#### Modelling and Simulation of the incidence of adverse events in clinical trials

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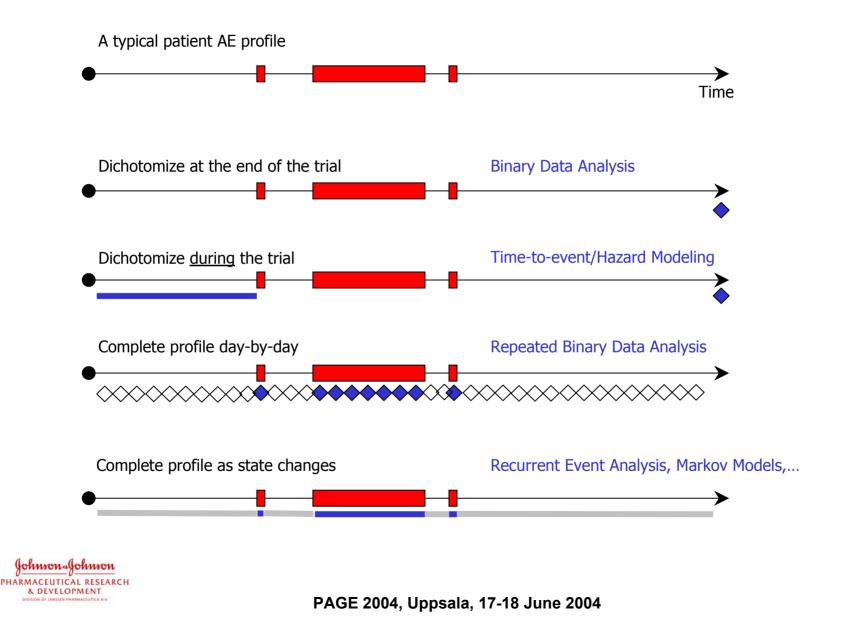
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## Introduction

- Drug Y is an improved version of a marketed drug X
- A specific adverse event is related to supra-efficacious drug levels and is expected for drug Y as well.
- In planned clinical trials with drug Y, we want to control the incidence of the adverse event, to balance efficacy and safety
- PK/PD model using data of drug X (~2500 patients, 10 trials)
- Predict adverse event in clinical trials with Y (based on a pharmacokinetic and pharmacological rationale)



### How to model adverse events?



# The Data of Drug X

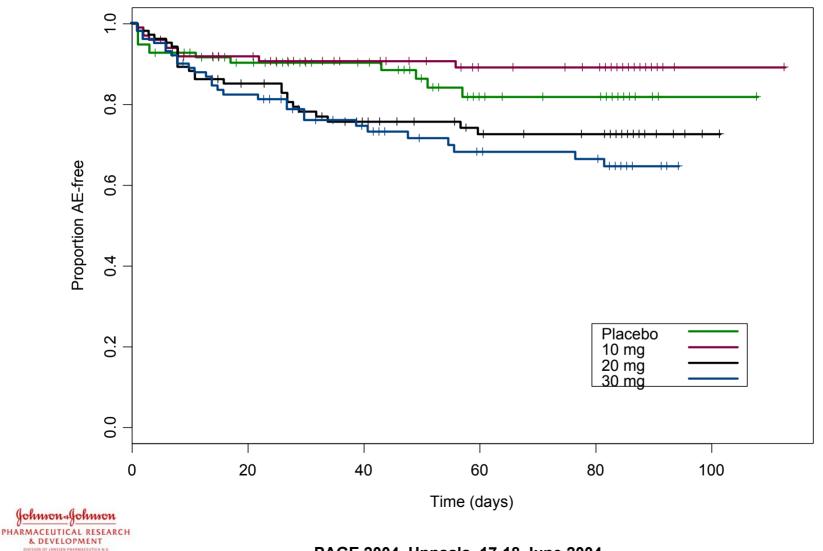
#### Double-blind placebo controlled trial with 3 doses

Treatment	N	Drop-out(%)	<u>AE(%)</u>
Placebo	98	67(68)	13(13)
10 mg	99	51(51)	10(10)
20 mg	103	54(51)	25(24)
<u>30 mg</u>	100	52(52)	29(29)

AE = # of patients with at least 1 AE-episode # of patients randomized

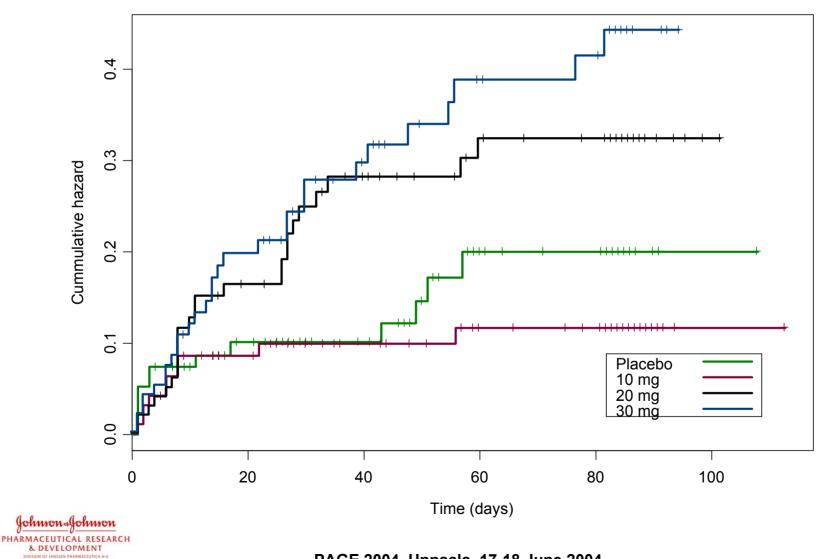


### Kaplan-Meier plot for time to first AE



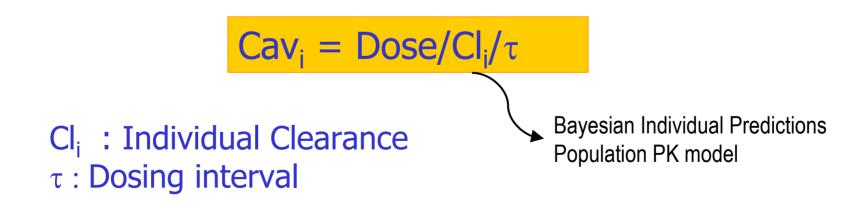
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#### Cumulative hazard



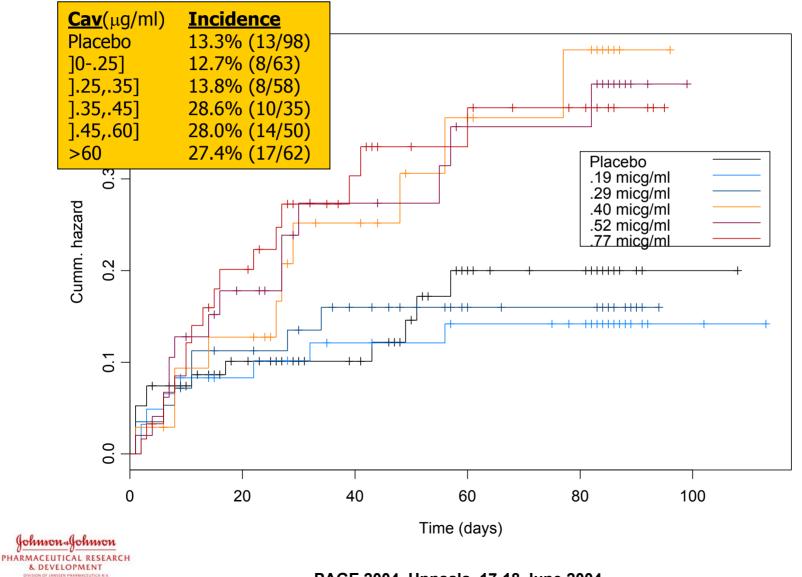
# What measure of drug exposure?

- No scientific rationale available
- As the adverse event develops over time, an integrated measure of long term exposure was chosen
- Individual Average Steady-State Concentration (Cav<sub>i</sub>)



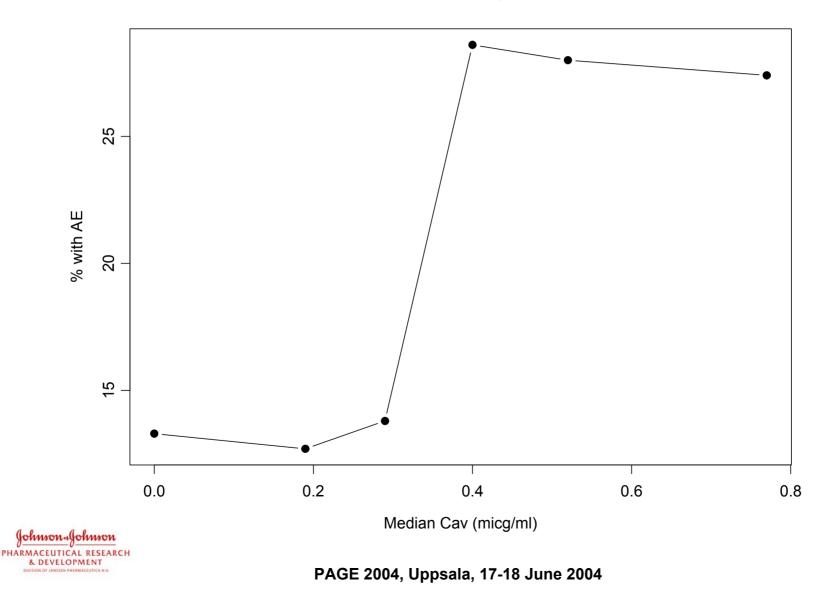
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### Cumulative hazard x Exposure



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### Incidence of AE x Exposure



# Modeling the AE risk

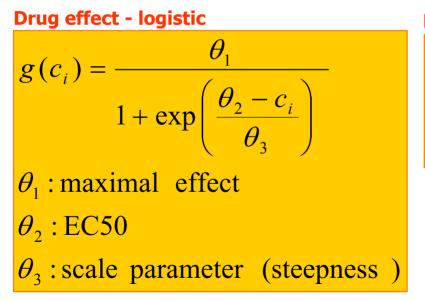
 $\log \lambda(t,c_i) = f(t) + g(t,c_i)$ 

*t* : time since trial start

c<sub>i</sub>:individual average steady state concentration

#### Time dependency

 $f(t) = \beta_0 + \beta_1 t$ 

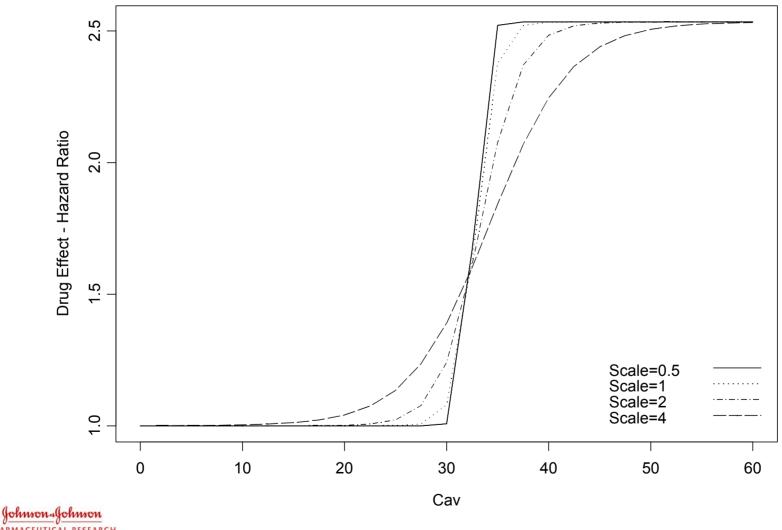


#### **Drug effect - threshold**

 $g(c_i) = I(c_i > \theta_1) \cdot \theta_2$   $\theta_1 : \text{threshold for risk increase}$  $\theta_2 : \log \text{ risk increase}$ 

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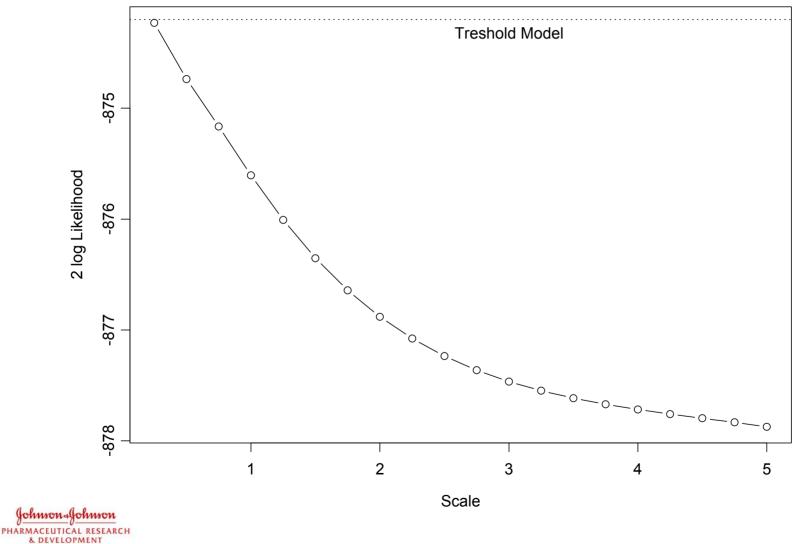
#### Functional form for various $\theta_3$



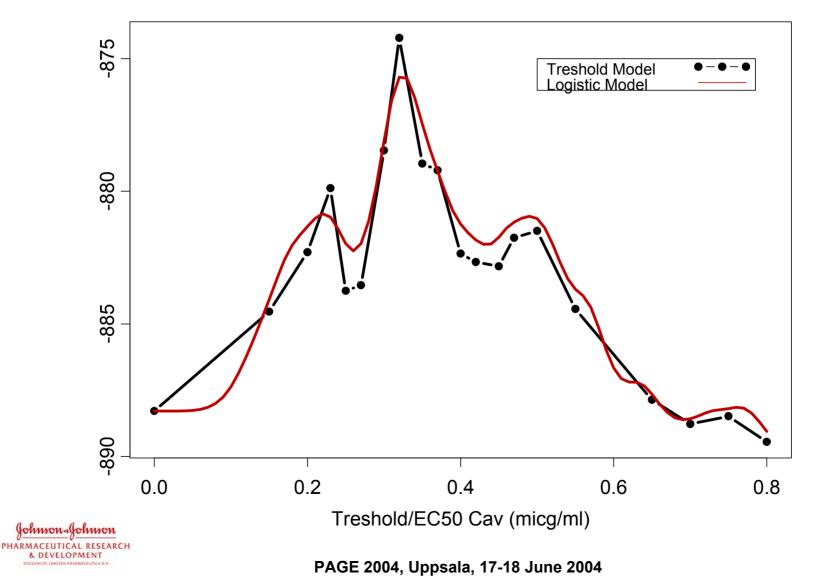
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# Likelihood profile for $\theta_3$

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# Threshold versus logistic model $(\theta_3=1)$



### Implementation in SAS 8.2

#### id time cav event;

1	1	12	0
1	2	12	0
1	3	12	0
1	60	12	0 = censored at Day 60
2	1	65	0
2	2	65	0
2	3	65	1 = has AE at Day 3

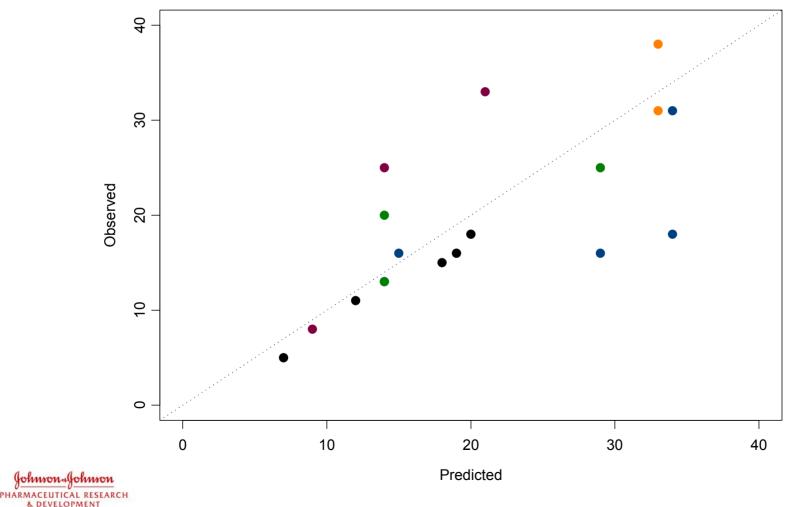
#### proc nlmixed; parms a=-4 b=-0.04 emax=1 ec50=3 scale=4; loghaz=a+b\*time+emax/(1+exp(ec50-cav)/scale); p=exp(loghaz); model event~binomial(1,p); run;



### **Model Validation**

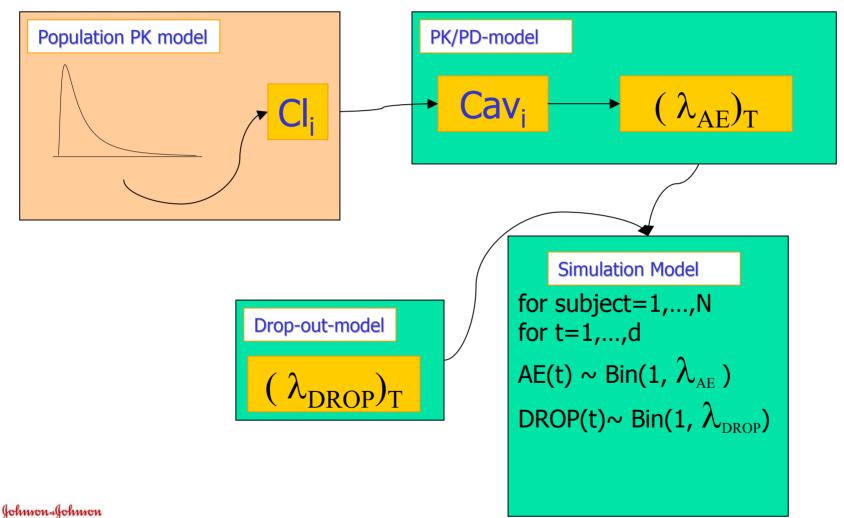
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AE incidence (%) in 5 independent clinical trials with drug X (total ±2000 pat.). Each point is a different dose, each color a different trial



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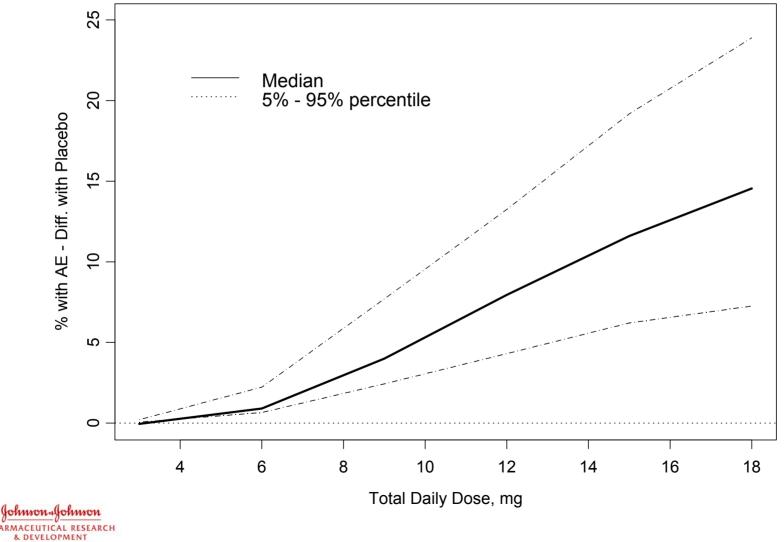
# Clinical Trial Simulation for Drug Y



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# Incidence of AE in the population

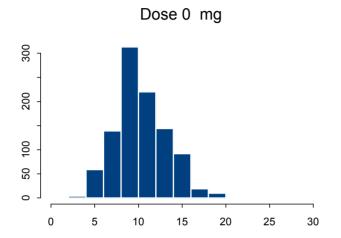
Simulation of 2000 patients/dose, no drop-out, 8-week trial



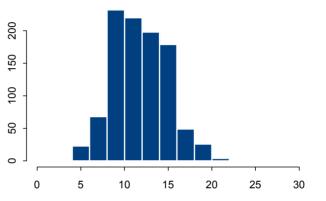
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# AE Incidence (%) in planned trials

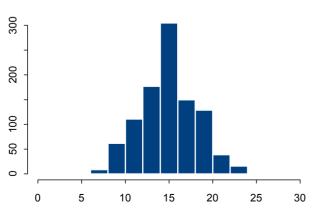
Simulation of 1000 trials, 100 patients/dose, drop-out, 8-weeks

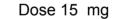


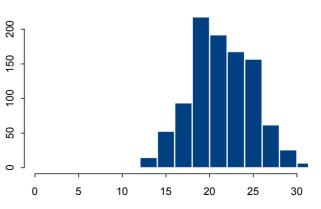
Dose 3 mg



Dose 9 mg



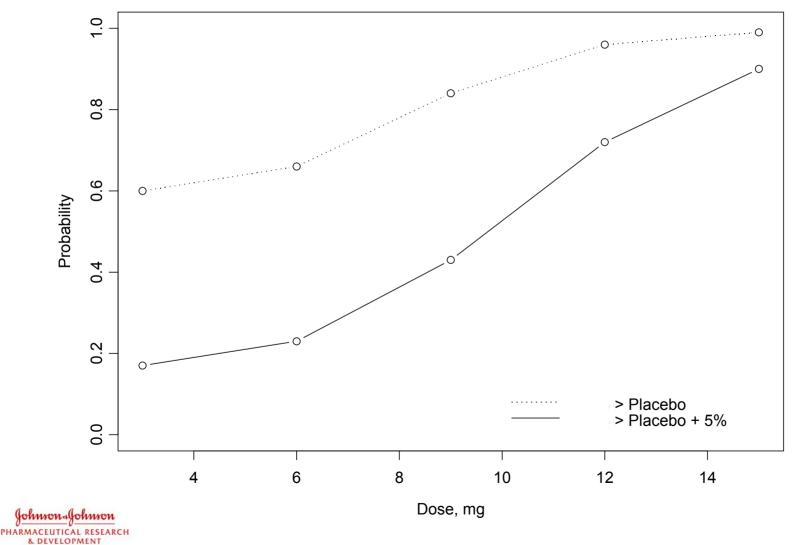




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# AE Incidence (%) in planned trials

Simulation of 1000 trials, 100 patients/dose, drop-out, 8-weeks



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### Conclusions

- Hazard modeling is a flexible tool to model the occurrence of side effects in clinical trials
- In the example presented here, the risk for a specific adverse event showed a steep (~on/off) relation with the patient-specific average steady state concentration
- Modeling allowed synthesis of data of a large number of studies of a marketed drug
- Clinical Trial Simulation allowed to study what can be expected in planned clinical trials, and optimize the dose range to study.

