\_2.1.2 htmltools\_0.3.6   
## [17] lazyeval\_0.2.2 yaml\_2.2.0 assertthat\_0.2.1 digest\_0.6.21   
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## [29] stringi\_1.4.3 pander\_0.6.3 compiler\_3.5.3 pillar\_1.4.2   
## [33] scales\_1.0.0 boot\_1.3-20 pkgconfig\_2.0.3