# Bayesian multivariate probability of success with applications to rare diseases

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September 25, 2020



### Introduction

- Increased interest among practitioners in computing the probability of having a successful clinical trial
- Framework: Chuang-Stein (*Pharmaceutical Statistics* 2006)
- Standard methods to compute sample size rely on statistical power
  - Power is a conditional value
  - Power is not the probability of a successful clinical trial
- Probability of success (POS) is the expected value of power with respect to a specified distribution for the effect size:

$$\mathsf{POS} = \int P(\mathsf{Trial} \; \mathsf{meets} \; \mathsf{success} \; \mathsf{critera}|\Delta) p(\Delta|D) d\Delta$$



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# **Case study**

- Phase 2 trial of Ivacaftor in subjects with cystic fibrosis (Vertex Pharmaceuticals, 2007-12)
- Primary objectives were to assess safety and dose tolerance, but some efficacy endpoints measured
- Phase 2 data suggested treatment efficacious, but sample size was very small
- Phase 3 trial conducted 2012-15:
  - Primary endpoint: Absolute change from baseline in percent predicted forced expiratory volume in 1 Second (FEV1)
  - Key secondary endpoints:
    - Change from baseline in sweat chloride
    - Change from baseline in Cystic Fibrosis Questionnaire-Revised (CFQ-R) respiratory domain score
- **Key question:** How can we exploit this phase 2 data to find a sample size that yields a high probability of success in a Phase 3 trial across the endpoints?



# **Seemingly Unrelated Regression (SUR)**

#### **SUR Model**

$$egin{aligned} oldsymbol{y}_i &= oldsymbol{X}_ieta + oldsymbol{u}_i \ egin{aligned} oldsymbol{u}_i &= oldsymbol{X}_j(oldsymbol{0}, oldsymbol{\Sigma}), \quad oldsymbol{\Sigma} \in \mathbb{R}^{J imes J} \ oldsymbol{y}_i &= (y_{i1}, \dots, y_{iJ})' \in \mathbb{R}^J \ oldsymbol{X}_i &= ext{blkdiag} \left\{ oldsymbol{x}_{i1}', \dots, oldsymbol{x}_{iJ}' 
ight\} \in \mathbb{R}^{J imes p}, \quad oldsymbol{p} &= \sum_{j=1}^J oldsymbol{p}_j \ oldsymbol{\beta} &= (oldsymbol{\beta}_1', \dots, oldsymbol{\beta}_J')' \in \mathbb{R}^p \end{aligned}$$

- Most general multivariate normal linear model
- Allows each response to have its own set of covariates



# Copula regression

#### Gaussian copula regression model

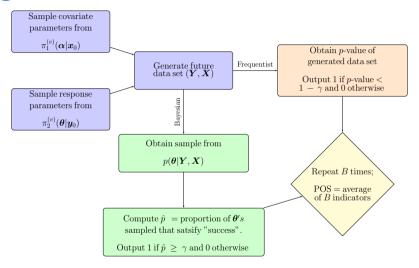
$$m{z}_i \sim N_J(0, \Gamma) \ y_{ij} = F_j^{-1}(\Phi(z_{ij})|m{ heta}, m{x}_{ij})$$

- $F_j(\cdot)$  is the CDF for the  $j^{th}$  margin
- If the  $j^{th}$  margin is a GLM,  $\theta = (\beta', \tau)$ , where  $\tau = 1$  in some cases
- **x**<sub>ij</sub> is a vector of covariates for subject i and endpoint j, i = 1, ..., n, j = 1, ..., J
- Explicitly models the correlation between endpoints of possibly mixed types
- Equivalent to SUR model if all endpoints are normally distributed



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# **POS Algorithm**





## A note on small historical data sets

- For rare diseases, Phase II sample sizes are typically very small
- Implausible treatment effects may be sampled if the sample size is too low
- There are several possible adjustments one can make:
  - 1 Restrict samples for efficacy in the treatment effect: Bayesian conditional expected power
  - Use informative priors for treatment effects
  - Restrict samples of treatment effects to the  $q^{th}$  highest posterior density (HPD) region for some 0 < q < 1.
- We focus on (3) and propose two different mechanisms:
  - HPD region of all parameters
  - 2 HPD region of only treatment effects estimated using KDE



## The simulated trial

- $n_0 = n_1 = 8$
- $\blacksquare E(\Delta y_{ij}) = \beta_{0j} + \beta_{1j}z_i + \mathbf{x}'_{ij}\beta_{2j}$
- $\beta_1 = (6.4, 3.5, -49.1)'$
- $\bullet$  diag( $\Sigma$ ) = (5.12, 7.05, 12.27)'
- $(\rho_{12}, \rho_{13}, \rho_{23}) = (0.25, -0.25, -0.33)$
- For all outcomes,  $\mathbf{x}_{ij}$  includes an intercept term, linear and square terms of age, weight, BMI, and sex
- Baseline levels for FEV1 and CFQ-R score are controlled for in their regressions
- Power computations yield  $\tilde{n}_1 = 22$ ,  $\tilde{n}_2 = 176$ , and  $\tilde{n}_3 = 14$  for 90% power



## **POS** simulation

■ The notion of "success" can be generalized to a set

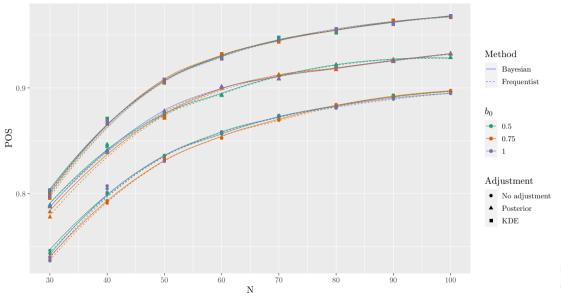
$$egin{aligned} \Omega_1 &:= \{ heta \mid eta_{11} > 0 \} \ \Omega_2 &:= \{ heta \mid eta_{12} < 0 \} \ \Omega_3 &:= \{ heta \mid eta_{13} > 0 \} \end{aligned}$$

$$lacksquare$$
  $\Omega_{1j} := \Omega_1 \cap \Omega_j, j = 1, 2$ 

$$\square$$
  $\Omega_{123} = \Omega_1 \cap \Omega_2 \cap \Omega_3$  (complete success)

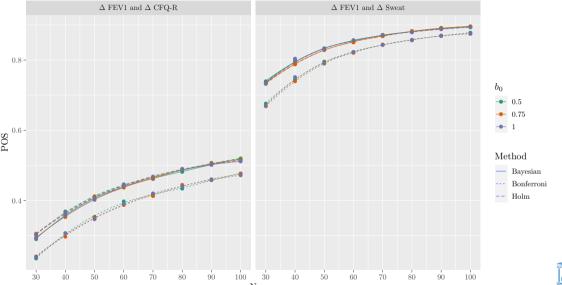


# POS for $\Delta$ FEV1



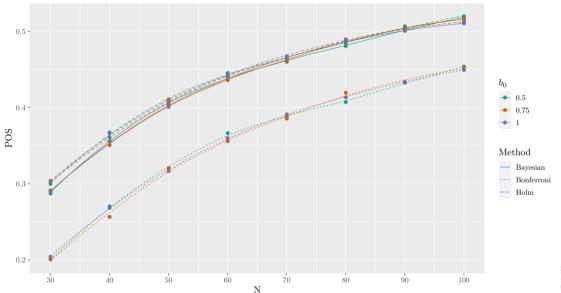


#### POS for Primary and one Secondary Endpoint

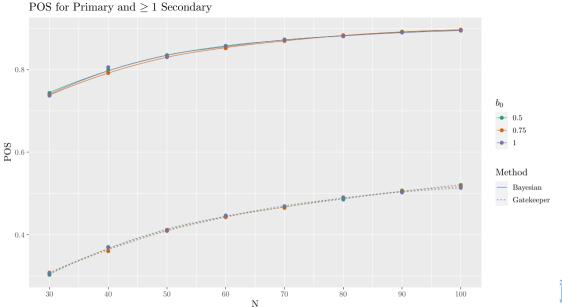




#### POS for Complete Success









# **Power and Type I Error Rate**

- In order to understand the increase in success, we must characterize the type I error rate of the method
- Amend the posterior samples of the historical data

$$\tilde{\pi}^{(\nu)}(\theta|D_0) \propto \pi^{(\nu)}(\theta|D_0)I(\theta \in \Theta)$$
 (1)

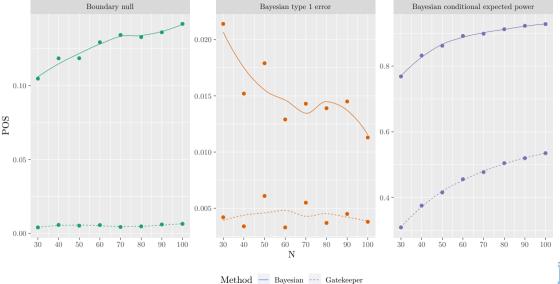
- Three important Θ's:
  - Boundary null:

$$\Theta_B = \{\theta | \beta_{12} = 0 \cap \beta_{13} = 0\}$$
 (for example)

- Bayesian conditional expected power:  $\Theta_{H_1} = \{\theta | \beta_{11} > 0 \cap \{\beta_{12} < 0 \cup \beta_{13} > 0\}\}$
- Bayesian type I error:  $\Theta_{H_0} = \overline{\Theta}_{H_1} = \{\theta | \{\beta_{11} \leq 0\} \cup \{\beta_{12} \geq 0 \cup \beta_{13} \leq 0\}\}$



#### Power and Type I Error for Primary and $\geq 1$ Secondary



#### Conclusion

- Only POS method that considers multiple endpoints
- Fully Bayesian approach to jointly model multivariate LMs and GLMs
- Unifies hypothesis testing into one framework
- Interpretation far simpler than frequentist methods
- Useful whether a frequentist or Bayesian analysis will be used
- Methods of Ibrahim et al. and Chaung-Stein can be seen as special cases
- R packages available on CRAN: surbayes and bayescopulareg

