n_i per ce

near Model

Unbalanced

Sum up1

alpha

```
ggarrange(


ggarrange(gg_nparcomp_alpha_balanced +theme(axis.text.x = element_text(color = "black", face="bold"), a
                                    legend.title = element_text(face = "bold"), legend.text = 

        #gg_nparcomp_alpha_unbalanced ,
```

```
        gg_nparcomp_unbalanced_alpha+theme(axis.text.x = element_text(color = "black", face="bold"), ax
                                           legend.title = element_text(face = "bold"), legend.text = 

        nrow=1,  #legend="bottom" ,
        labels=c("C", "D")  ,  font.label=list(color="black",size=order_legend)

    ) %>% annotate_figure( top = text_grob("Continuous",
            color = "black", face = "bold", size = 90)),



ggarrange(gg_ordinal_alpha_balanced +theme(axis.text.x = element_text(color = "black", face="bold"), ax
                                           legend.title = element_text(face = "bold"), legend.text = 

        gg_ordinal_alpha_unbalanced +theme(axis.text.x = element_text(color = "black", face="bold"), ax
                                           legend.title = element_text(face = "bold"), legend.text = 

        nrow=1 ,  #legend="bottom",
        labels=c("E", "F")   ,  font.label=list(color="black",size=order_legend)

    ) %>% annotate_figure( top = text_grob("Ordinal",
            color = "black", face = "bold", size = 90)),
nrow = 2

)
```
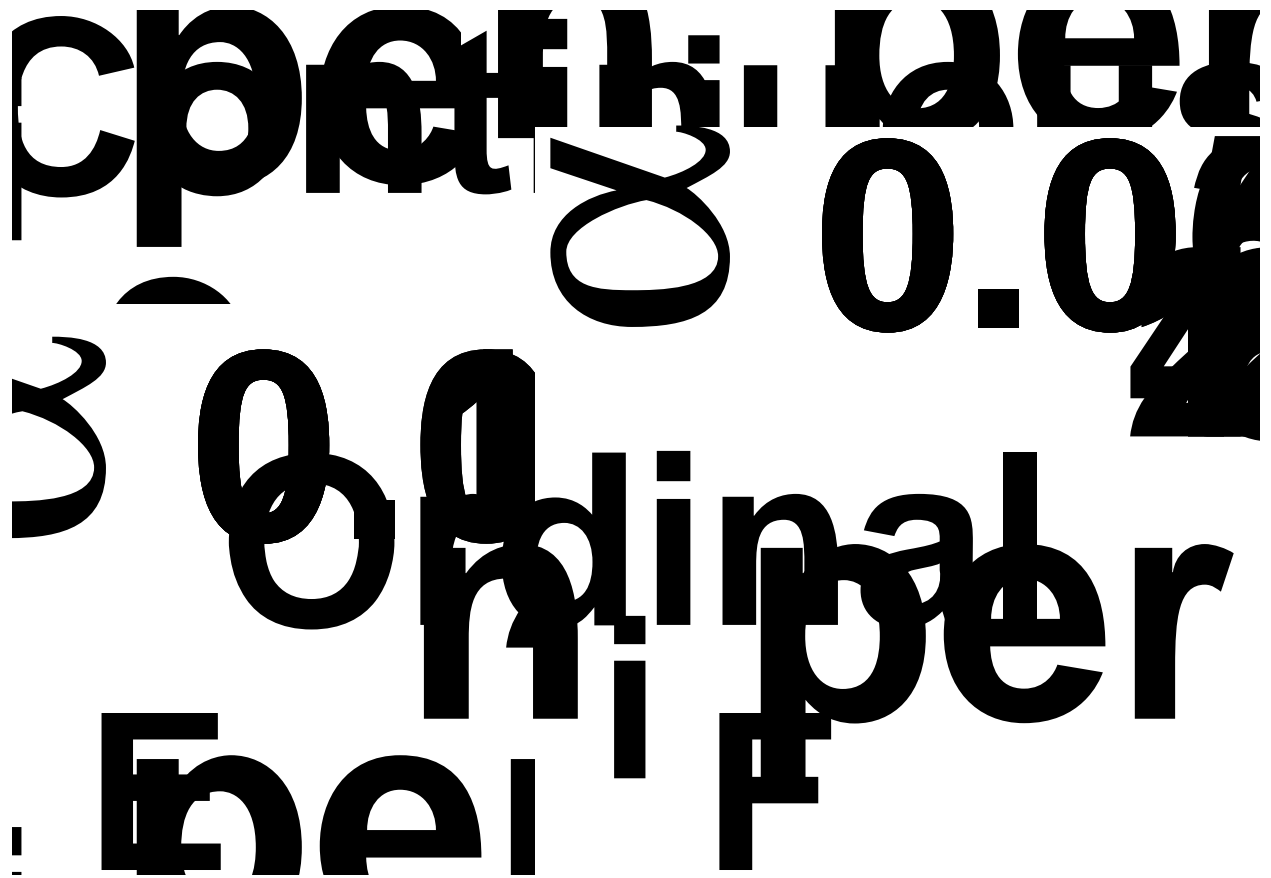
The probability of falsely rejecting the null hypothesis for at least one center as a function of sample size for each method applied on relevant response outcome for balanced (left panel) and unbalanced designs (right panel). The nominal type I error rate (alpha=0.05) is shown as a horizontal line. Dotted blue lines indicate error margins for simulations with 5000 runs. Simulated type-I-errors falling outside [0.044; 0.056] indicate a significant deviation from the prespecified level alpha=0.05).