



# Rapid sample size calculations for a defined likelihood ratio test-based power in mixed effects models

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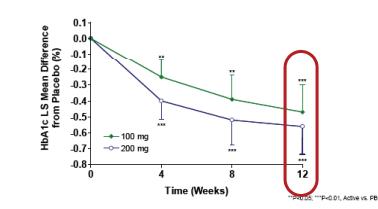


## Motivating example

### Phase II study in Diabetes

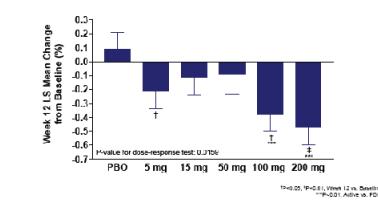
- Power to detect a significant drug effect on reduction in HbA1c
- 12 week study
- FPG and HbA1c
- Placebo + 5 dose groups

Placebo-Adjusted HbA1c Change from Baseline to Week 12 in the 100 mg and 200 mg Treatment Arms



### HbA1c Efficacy

Week 12 Change from Baseline in HbA1c



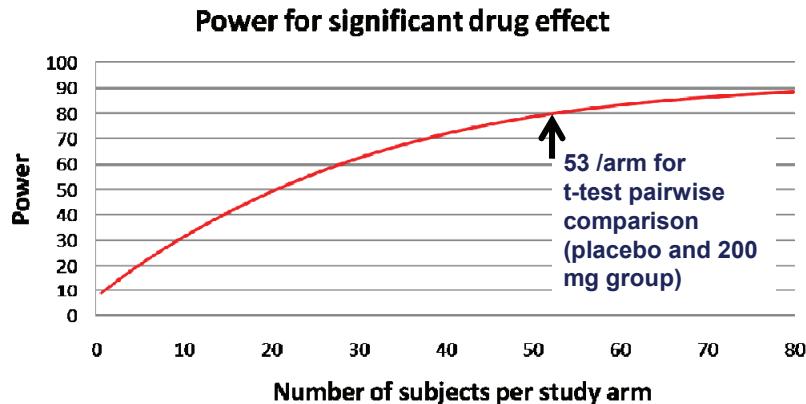
\*P<0.05, \*\*P<0.01, \*\*\*P<0.001, Week 12 vs. Baseline  
†P<0.05, ‡P<0.01, Active vs. PBO

Rosenstock et al., 69th ADA Scientific Sessions, 2009

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## Power with traditional group wise comparison (t-test)



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## Model-based approach

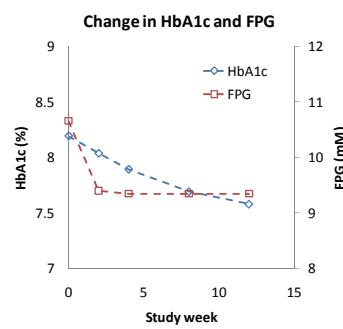
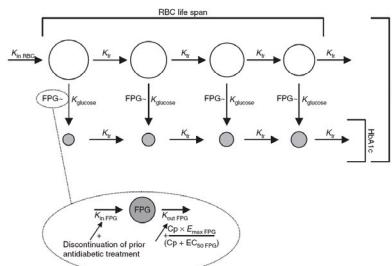
### Models for Plasma Glucose, HbA1c, and Hemoglobin Interrelationships in Patients with Type 2 Diabetes Following Tesaglitazar Treatment

B Hamren<sup>1,2</sup>, E Björk<sup>3</sup>, M Sunzel<sup>4</sup> and MO Karlsson<sup>2</sup>

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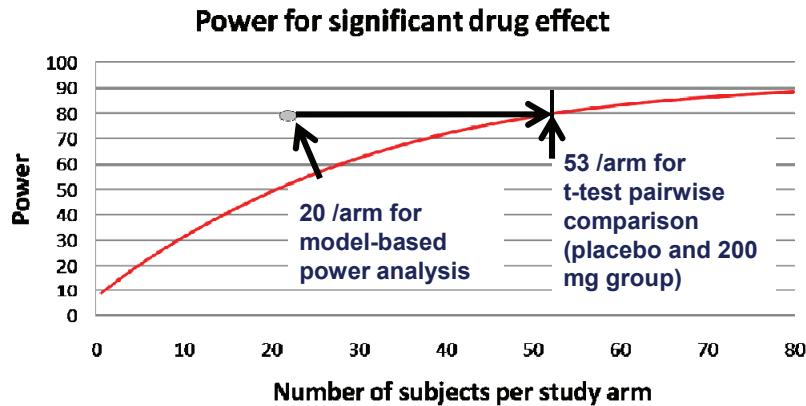
Received 31 October 2007; accepted 2 January 2008; advance online publication 19 March 2008; doi:10.1538/pq.2007.0293



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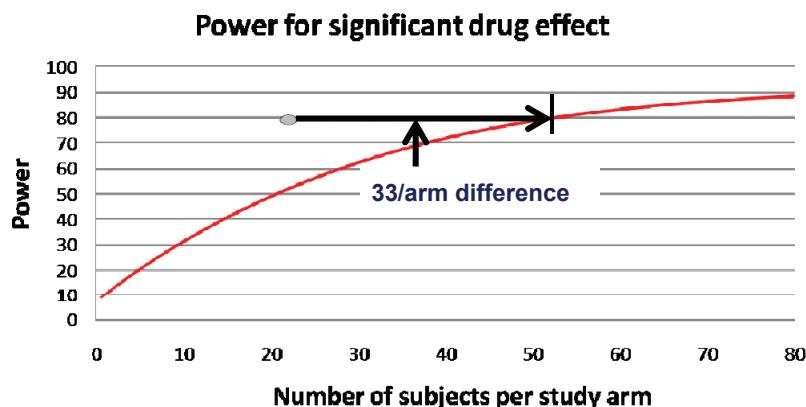
## Power with traditional group wise comparison (t-test)



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## Power with traditional group wise comparison (t-test)



⇒ Higher power with NLME models

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## Time computation comparison

**DESIGN is a moving target**

**Testing of assumptions and/or effect size**

**Guess of N for 80% power**

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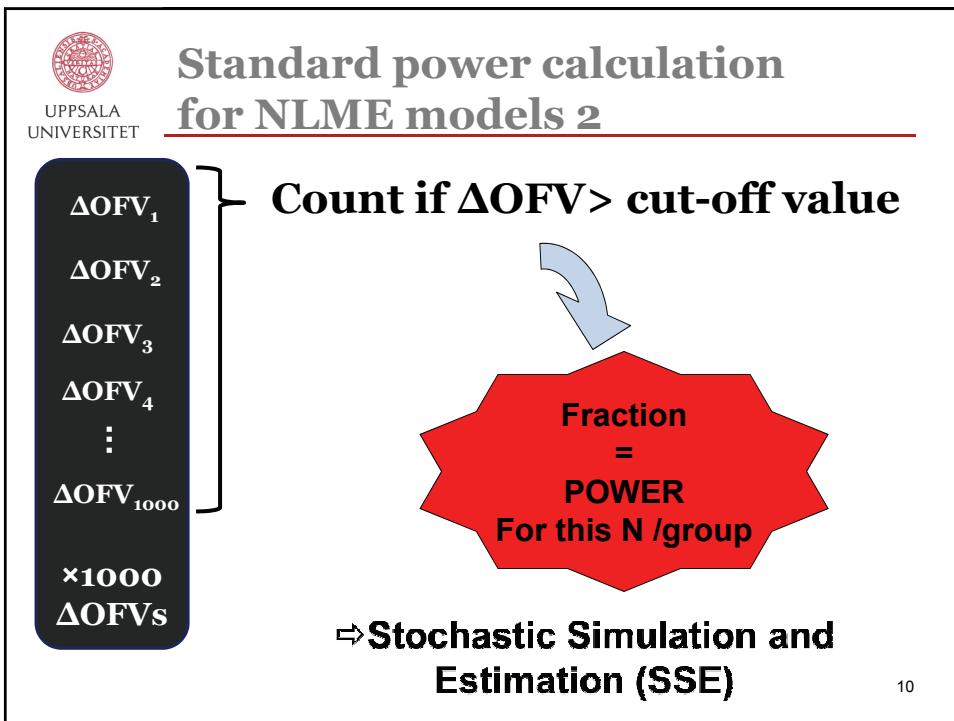
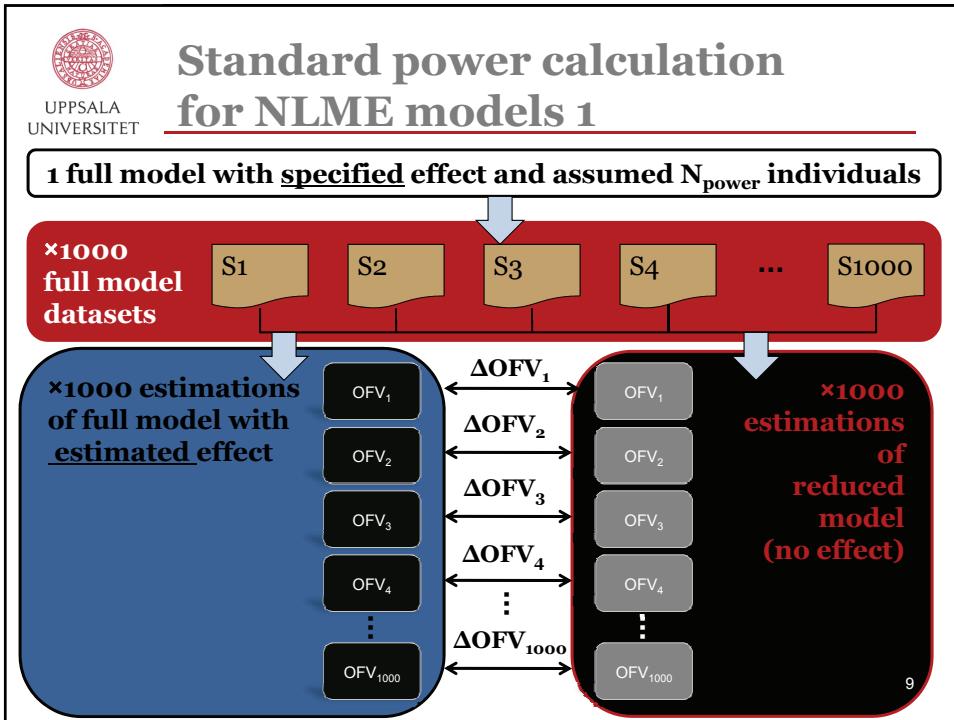
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## Objectives

- Power for Likelihood Ratio Test (LRT)
- Fast and easy method to map **complete** power curve

9 hours

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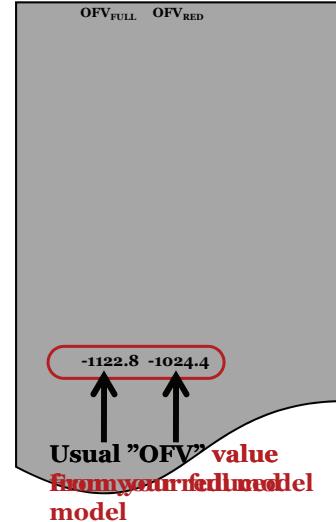




## Methodology

- Likelihood minimized during a NONMEM 7® run:

Objective Function Value =



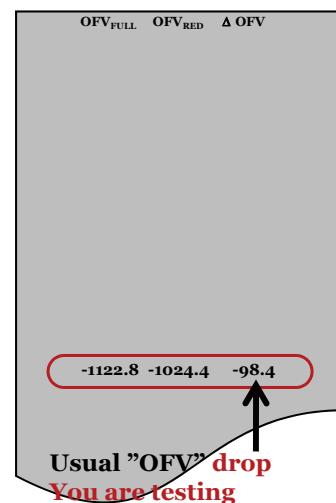
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## Methodology

- Likelihood minimized during a NONMEM 7® run:

Objective Function Value =



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## Methodology

- Likelihood minimized during a NONMEM 7® run:

$$\text{Objective Function Value} = \sum_{i=1}^n iOFV$$

- Can be directly found in NM7 in .phi file
- Can be computed in NM6 with –iofv in PsN

ID	iOFV <sub>FULL</sub>	iOFV <sub>RED</sub>
1	-2.461	-2.012
2	-2.413	-2.033
3	-2.358	-1.807
4	-2.367	-1.896
5	-2.26	-2.016
6	-2.094	-2.102
7	-2.48	-1.898
8	-2.07	-1.946
9	-2.453	-2.05
10	-2.193	-1.963
11	-2.127	-2.256
12	-2.409	-1.95
⋮	⋮	⋮
1000	-2.028	-1.941
$\Sigma$	-1122.8	-1024.4

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## Methodology

- Likelihood minimized during a NONMEM 7® run:

$$\text{Objective Function Value} = \sum_{i=1}^n iOFV$$

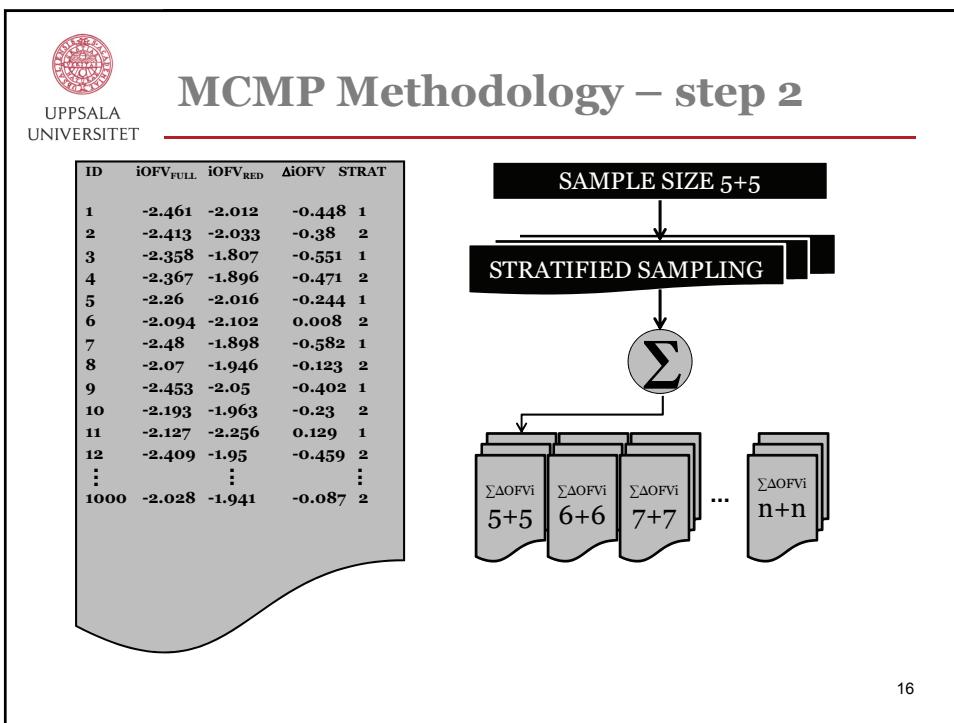
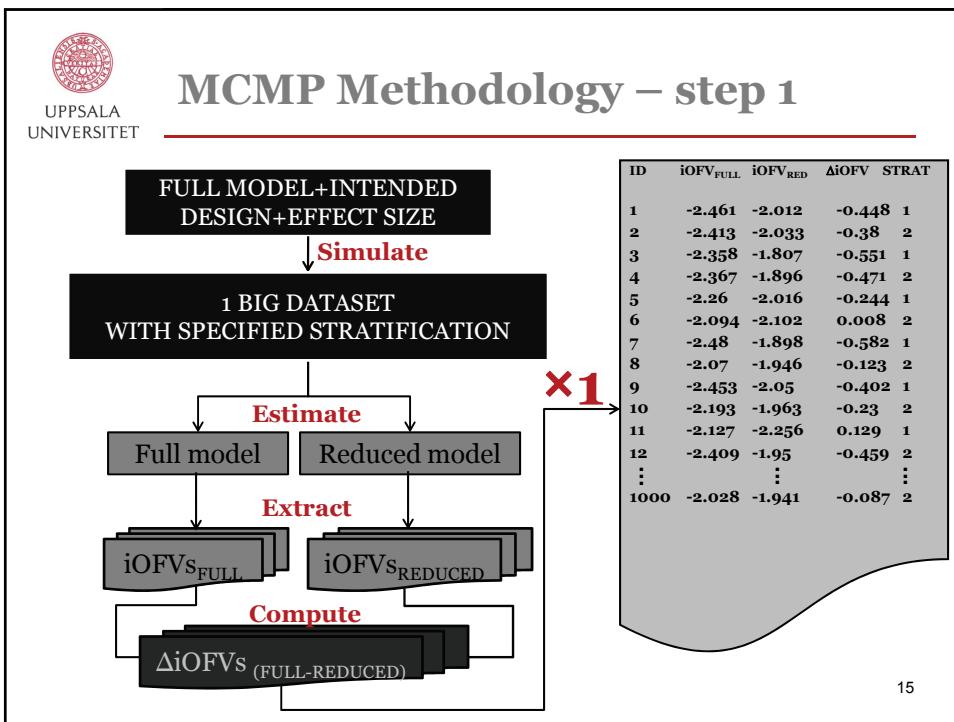
- Drop between two nested models (i.e.  $\chi^2$ -distribution):

$$\Delta OFV_{(FULL - REDUCED)} = \sum_{i=1}^n (iOFV_{FULL} - iOFV_{REDUCED})$$

ID	iOFV <sub>FULL</sub>	iOFV <sub>RED</sub>	$\Delta iOFV$	STRAT
1	-2.461	-2.012	-0.448	1
2	-2.413	-2.033	-0.38	2
3	-2.358	-1.807	-0.551	1
4	-2.367	-1.896	-0.471	2
5	-2.26	-2.016	-0.244	1
6	-2.094	-2.102	0.008	2
7	-2.48	-1.898	-0.582	1
8	-2.07	-1.946	-0.123	2
9	-2.453	-2.05	-0.402	1
10	-2.193	-1.963	-0.23	2
11	-2.127	-2.256	0.129	1
12	-2.409	-1.95	-0.459	2
⋮	⋮	⋮	⋮	⋮
1000	-2.028	-1.941	-0.087	2
$\Sigma$	-1122.8	-1024.4	-98.4	

Principle  
of MCMP

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## MCMP Methodology – step 2

ID	iOFV <sub>FULL</sub>	iOFV <sub>RED</sub>	$\Delta$ iOFV	STRAT
1	-2.461	-2.012	-0.448	1
2	<b>-2.413</b>	<b>-2.033</b>	<b>-0.38</b>	<b>2</b>
3	-2.358	-1.807	-0.551	1
4	-2.367	<b>-1.896</b>	<b>-0.471</b>	<b>2</b>
5	-2.26	-2.016	-0.244	1
6	-2.094	<b>-2.102</b>	<b>0.008</b>	<b>2</b>
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9	-2.453	-2.05	-0.402	1
10	<b>-2.193</b>	<b>-1.963</b>	<b>-0.23</b>	<b>2</b>
11	-2.127	-2.256	0.129	1
12	<b>-2.409</b>	<b>-1.95</b>	<b>-0.459</b>	<b>2</b>
⋮	⋮	⋮	⋮	⋮
1000	-2.028	-1.941	-0.087	2

```

graph TD
    A["SAMPLE SIZE 5+5"] --> B["STRATIFIED SAMPLING"]
    B --> C["Σ"]
    C --> D["ΣΔOFVi  
5+5"]
    C --> E["ΣΔOFVi  
6+6"]
    C --> F["ΣΔOFVi  
7+7"]
    C --> G["..."]
    C --> H["ΣΔOFVi  
n+n"]
  
```

The flowchart illustrates the MCMP Methodology Step 2 process. It starts with a 'SAMPLE SIZE 5+5' box, which leads to a 'STRATIFIED SAMPLING' box. This is followed by a summation symbol ( $\Sigma$ ). Below the summation symbol are four boxes labeled  $\Sigma\Delta OFVi$  with sizes 5+5, 6+6, 7+7, and n+n, separated by ellipses (...).

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## MCMP Methodology – step 2

ID	iOFV <sub>FULL</sub>	iOFV <sub>RED</sub>	$\Delta$ iOFV	STRAT
1	-2.461	-2.012	-0.448	1
2	<b>-2.413</b>	<b>-2.033</b>	<b>-0.38</b>	<b>2</b>
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10	<b>-2.193</b>	<b>-1.963</b>	<b>-0.23</b>	<b>2</b>
11	-2.127	-2.256	0.129	1
12	<b>-2.409</b>	<b>-1.95</b>	<b>-0.459</b>	<b>2</b>
⋮	⋮	⋮	⋮	⋮
1000	-2.028	-1.941	-0.087	2

```

graph TD
    A["SAMPLE SIZE 5+5"] --> B["STRATIFIED SAMPLING"]
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```

The flowchart illustrates the MCMP Methodology Step 2 process. It starts with a 'SAMPLE SIZE 5+5' box, which leads to a 'STRATIFIED SAMPLING' box. This is followed by a summation symbol ( $\Sigma$ ). Below the summation symbol are four boxes labeled  $\Sigma\Delta OFVi$  with sizes 5+5, 6+6, 7+7, and n+n, separated by ellipses (...).

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## MCMP Methodology – step 2

ID	iOFV <sub>FULL</sub>	iOFV <sub>RED</sub>	$\Delta$ iOFV	STRAT
1	-2.461	-2.012	-0.448	1
2	<b>-2.413</b>	<b>-2.033</b>	<b>-0.38</b>	<b>2</b>
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10	<b>-2.193</b>	<b>-1.963</b>	<b>-0.23</b>	<b>2</b>
11	-2.127	-2.256	0.129	1
12	<b>-2.409</b>	<b>-1.95</b>	<b>-0.459</b>	<b>2</b>
⋮	⋮	⋮	⋮	⋮
1000	<b>-2.028</b>	<b>-1.941</b>	<b>-0.087</b>	<b>2</b>

$\Sigma \Delta iOFV = -2.278$

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## MCMP Methodology – step 2

$\Sigma \Delta iOFV = -2.278$

$\Sigma \Delta iOFV = -5.037$

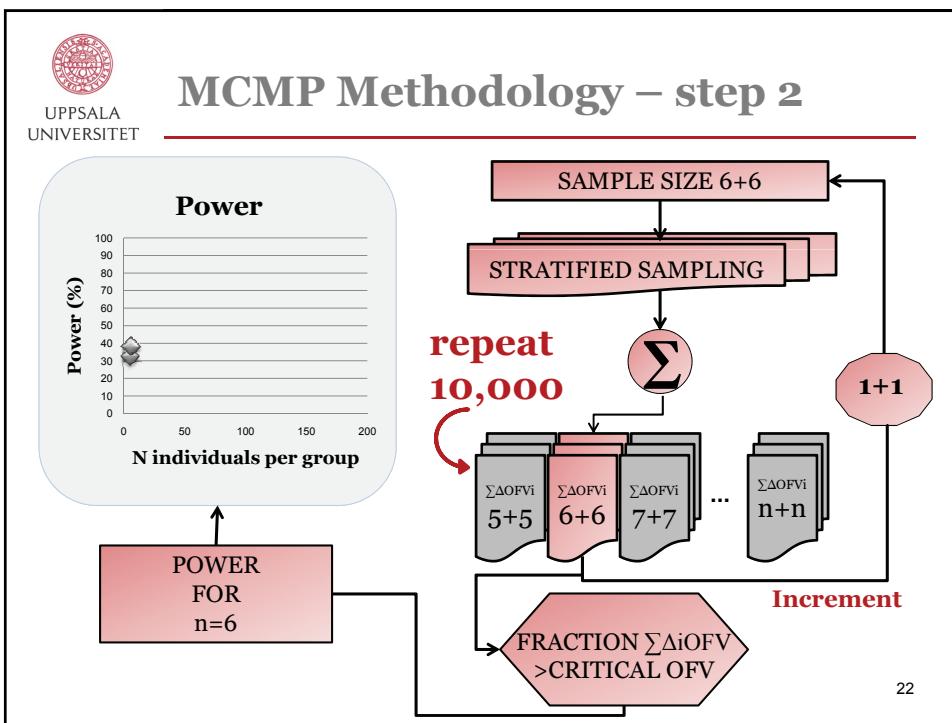
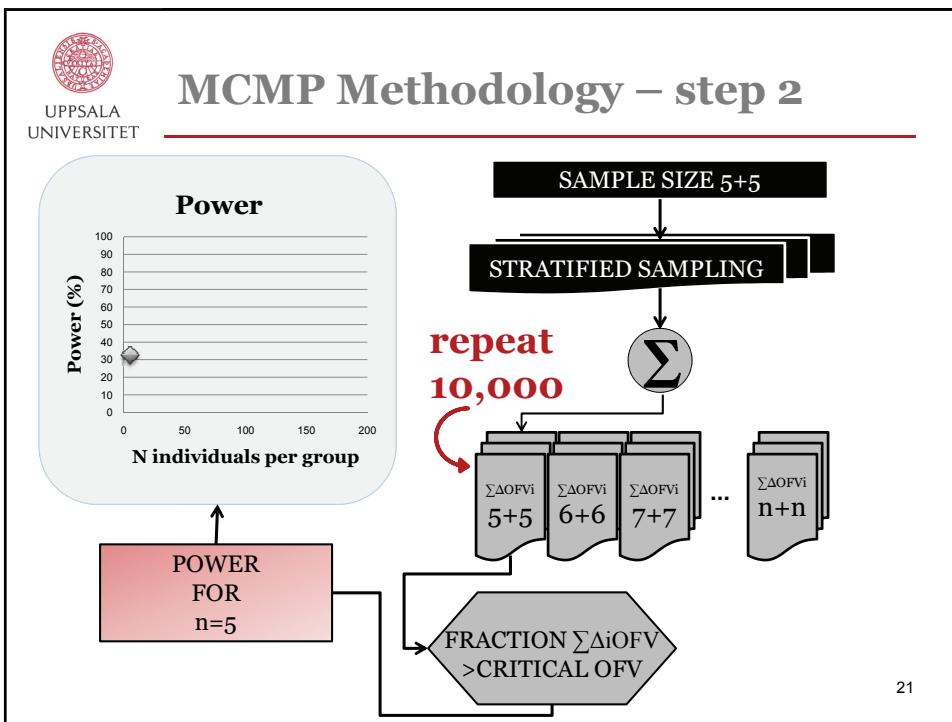
$\Sigma \Delta iOFV = -0.641$

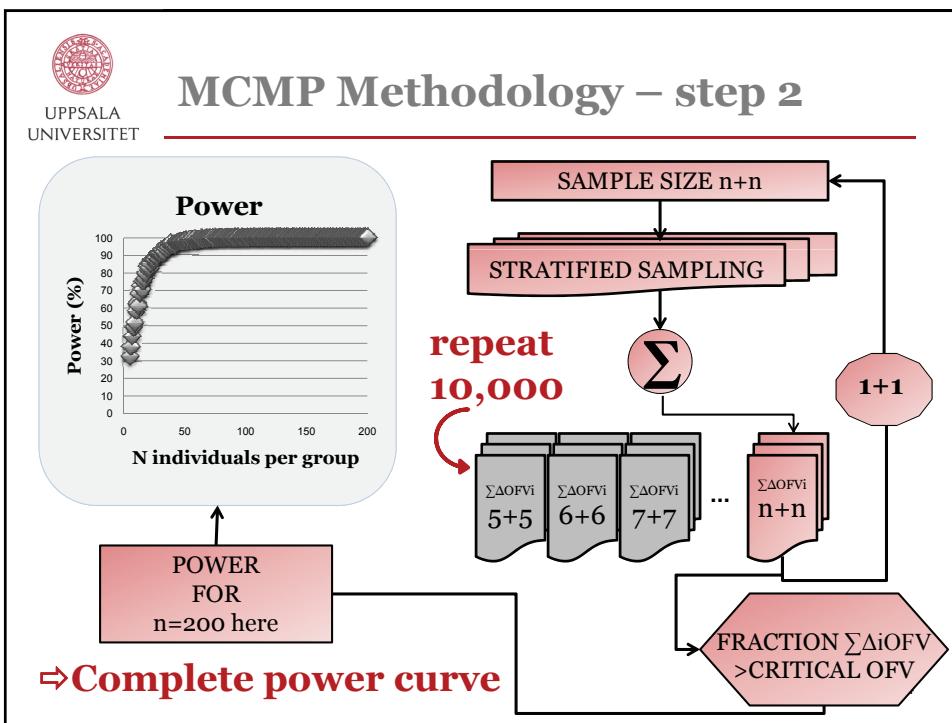
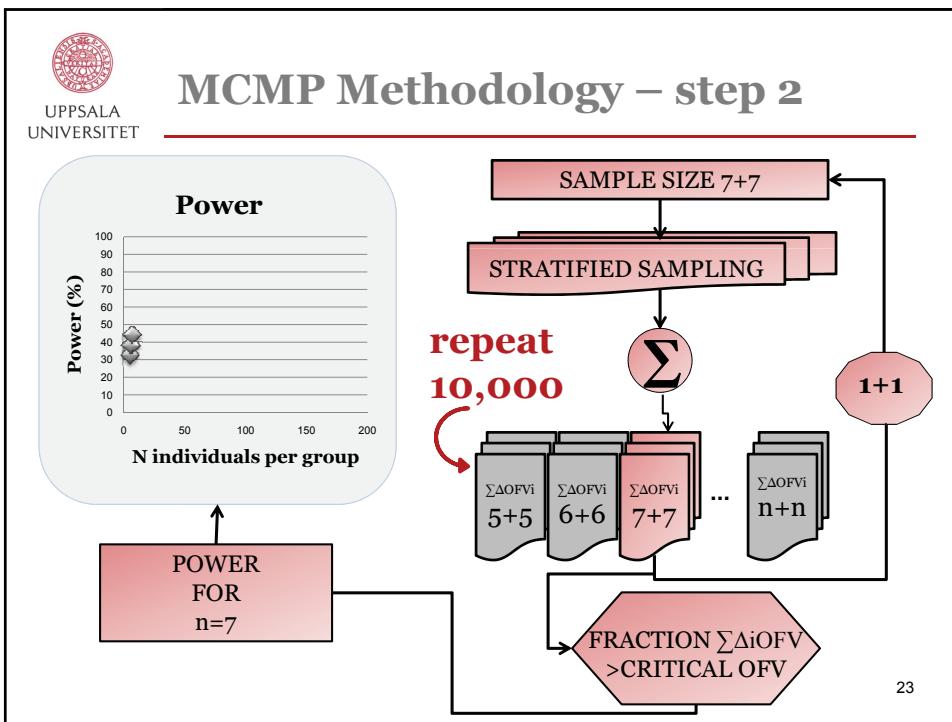
$\Sigma \Delta iOFV = 0.488$

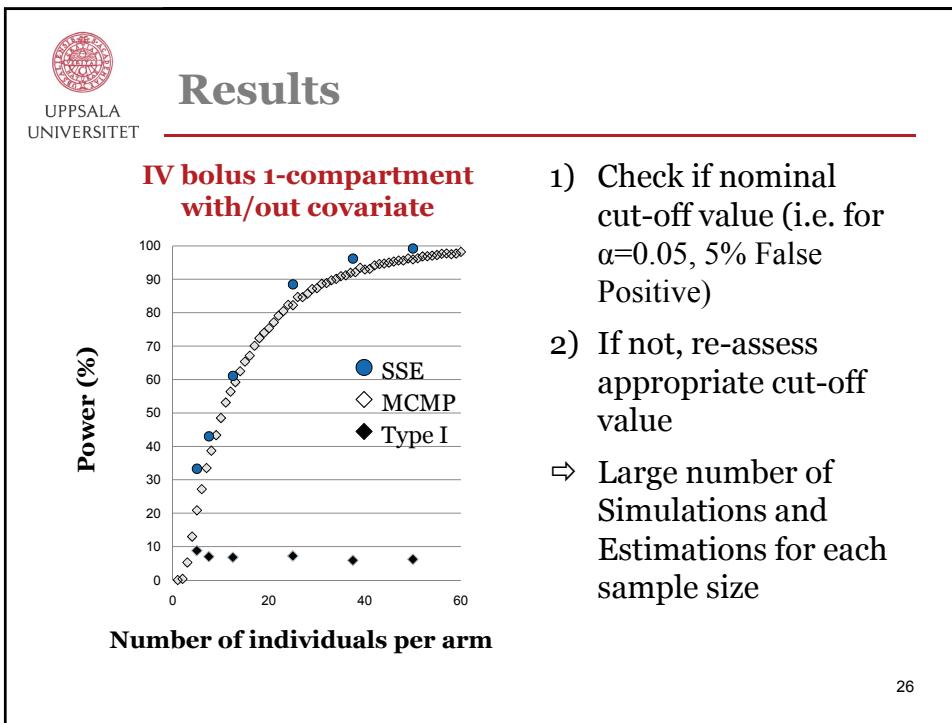
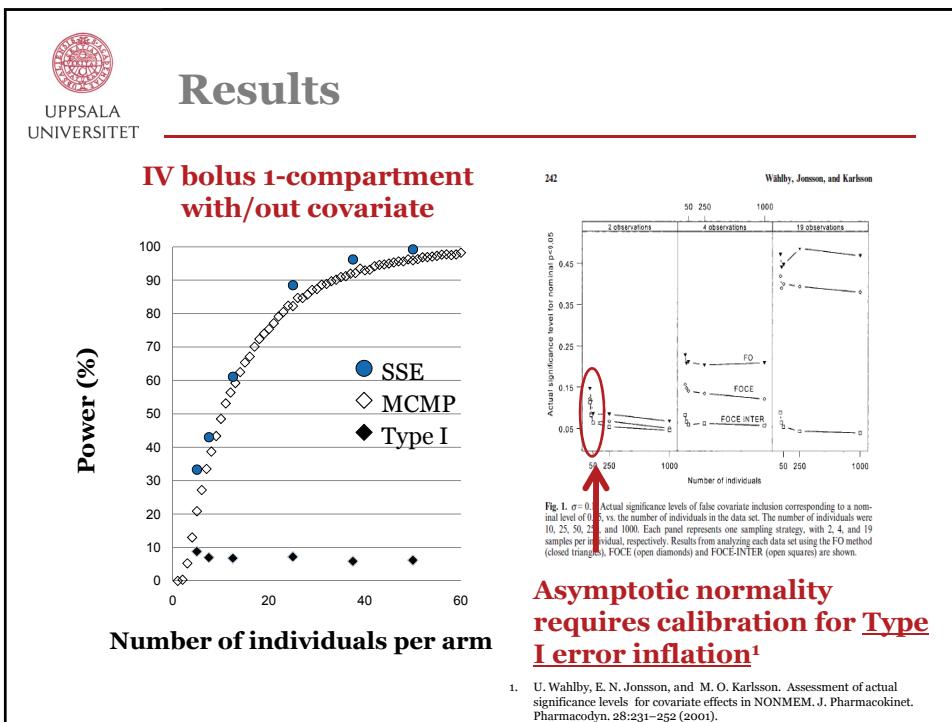
...

$\Sigma \Delta iOFV = -3.694$

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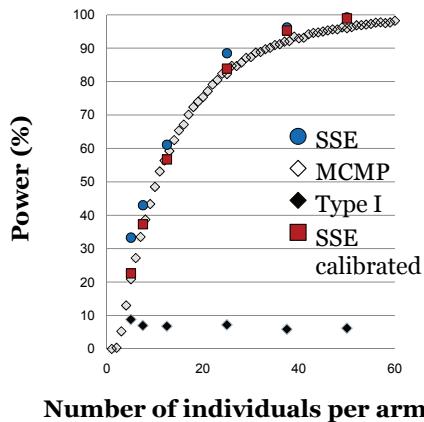






## Results

### IV bolus 1-compartment with/out covariate



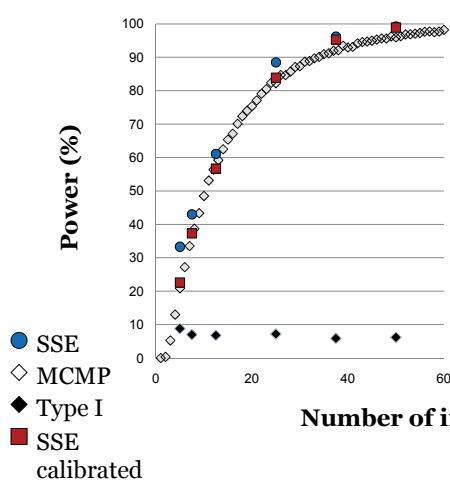
- 1) Check if nominal cut-off value (i.e. for  $\alpha=0.05$ , 5% False Positive)
  - 2) If not, re-assess appropriate cut-off value
- ⇒ Large number of Simulations and Estimations for each sample size

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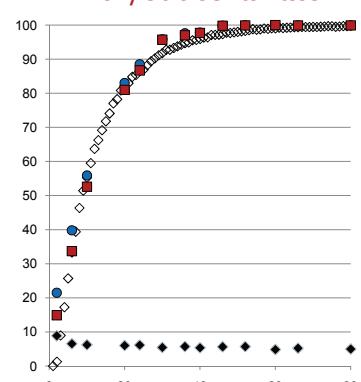


## Results

### IV bolus 1-compartment with/out covariate



### Infusion 1-compartment with/out covariate

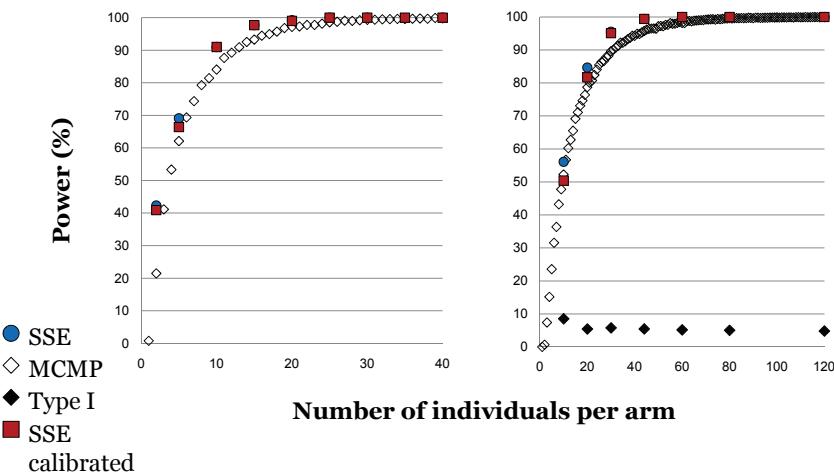


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## Results

FPG-HbA1c model with/out drug effect on Kout

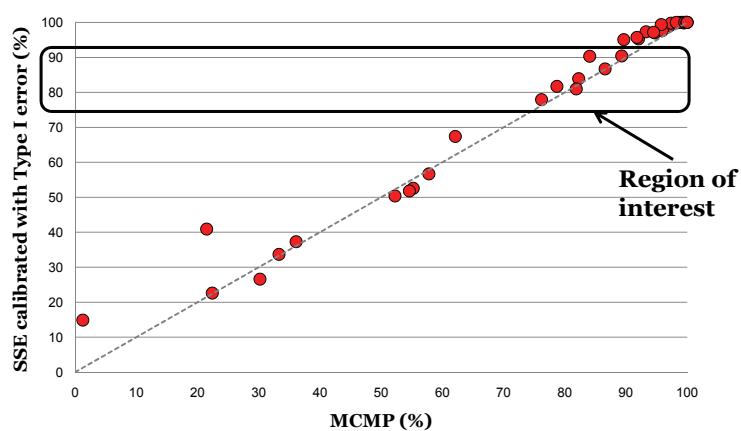


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## Pool of all tested models results

Calibrated SSE vs. MCM Power



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**2<sup>nd</sup> Application**

**ARTICLES**

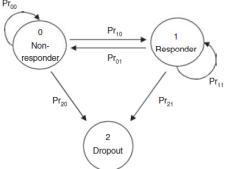
A Pharmacodynamic Markov Mixed-Effects Model for Determining the Effect of Exposure to Certolizumab Pegol on the ACR20 Score in Patients With Rheumatoid Arthritis

BD Lacout<sup>1,2</sup>, MR Lorenz<sup>1</sup>, A Stocks<sup>1</sup>, ML Sargentini-Mäder<sup>1</sup>, MO Karlsson<sup>3</sup> and LE Friberg<sup>2</sup>

Pharmometrics, Department of Global Exploratory Development, UCB Pharma SA, Braine-Milleville, Belgium; Department of Pharmaceutical Biostatistics, Uppsala University, Uppsala, Sweden. Correspondence: BD Lacout (lacout.bright@bright.be) or lefrig@friberg.se

Received 1 April 2008; accepted 3 June 2008; advance online publication 22 July 2008; doi:10.1038/cpt.2008.16

CLINICAL PHARMACOLOGY & THERAPEUTICS | VOLUME 84 NUMBER 4 | OCTOBER 2008

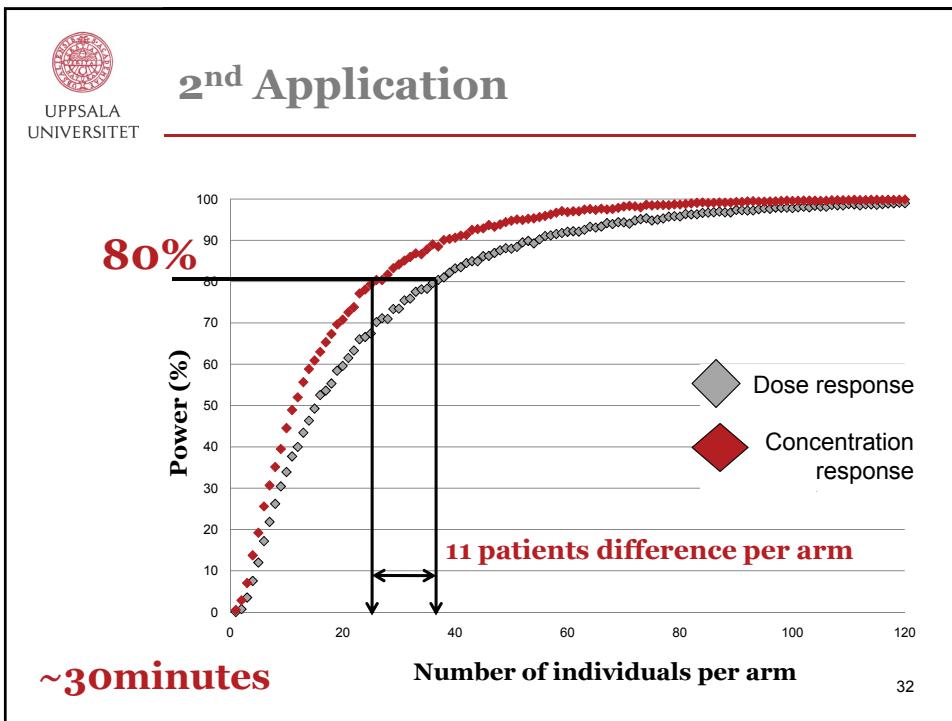


**Figure 1** Transitions between the three possible states (ACR20) defined by the scores 0, 1, and 2, respectively. ACR20, American College of Rheumatology 20% preliminary definition of improvement in rheumatoid arthritis.

**Proof of Concept study with categorical data**

- Power to detect difference with PK samples vs. only dose
- Placebo + 4 dose groups
- GO/NO GO criterion : number of inclusion between the two studies

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## Summary

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**A fast method for powering LRT**

- ✓ Possibility to obtain a complete power curve
- ✓ No calibration of type I error
- ✓ Opportunity for rapid response to design changes proposed by study team
- ✓ Increase feasibility for sensitivity analyses

⇒ **Increase possibility to demonstrate added value of mechanism-based models**

**Future work**

- ✓ Soon to be embedded in PsN software

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## Acknowledgment

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⌘ My co-authors: Mats O. Karlsson and Martin Bergstrand

⌘ Kristin Karlsson (<http://www.page-meeting.org/default.asp?abstract=1846>)

⌘ Sebastian Ueckert, Joakim Nyberg

⌘ The Pharmacometrics Group at Uppsala University

⌘ Institut de Recherches Internationales SERVIER for research funding

And... 34

