

Guiding clinical trial design for a rare disease using natural history data and Bayesian disease progression modeling



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 - Julie Sapp, Leslie Biesecker

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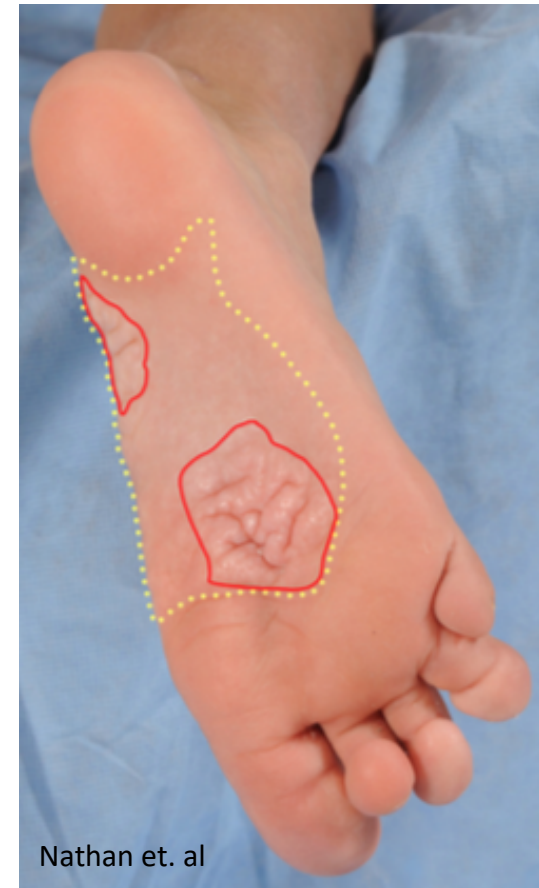
Pathogenetic insights from quantification of the cerebriform connective tissue nevus in Proteus syndrome

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Rare disease

Proteus syndrome

- Disease characterization and manifestation
 - Genetic mutation
 - Overgrowth of skin, bone, and other tissues
 - Plantar cerebriiform connective tissue nevus (CCTN)
- Challenges in clinical trial design
 - Small, heterogenous patient populations
 - Insufficient understanding of disease etiology
 - Poorly developed study endpoints



Nathan et. al

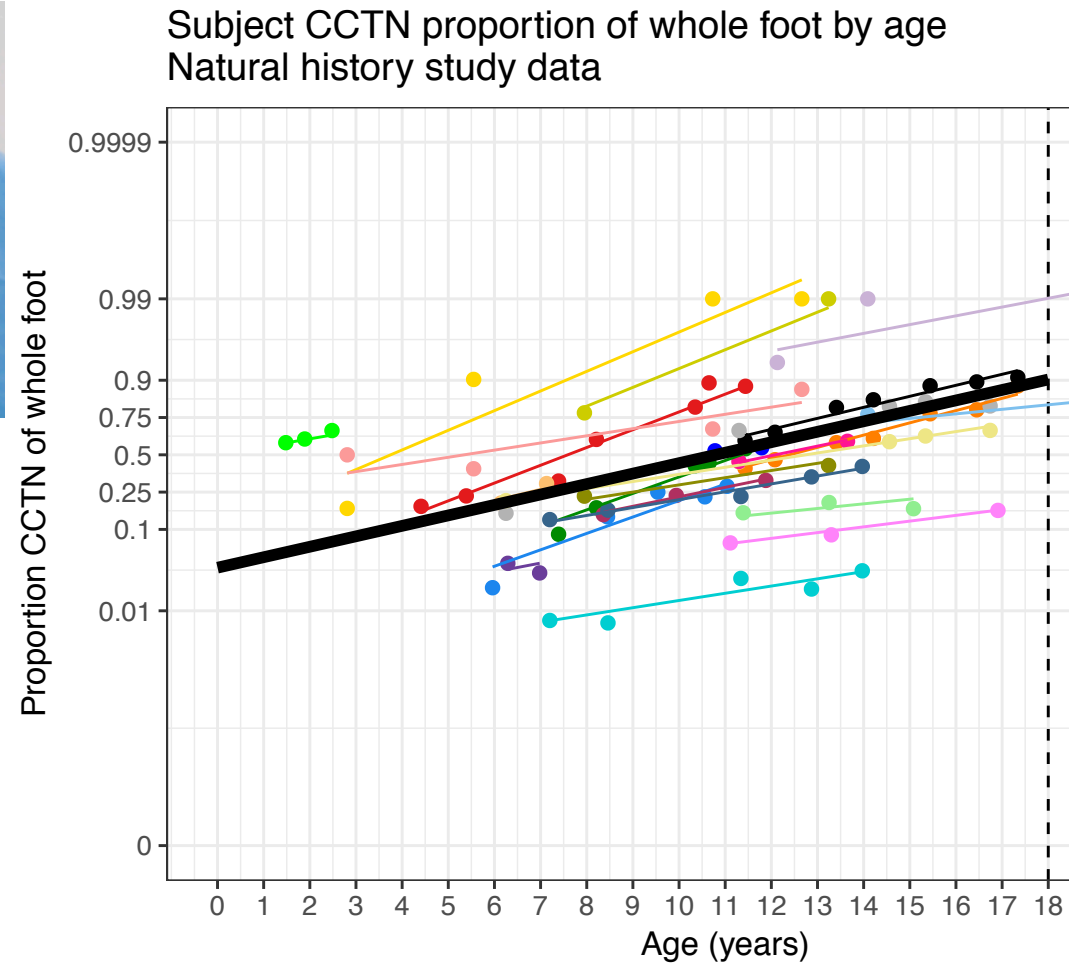
Natural history study

CCTN disease progression



Natural history study

CCTN disease progression

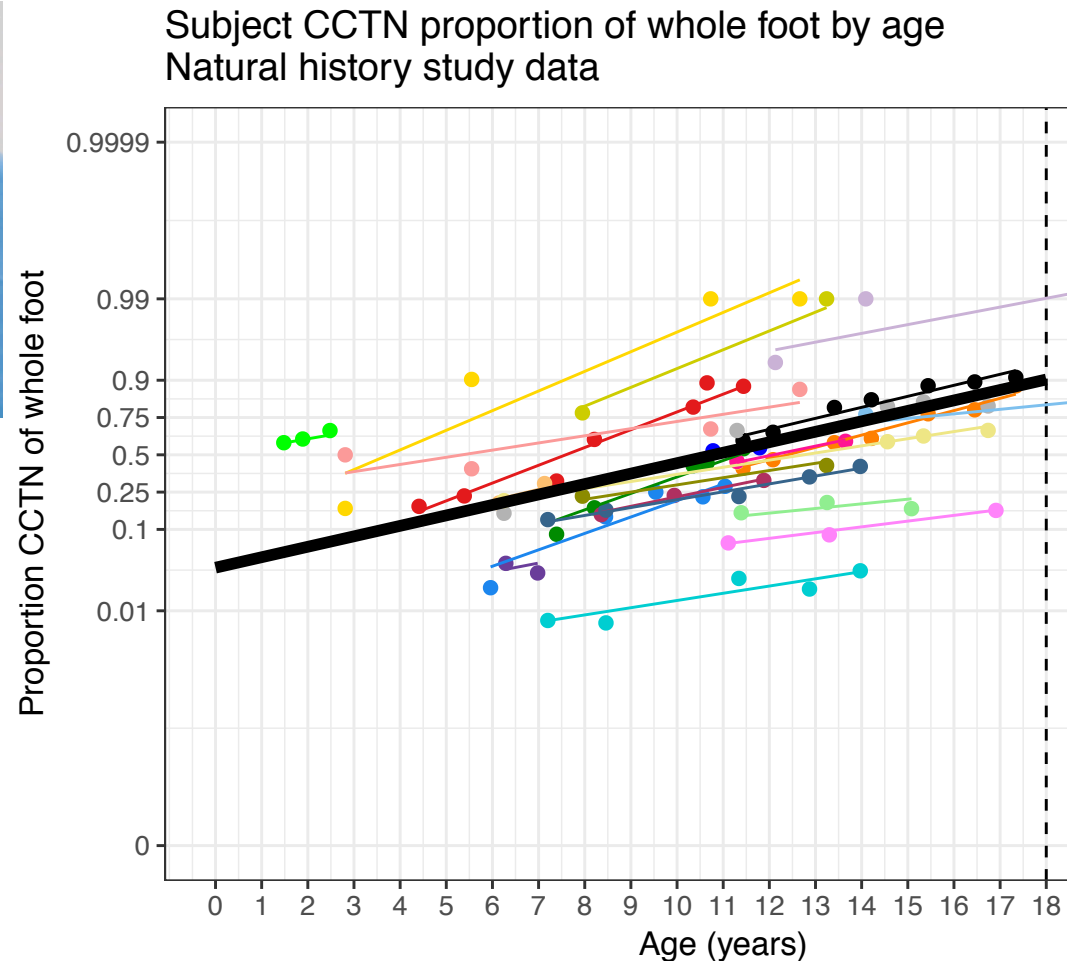


Natural history study

CCTN disease progression



Can we leverage data from this natural history study (NHS) to:
-understand natural rate of progression



Natural history study

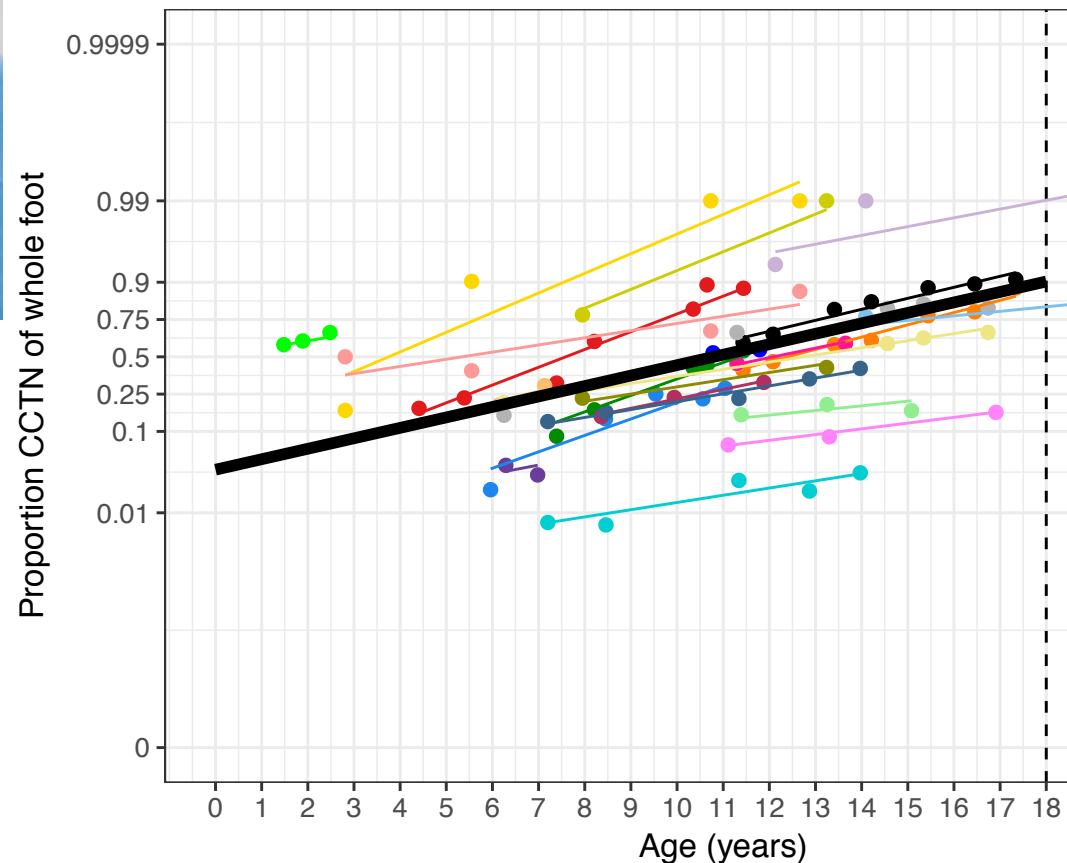
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Can we leverage data from this natural history study (NHS) to:

- understand natural rate of progression
- create a virtual subject simulator

Subject CCTN proportion of whole foot by age
Natural history study data



Natural history study

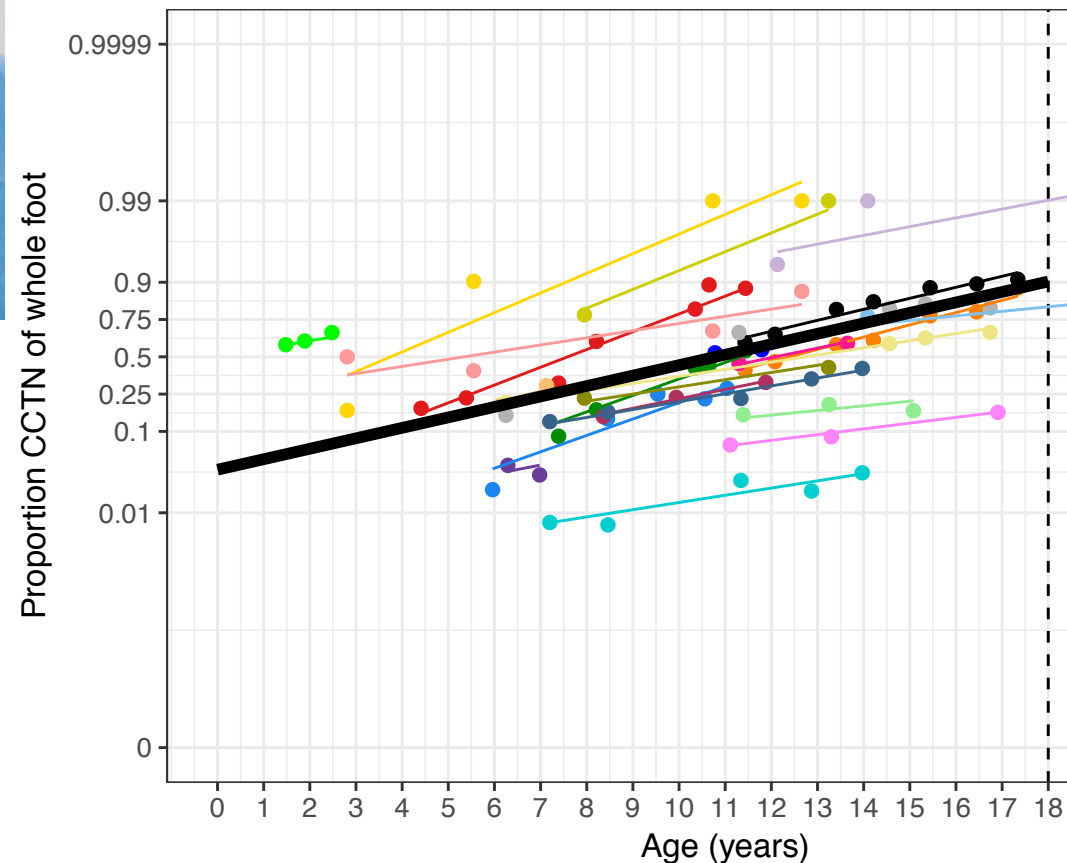
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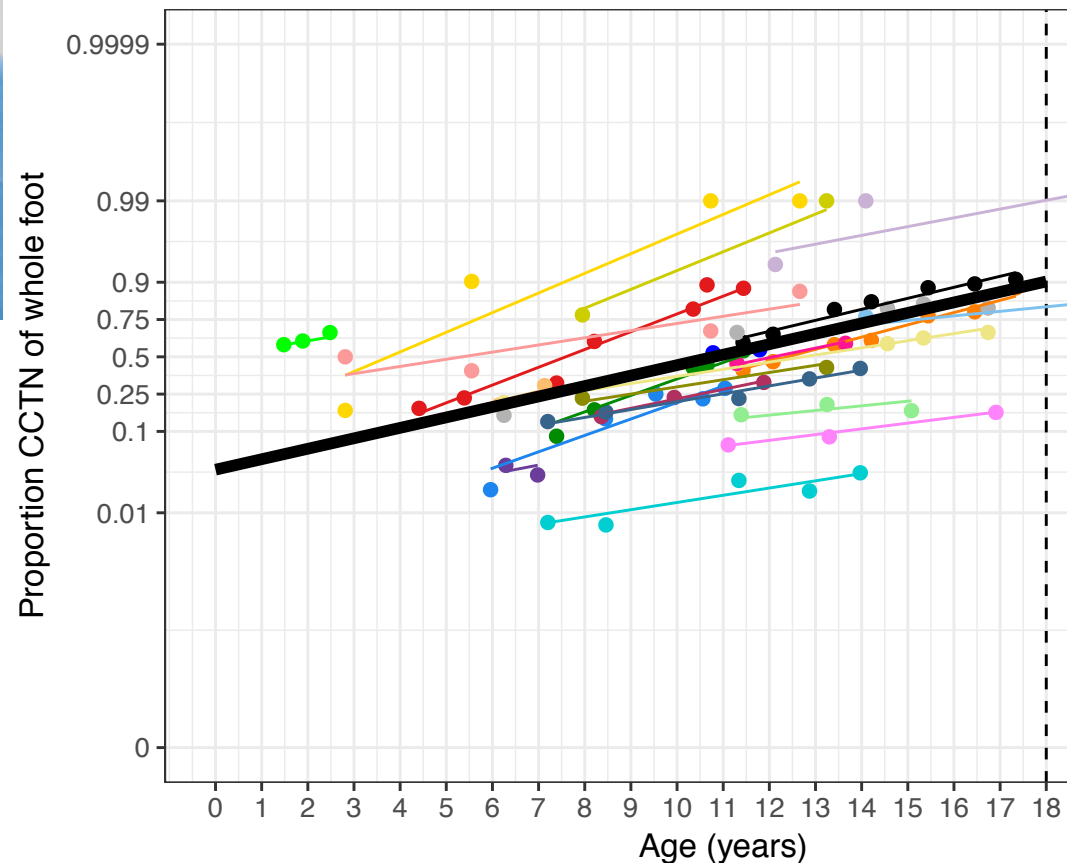
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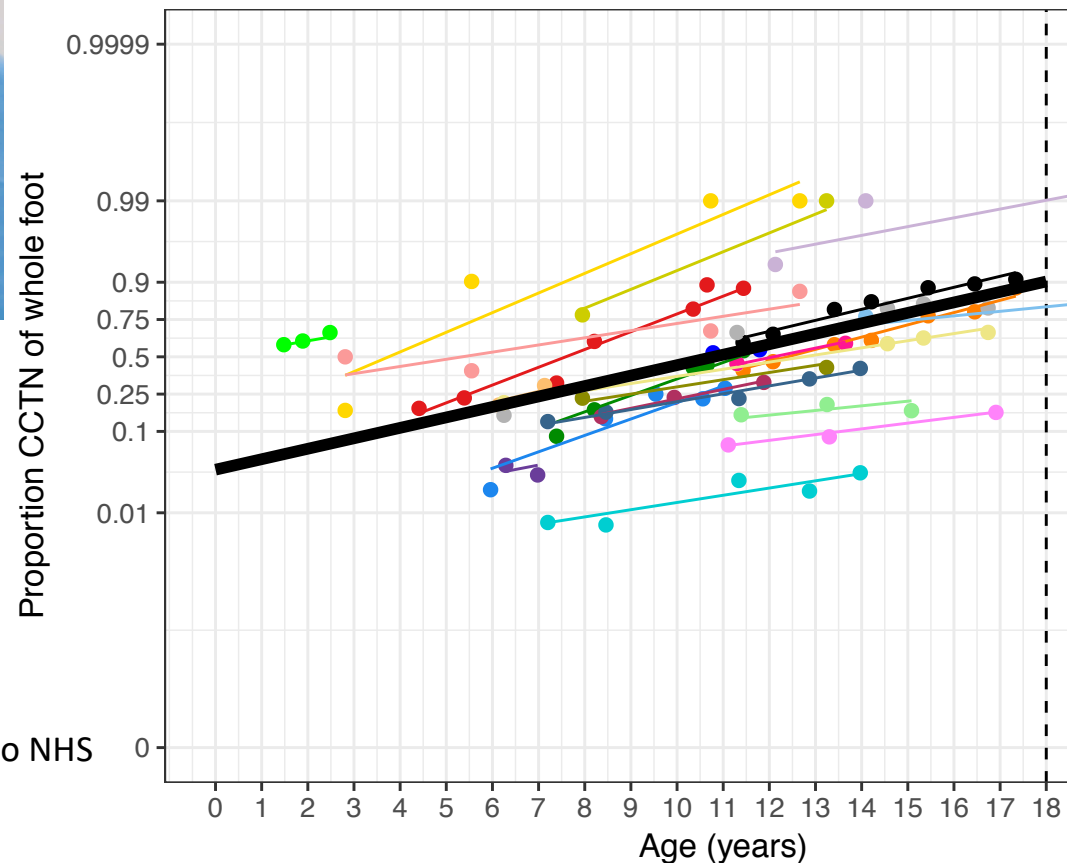
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Can we leverage data from this natural history study (NHS) to:

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- create a virtual subject simulator
- simulate a treatment effect
- build a Bayesian disease progression model (DPM)
- design a single arm trial that
 - compares disease progression of treated patients to NHS
 - defines a final analysis using the DPM

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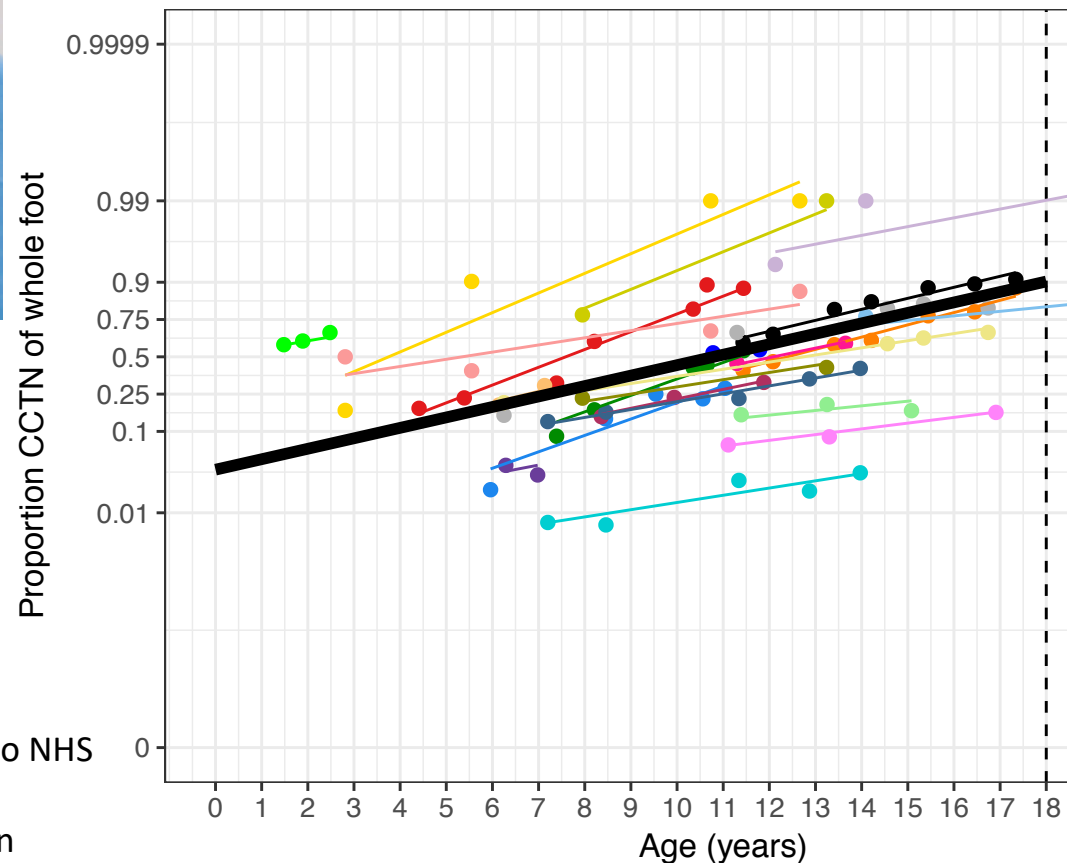
CCTN disease progression



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 - compares disease progression of treated patients to NHS
 - defines a final analysis using the DPM
- understand the operating characteristics of this design

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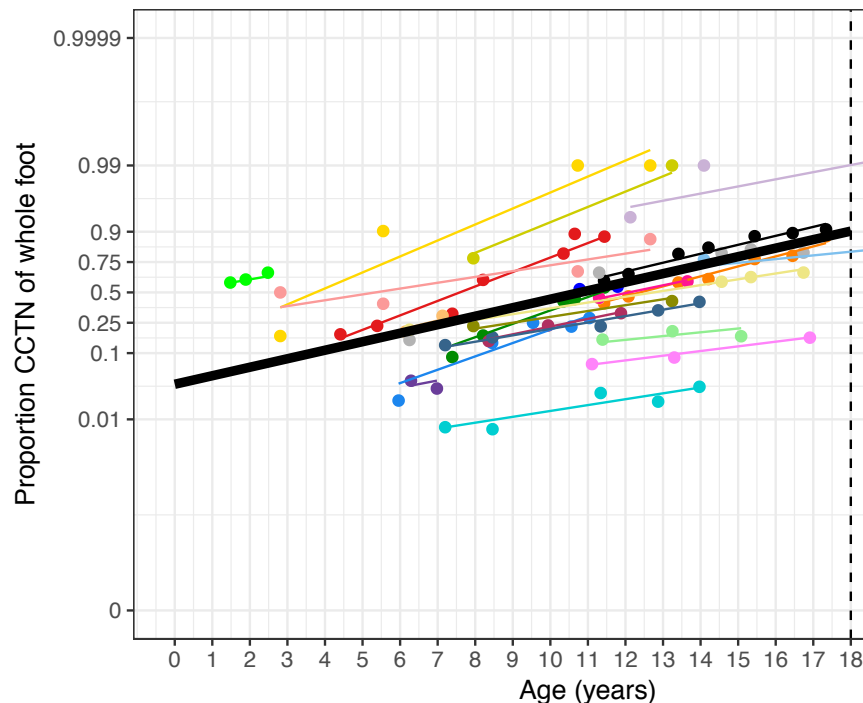
Natural history study

CCTN disease progression

Fit a mixed model to estimate random slope and intercept for age

For subject s at visit i : $\text{logit}(\text{CCTN}_{si}) = \beta_{0,s} + \beta_{1,s} * \text{Age}_{si} + \varepsilon_{si}$

Subject CCTN proportion of whole foot by age
Natural history study data



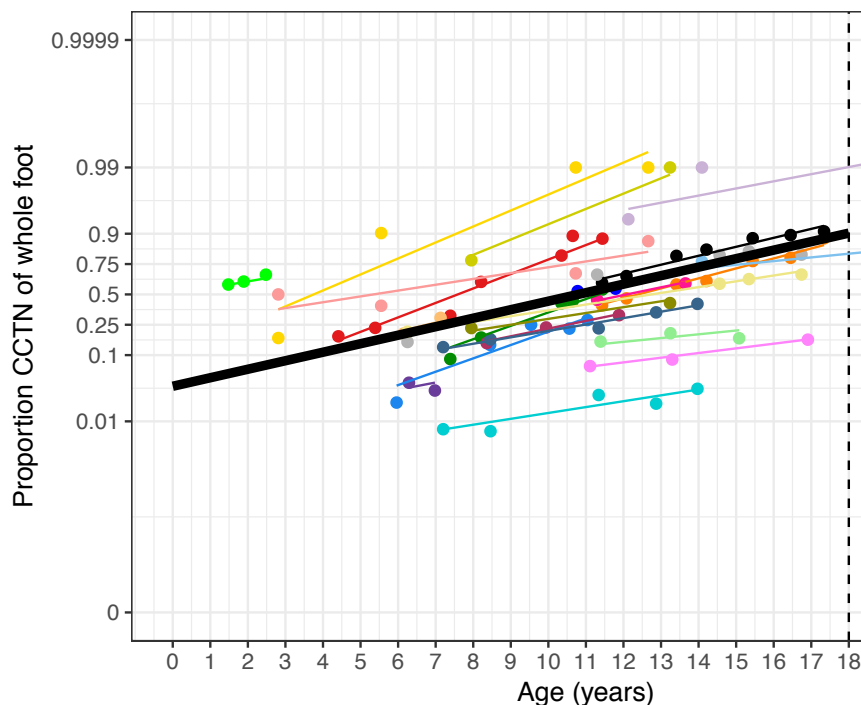
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Estimates:


- μ_{β_0} : mean random intercept
- $\sigma_{\beta_0}^2$: variance random intercept
- μ_{β_1} : mean random slope
- $\sigma_{\beta_1}^2$: variance random slope
- σ_{ε}^2 : residual error

CCTN simulation model

Virtual patient simulator

Use mixed model estimates to simulate virtual patients

For subject s at visit i : $\text{logit}(CCTN_{si}) = \beta_{0,s} + \beta_{1,s} * Age_{si} + \epsilon_{si}$


Natural history of
disease progression

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Natural history of
disease progression

$$\beta_{0,s} \sim \text{Normal}(\mu_{\beta_0}, \sigma_{\beta_0}^2)$$

$$\beta_{1,s} \sim \text{Gamma}\left(\frac{\mu_{\beta_1}^2}{\sigma_{\beta_1}^2}, \frac{\mu_{\beta_1}}{\sigma_{\beta_1}^2}\right)$$

$$\varepsilon_{si} \sim \text{Normal}(0, \sigma_{\varepsilon}^2)$$

CCTN simulation model

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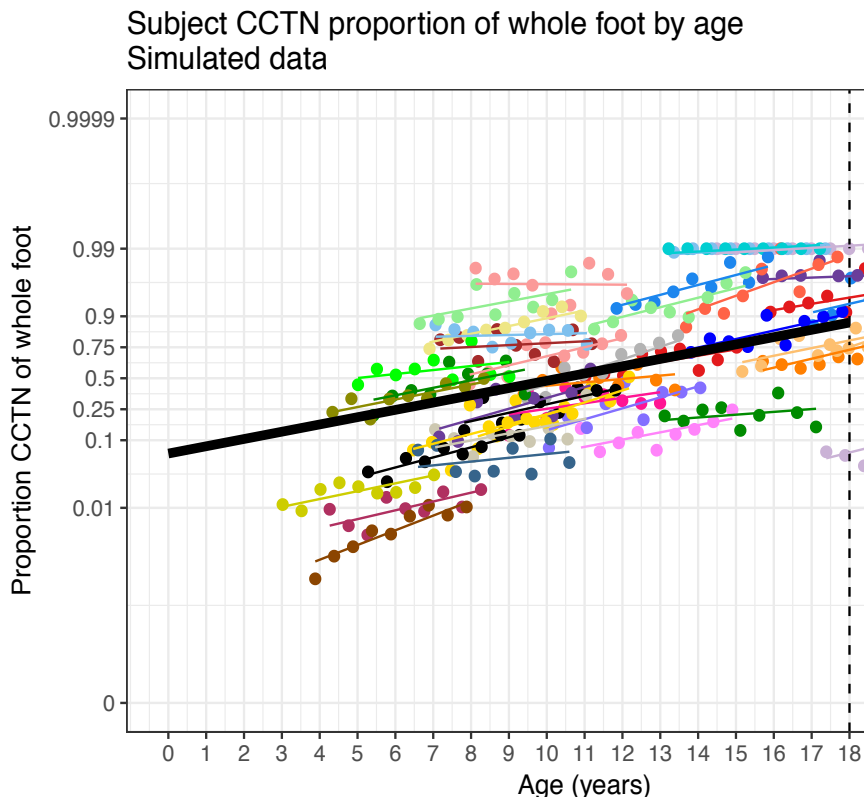
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Use mixed model parameter estimates to create a
virtual patient simulator that can generate patients
with the same characteristics as the NHS patients

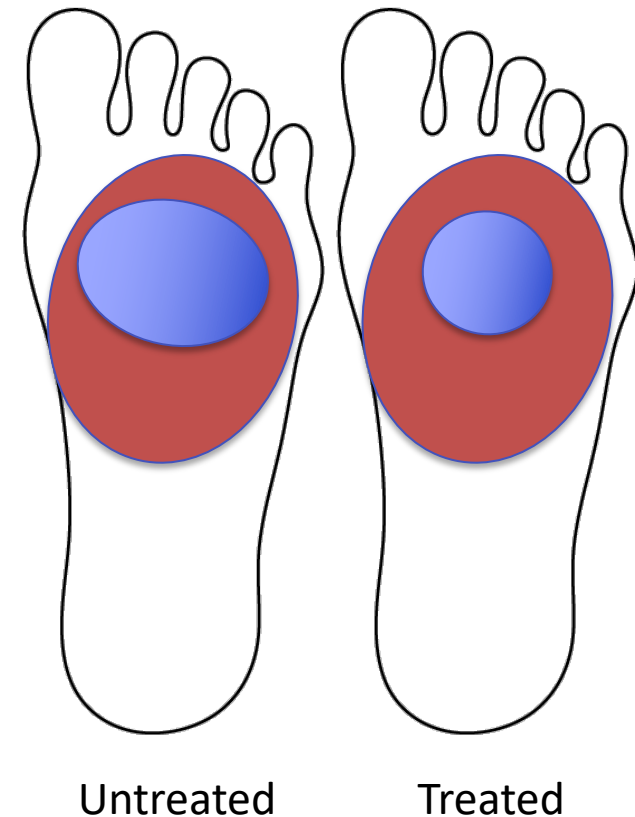
Assume that baseline age is distributed as a truncated normal.



Simulating a treatment effect

Proportional slowing of CCTN progression

- Treatment effect may *slow, stop, or reduce* disease progression of CCTN (measured as a proportion of the whole foot)
- Here, we are simulating CCTN and examining treatment effects applied to CCTN measurements



Simulating a treatment effect

Proportional slowing of CCTN progression

- Treatment effect, θ , is applied to the slope parameter of the simulation model
 - Only for the years during which the patient was treated

$$\text{logit}(\text{CCTN}_{si}) = \beta_{0,s} + \underbrace{(\beta_{1,s} * \text{Age}_{s0})}_{\text{Natural history of disease progression}} + \underbrace{(\theta * \beta_{1,s} * (\text{Age}_{si} - \text{Age}_{s0}))}_{\text{Treated disease progression}} + \epsilon_{si}$$

Years treated

Simulating a treatment effect

Proportional slowing of CCTN progression

- Treatment effect, θ , is applied to the slope parameter of the simulation model
 - Only for the years during which the patient was treated
- The addition of θ effectively models proportional slowing of CCTN progression

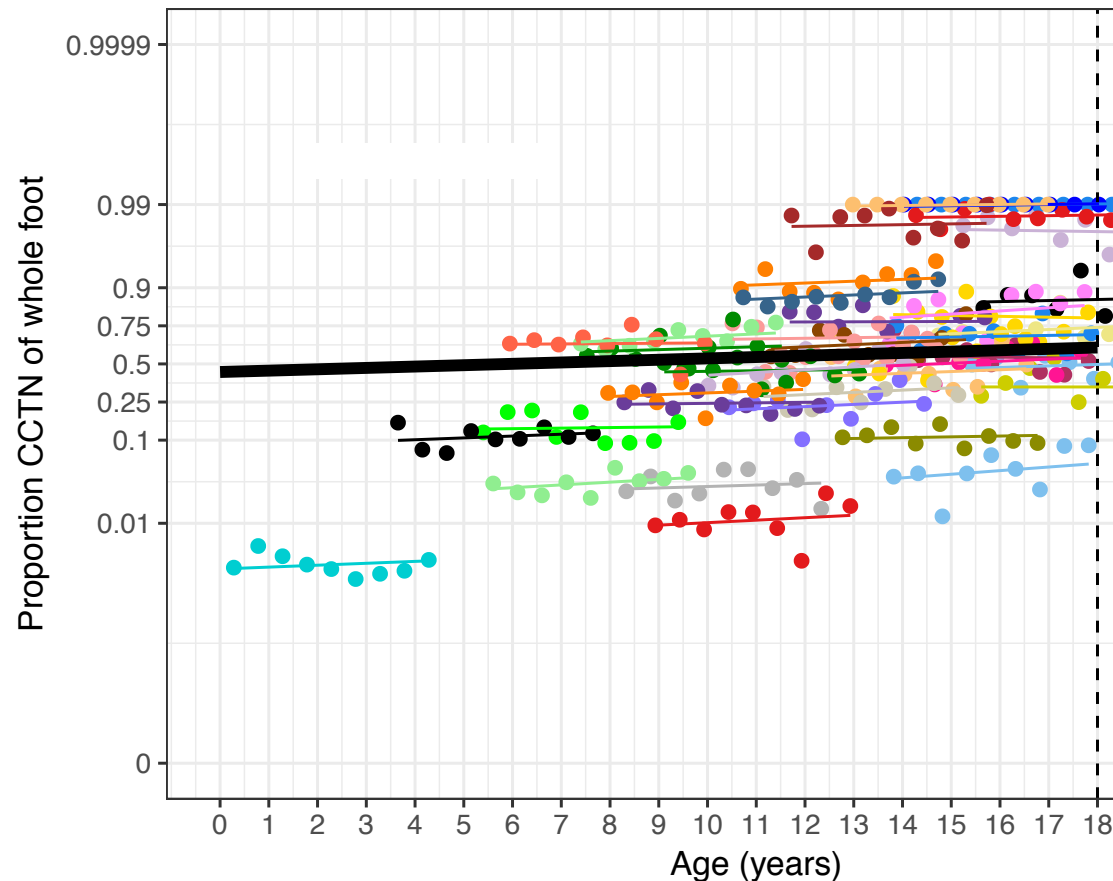
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Years treated

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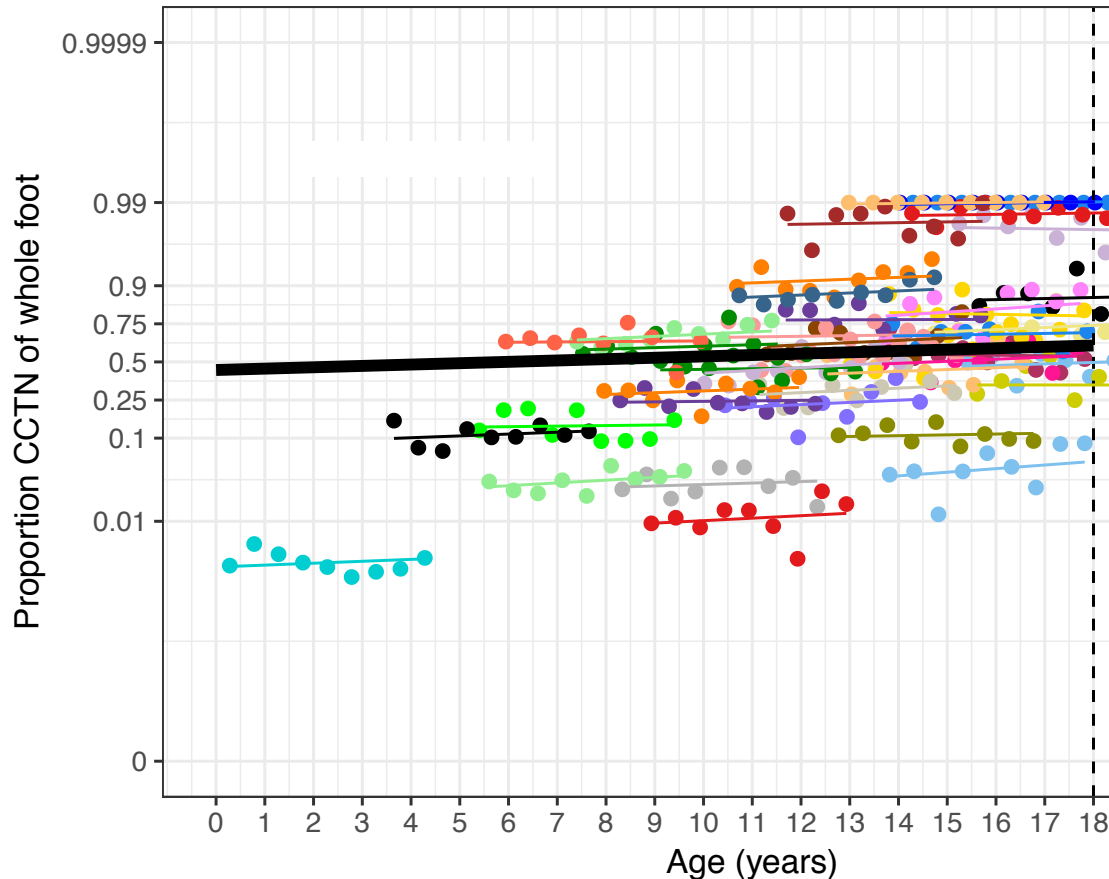
Subject CCTN proportion of whole foot by age
Simulated data, treated: $\theta = 0.1$



Simulating a treatment effect

Proportional slowing of CCTN progression

Subject CCTN proportion of whole foot by age
Simulated data, treated: $\theta=0.1$



Theta θ	Mean change in proportion CCTN of whole foot per year*
1	0.032
0.9	0.029
0.8	0.026
0.7	0.024
0.6	0.020
0.5	0.017
0.4	0.014
0.3	0.010
0.2	0.007
0.1	0.004
0	0.000

*based on 10,000 simulated trials

Bayesian disease progression model (DPM)

Primary analysis

For each subject, s , at visit, i , assume:

Quantifies rate of disease progression

$$\text{logit}(CCTN) \sim \text{Normal}(\mu_s, \sigma^2)$$

$$\mu_s = \alpha_s + \beta_s \text{Age}_{s,0} + \gamma \beta_s (\text{Age}_{s,i} - \text{Age}_{s,0})$$



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$$\text{Test } \Pr(\gamma < 1) \geq 0.994^*$$

* This threshold, found via simulation ensures 2.5% Type I error control

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This model integrates NHS patients into the analysis and allows for differential length of follow up

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Quantifies rate of disease progression

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$$\mu_s = \alpha_s + \beta_s \text{Age}_{s,0} + \gamma \beta_s (\text{Age}_{s,i} - \text{Age}_{s,0})$$

$$\alpha_s \sim \text{Normal}(\mu_\alpha, \sigma_\alpha^2) \quad \mu_\alpha \sim \text{Normal}(-3, 1^2) \quad \sigma_\alpha \sim \text{Uniform}(0, 10)$$

Priors

$$\beta_s \sim \text{Gamma}\left(\frac{\mu_\beta^2}{\sigma_\beta^2}, \frac{\mu_\beta}{\sigma_\beta^2}\right) \quad \mu_\beta \sim \text{Gamma}(0.3^2, 0.3) \quad \sigma_\beta \sim \text{Uniform}(0, 1)$$

$$\sigma \sim \text{Uniform}(0, 10)$$

$$\gamma \sim \text{Uniform}(0, 2)$$

This model integrates NHS patients into the analysis and allows for differential length of follow up

$$\text{Test } \Pr(\gamma < 1) \geq 0.994^*$$

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Trial operating characteristics

$$\Pr(\gamma < 1) \geq 0.994^*$$

Rate of disease progression, γ	4 years of follow up on treated patients	
	30 treated feet	40 treated feet
1	0.016	0.026
0.9	0.088	0.15
0.8	0.362	0.46
0.7	0.696	0.796
0.6	0.928	0.968
0.5	0.996	0.998
0.4	>0.999	>0.999
0.3	>0.999	>0.999
0.2	>0.999	>0.999
0.1	>0.999	>0.999
0	>0.999	>0.999

Trial - using Bayesian model

- All natural history data included
- 4 years of follow up for each treated subject
- 53 OR 63 (unique) feet:
 - 23 from natural history
 - 30 OR 40 treated
- Analysis of a single parameter, γ , which quantifies disease progression defined by proportion of whole foot CCTN

*Threshold selected to ensure one-sided 2.5% Type I error control

500 simulations per scenario

Design comparison

OPC vs. DPM

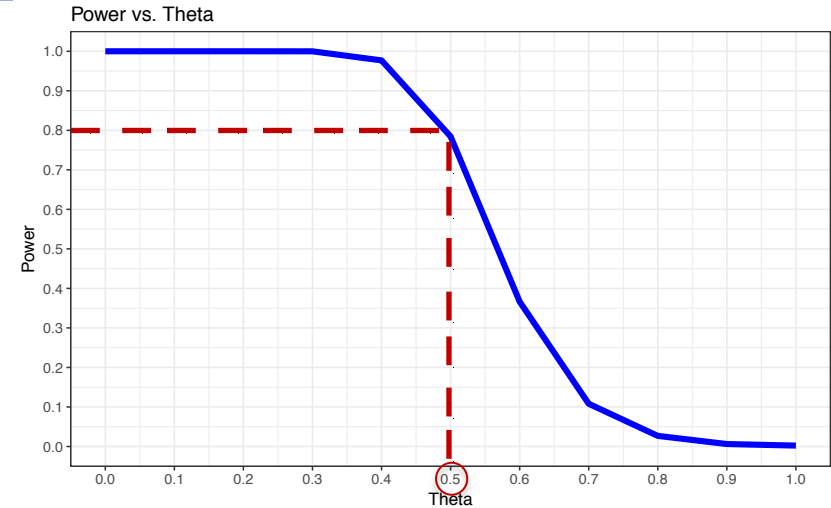
OPC analysis

40 treated feet

4 years of follow up

Analysis of lower confidence bound

Powered to detect a treatment effect equivalent
to at least 50% slowing in CCTN progression



Design comparison

OPC vs. DPM

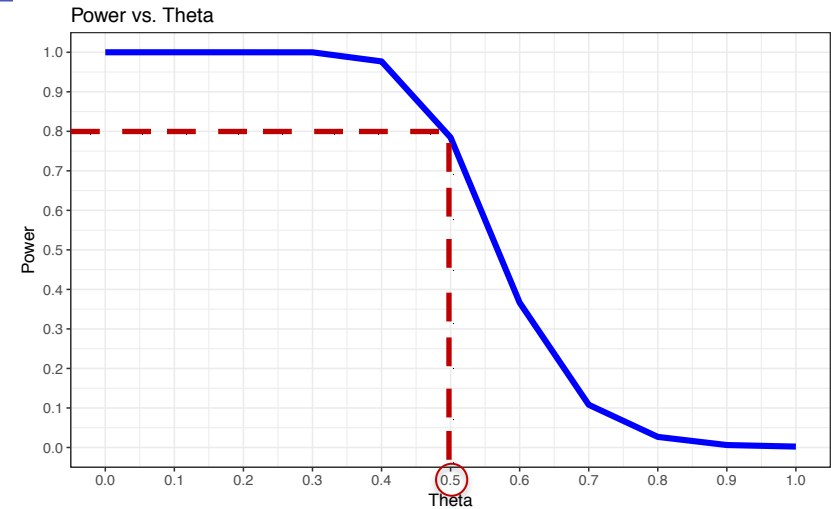
OPC analysis

40 treated feet

4 years of follow up

Analysis of lower confidence bound

Powered to detect a treatment effect equivalent to at least 50% slowing in CCTN progression



DPM analysis

40 treated feet

4 years of follow up

Analysis of Bayesian disease progression model

Powered to detect a treatment effect equivalent to at least 30% slowing in CCTN progression

