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# *Evaluation of a transit compartment model versus a lag time model for describing drug absorption delay*

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# Absorption delay

A delay in the initial appearance of drug in plasma

*Of interest:*

- **Facilitate modeling of pharmacokinetic profiles**
- Impact on predicted time-effect profile
- To learn about absorption properties



# *Absorption delay modelling*

Two models were evaluated:

- 1. Lag time model**

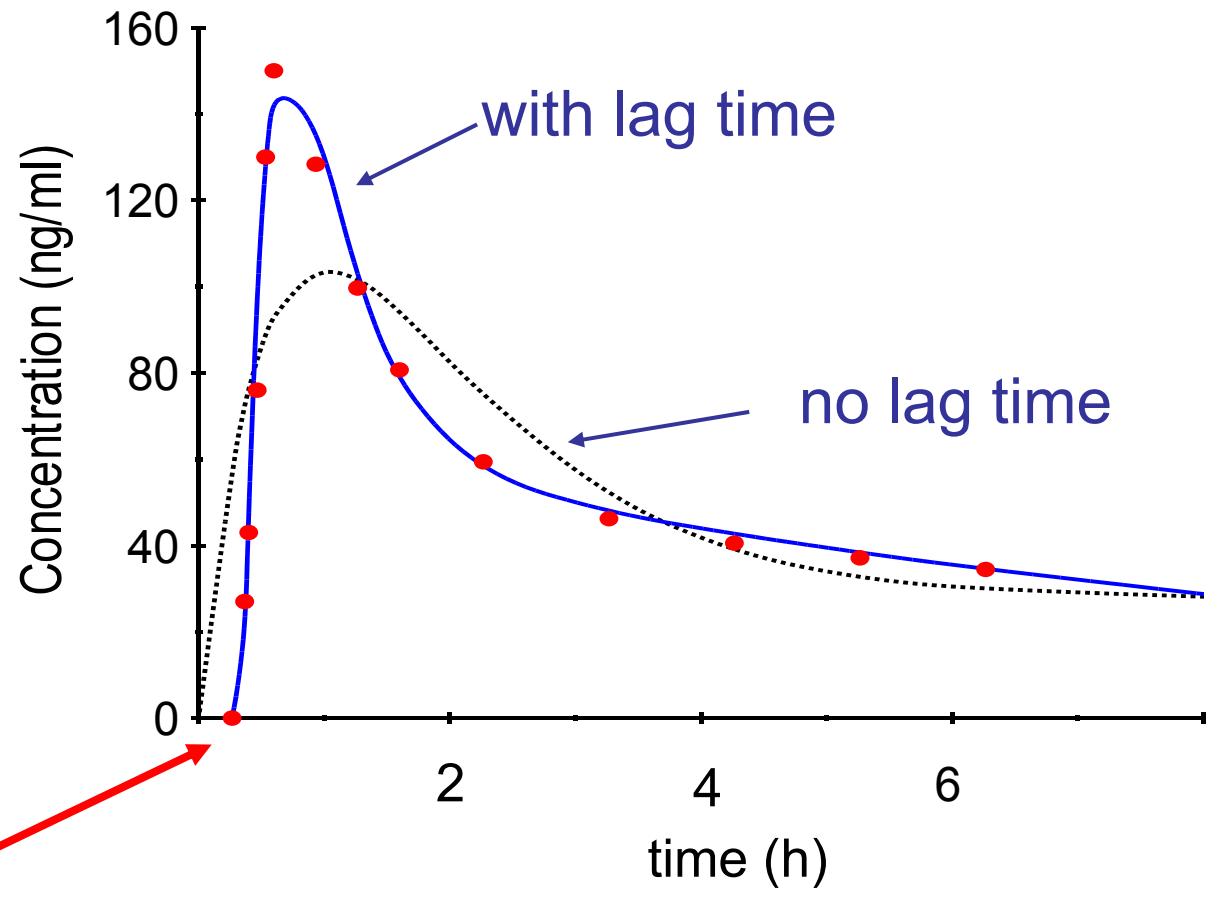
Estimation of lag time

- 2. Transit compartment model**

Delay due to passage of drug through a chain of transit compartments



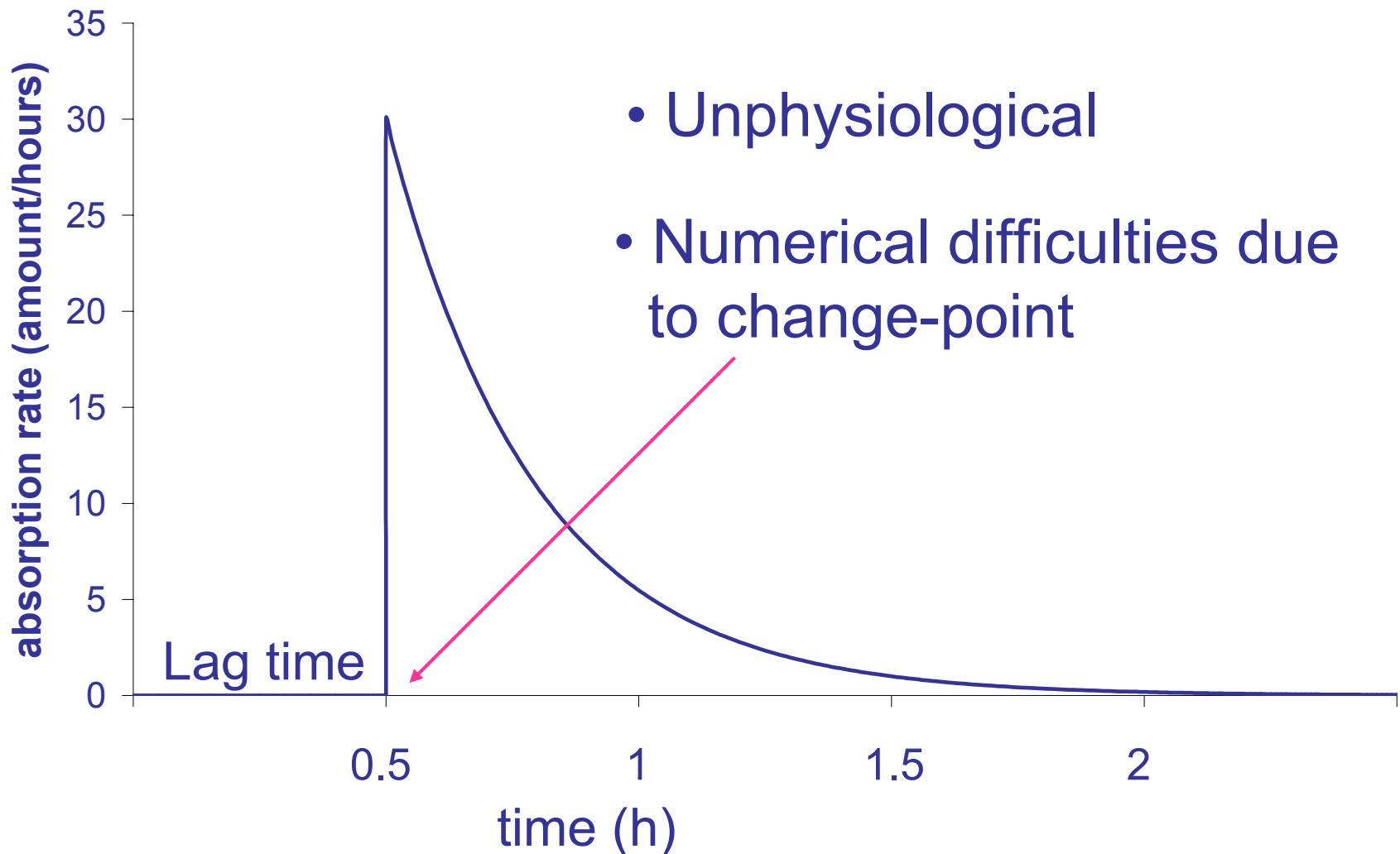
# *Improvement in the fit with a lag time*



*Shift of the dose time*

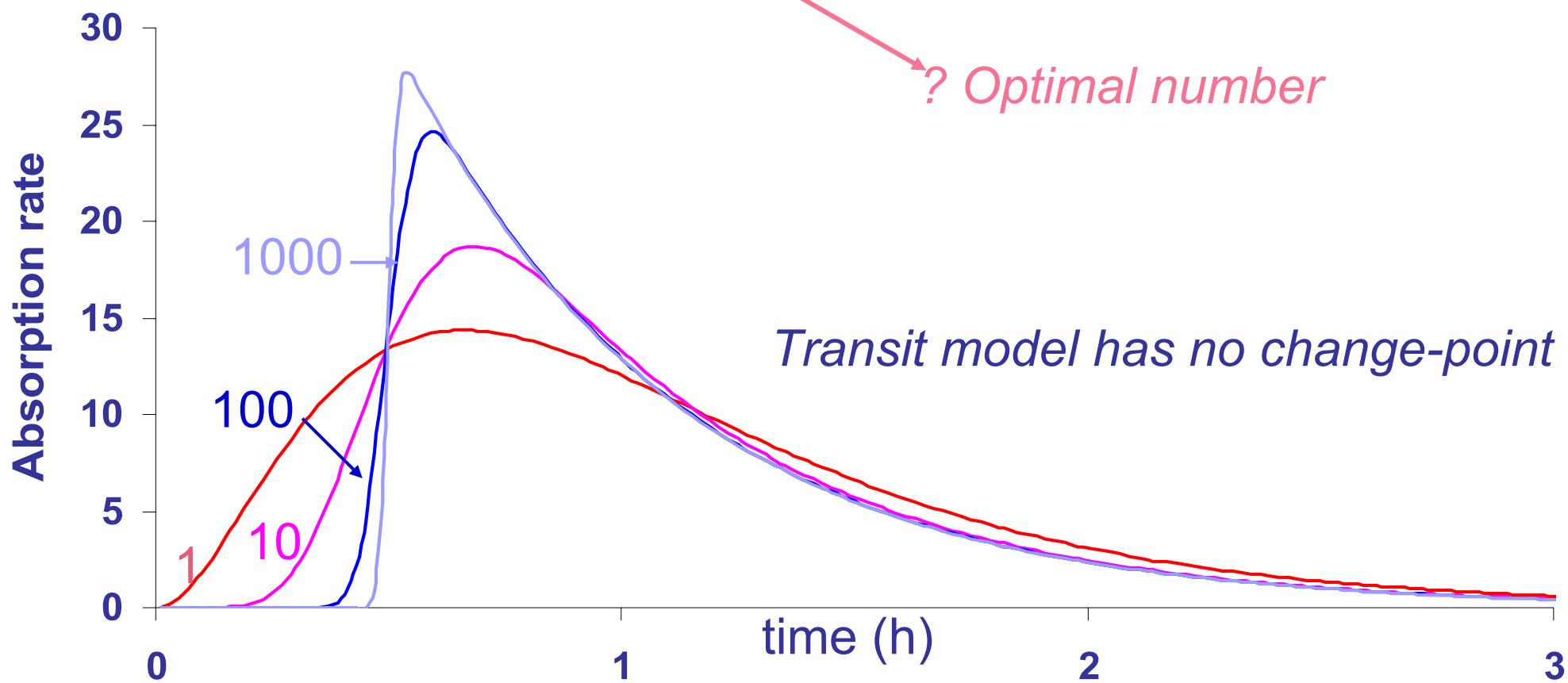
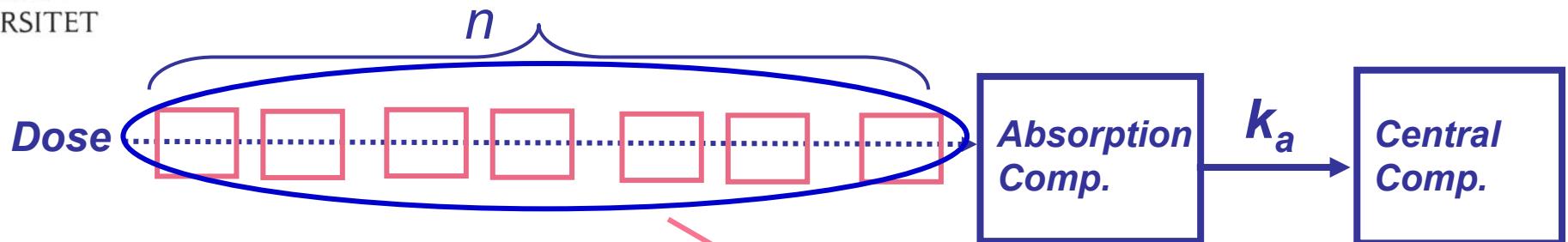


# *Drawbacks with the Lag time model*





# Transit compartment model





# Step-wise addition

Dose *bolus*



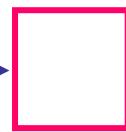
$k_{tr}$



$k_a$



Dose *bolus*



$k_{tr}$



$k_{tr}$



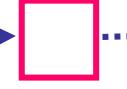
$k_a$



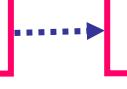
Dose *bolus*



$k_{tr}$



$k_{tr}$



$k_{tr}$

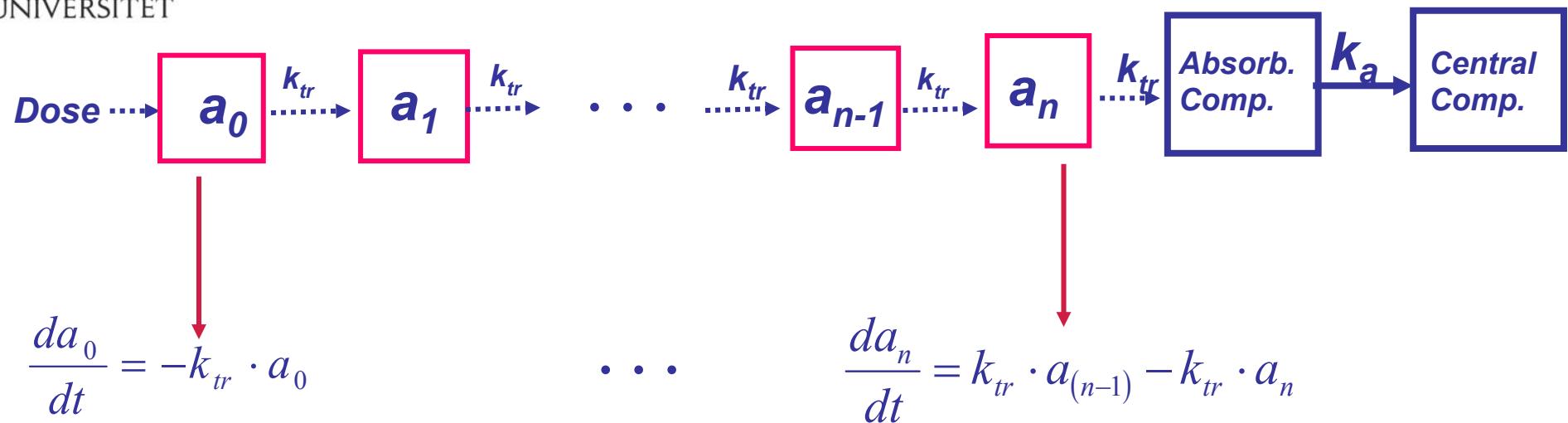


$k_a$





# Estimating the number of transit compartments



Mathematical solution for this system:

$$a_n(t) = Dose \cdot \frac{(k_{tr} \cdot t)^n}{n!} \cdot e^{-k_{tr} \cdot t} ; \text{ amount of drug in the } n^{\text{th}}\text{-compartment at time } t$$



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# *Implementation in NONMEM*

$$\frac{dA(1)}{dt} = Dose \cdot \frac{(k_{tr} \cdot t)^n \cdot e^{-k_{tr} \cdot t}}{n!} \cdot k_{tr} - k_a \cdot A(1)$$

Mean Transit Time to the absorption compartment:

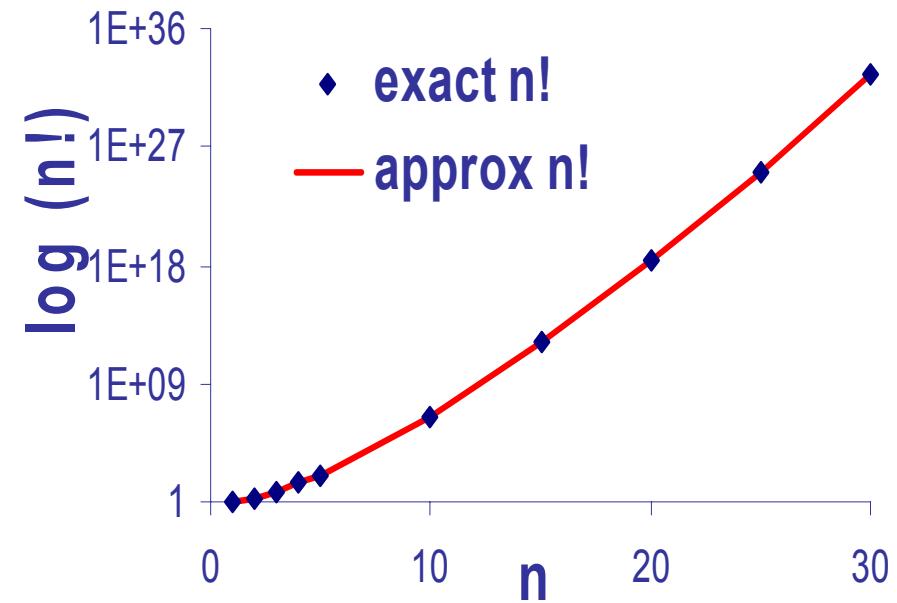
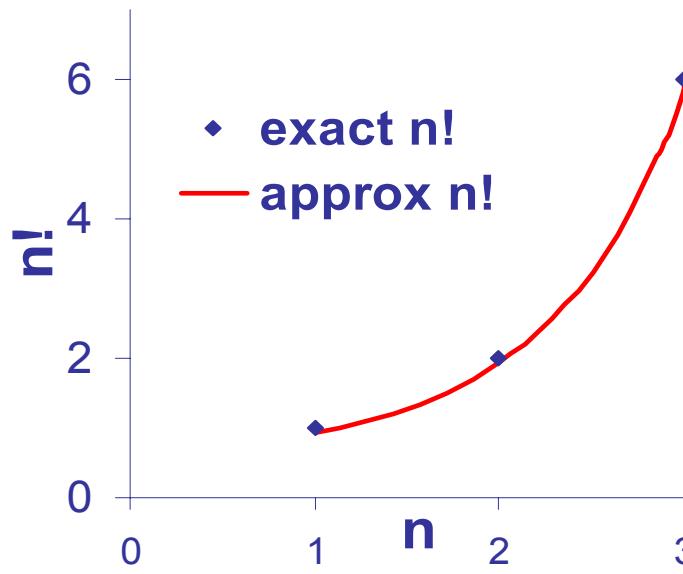
$$MTT = \frac{n + 1}{k_{tr}}$$



# Stirling approximation

$$\frac{dA(1)}{dt} = Dose \cdot \frac{(k_{tr} \cdot t)^n \cdot e^{-k_{tr} \cdot t}}{n!} \cdot k_{tr} - k_a \cdot A(1)$$

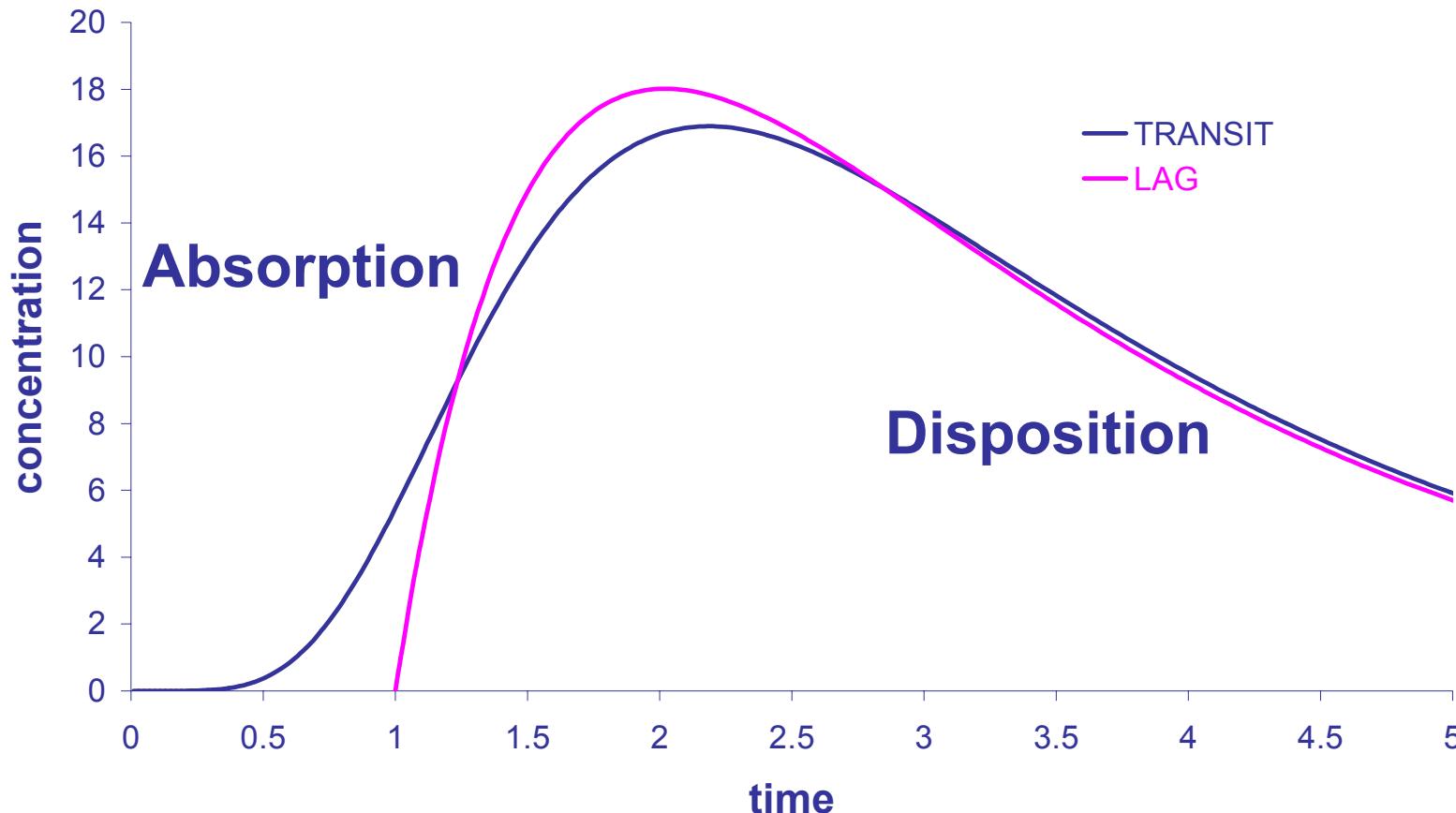
$$n! = \sqrt{2\pi} \cdot n^{n+0.5} \cdot e^{-n}$$





# Simulation – concentration-time profile

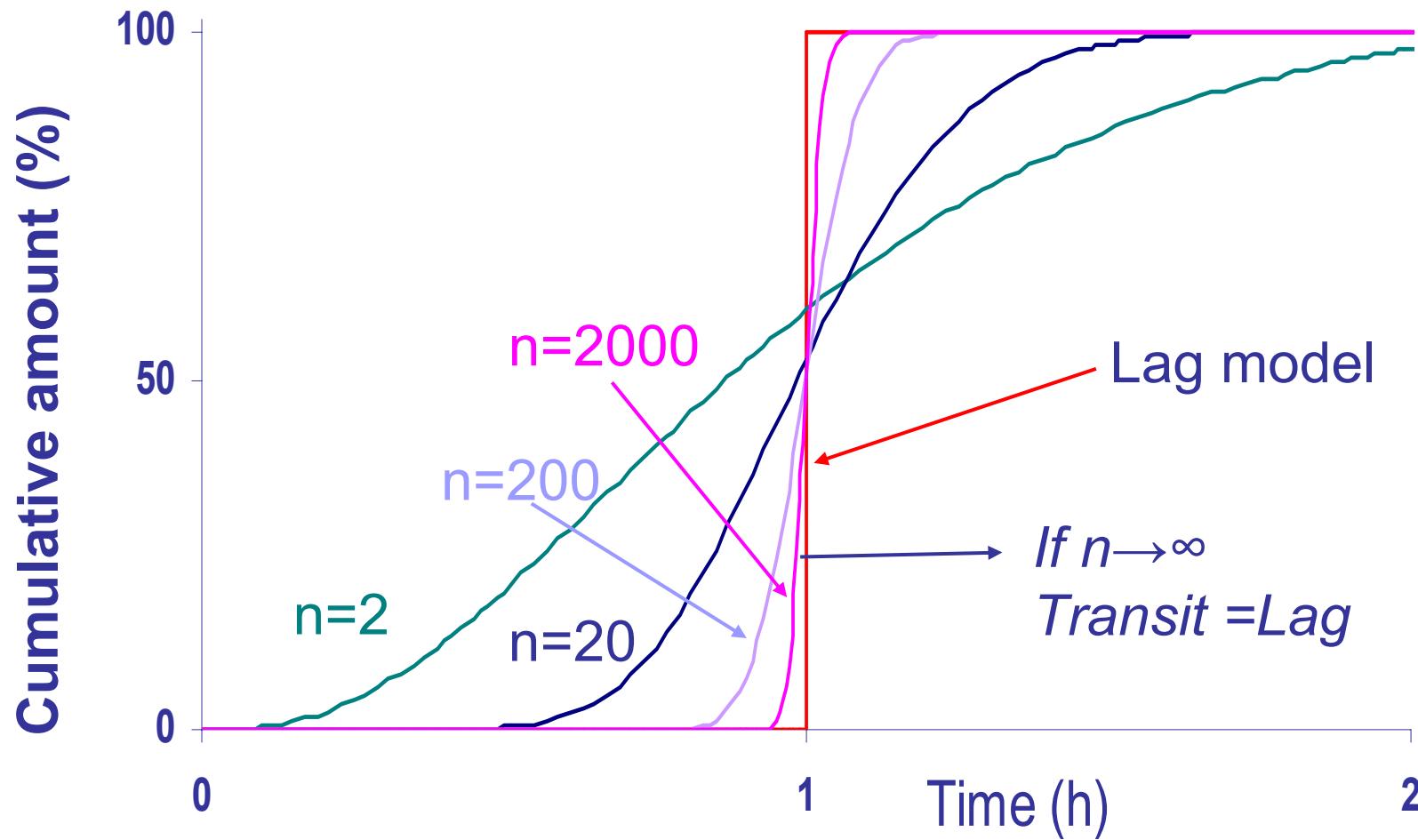
## LAG vs TRANSIT





# Simulation – amount in absorption compartment

## LAG vs. TRANSIT





# *Application to data*

## **Objective:**

- *to compare the performance of a TRANSIT model with the LAG model*

## **Data sets:**

- *glibenclamide, moxonidine, furosemide, amiloride*

## **Method:** *Population analysis in NONMEM*

## **Goodness of fit:**

*By eye: Diagnostic graphs*

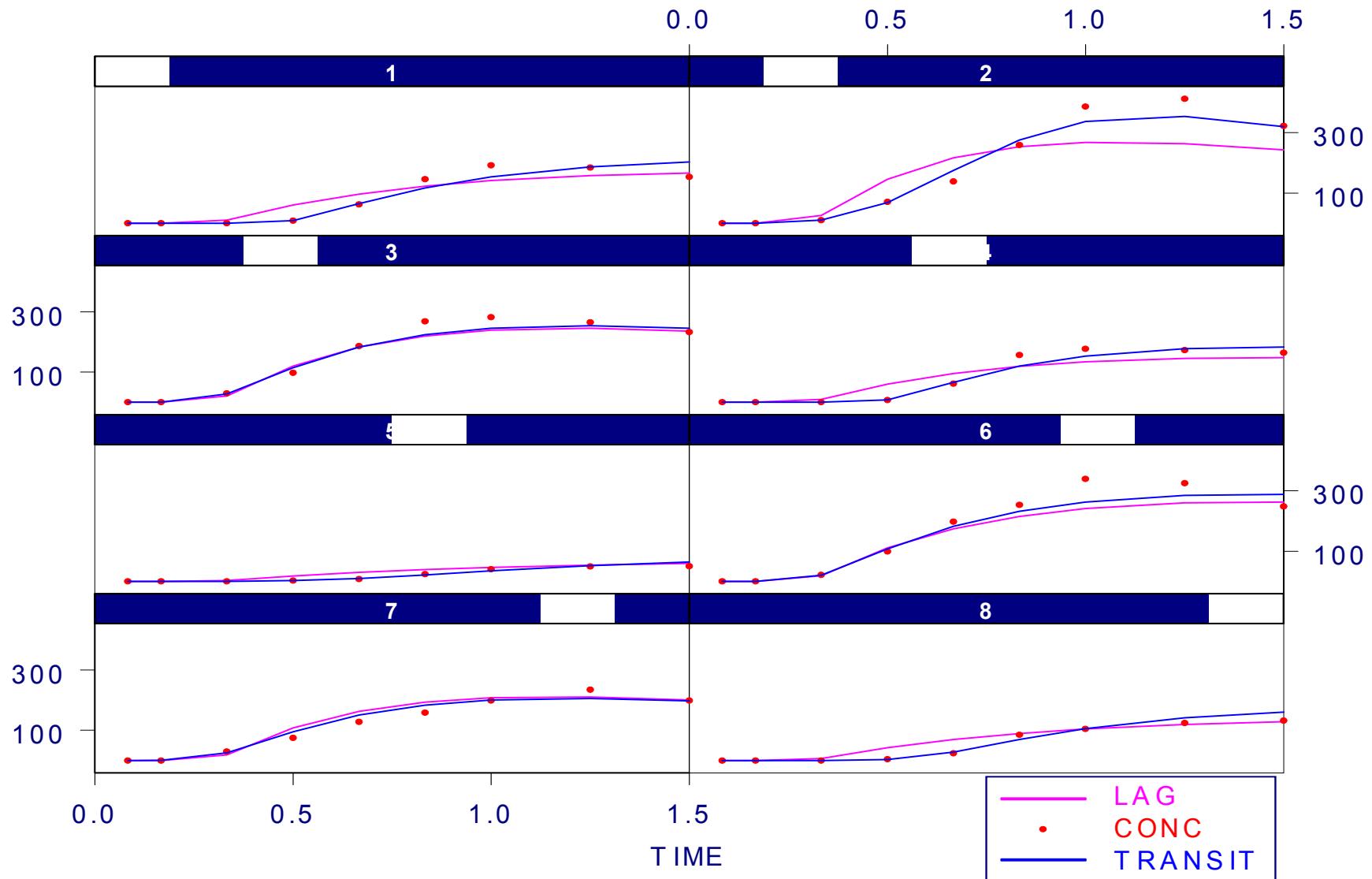
*Numerical: Objective Function Value (OFV)*

## **Example:** *glibenclamide*



# Glibenclamide - absorption

## LAG vs. TRANSIT





# Parameter Estimates

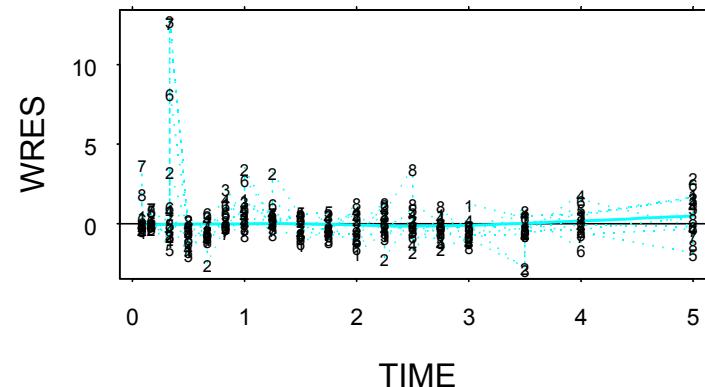
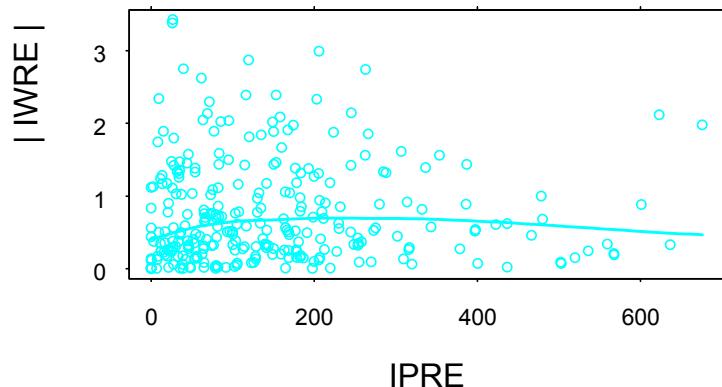
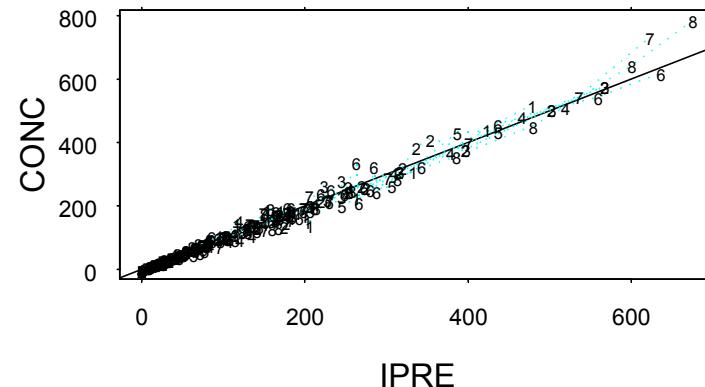
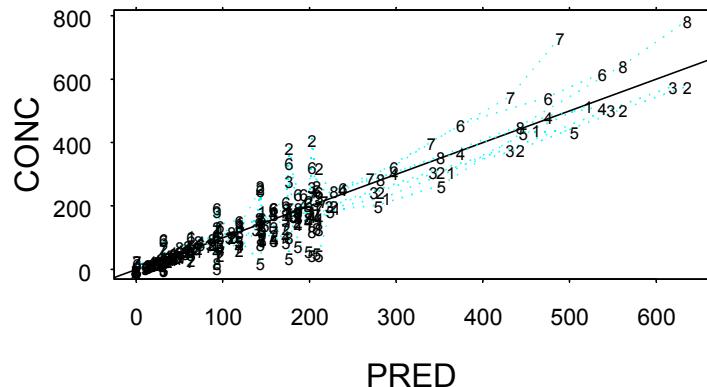
Est. (RSE %)	LAG model	TRANSIT model	TRANSIT model IIV (n)
OFV	1840	1676	1649
<i>Absorption</i>			
$k_a$	0.51 (29)	0.626 (27)	0.652 (31)
$t_{lag} / MTT$	0.306 (2.4)	0.438 (10)	0.458 (12)
$F$	0.948 (11)	0.96 (9.8)	0.959 (10)
n	-	23.3 (45)	22.9 (41)
IIV (n)	-	-	89% (57)
IIV(LAG/MTT)	-	29% (18)	30% (21)
<i>Disposition</i>			
$k$	1.13 (5)	1.14 (4.5)	1.14 (4.3)
$v$	3.84 (6.5)	3.81 (6.1)	3.79 (6)
$k_{23}$	0.34 (9.2)	0.356 (8.3)	0.363 (8.3)
$K_{32}$	0.66 (12)	0.681 (11)	0.691 (12)

Estimation method: FOCE with interaction



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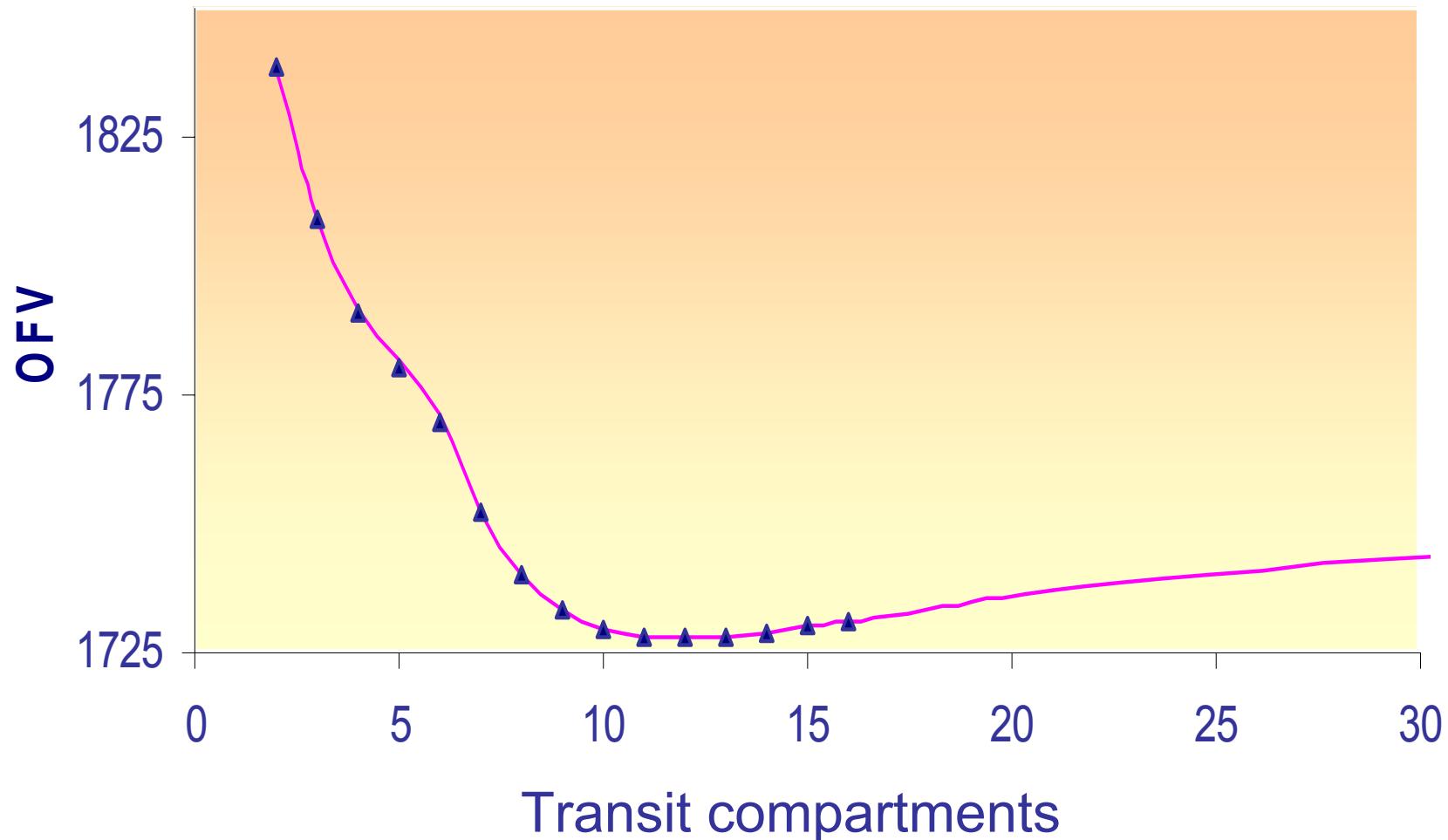
# Goodness-of-fit



FOCE with interaction



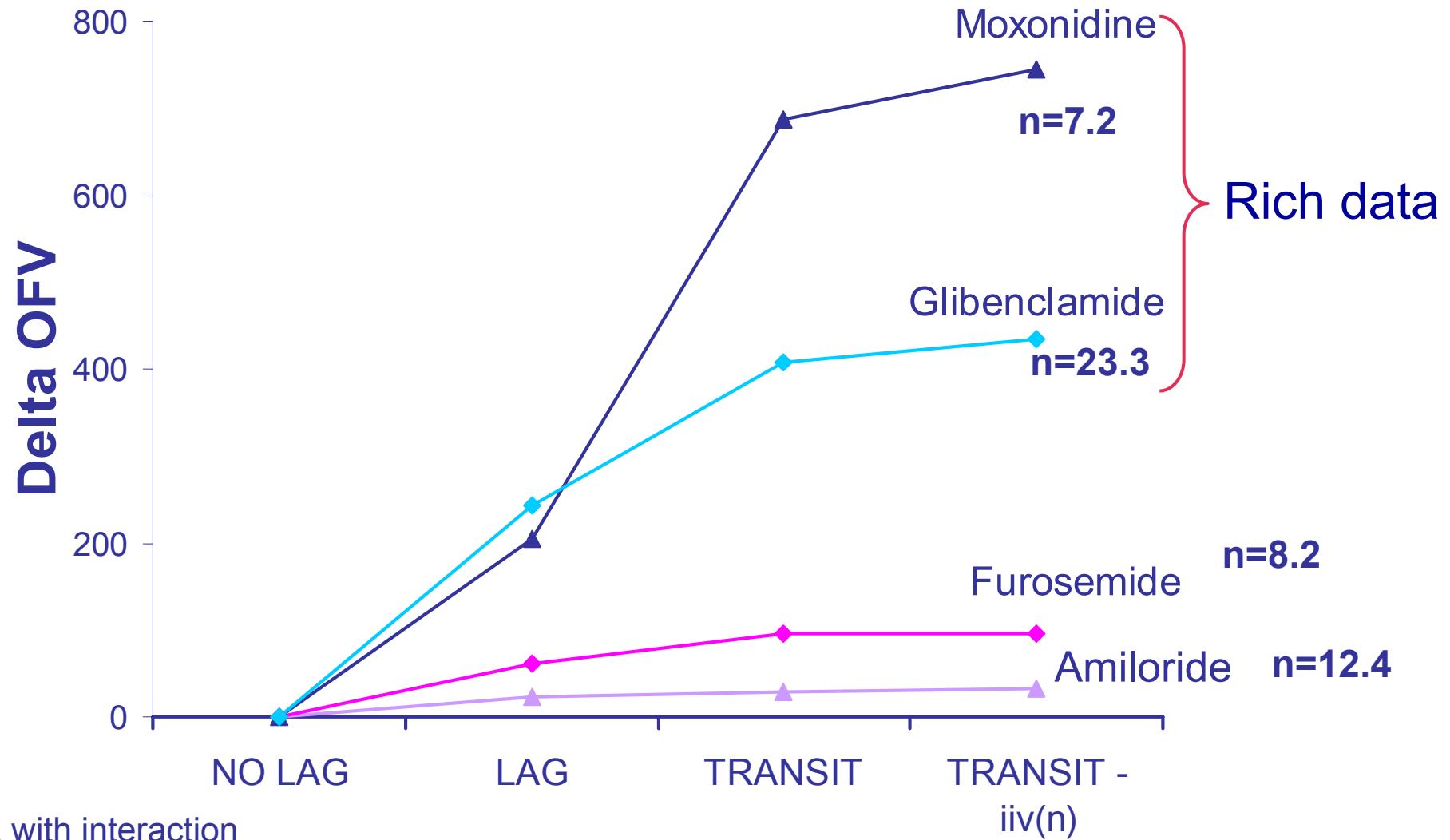
# Stepwise addition vs. Estimation



Estimation method: FO

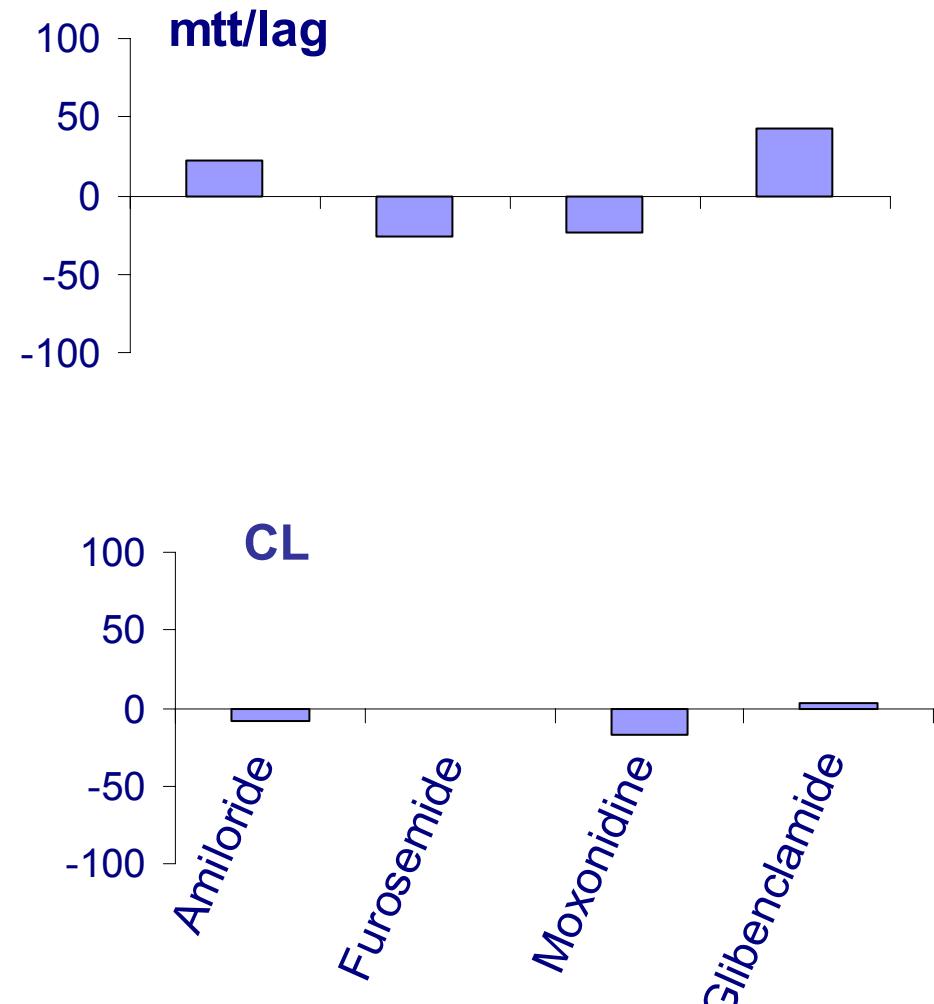
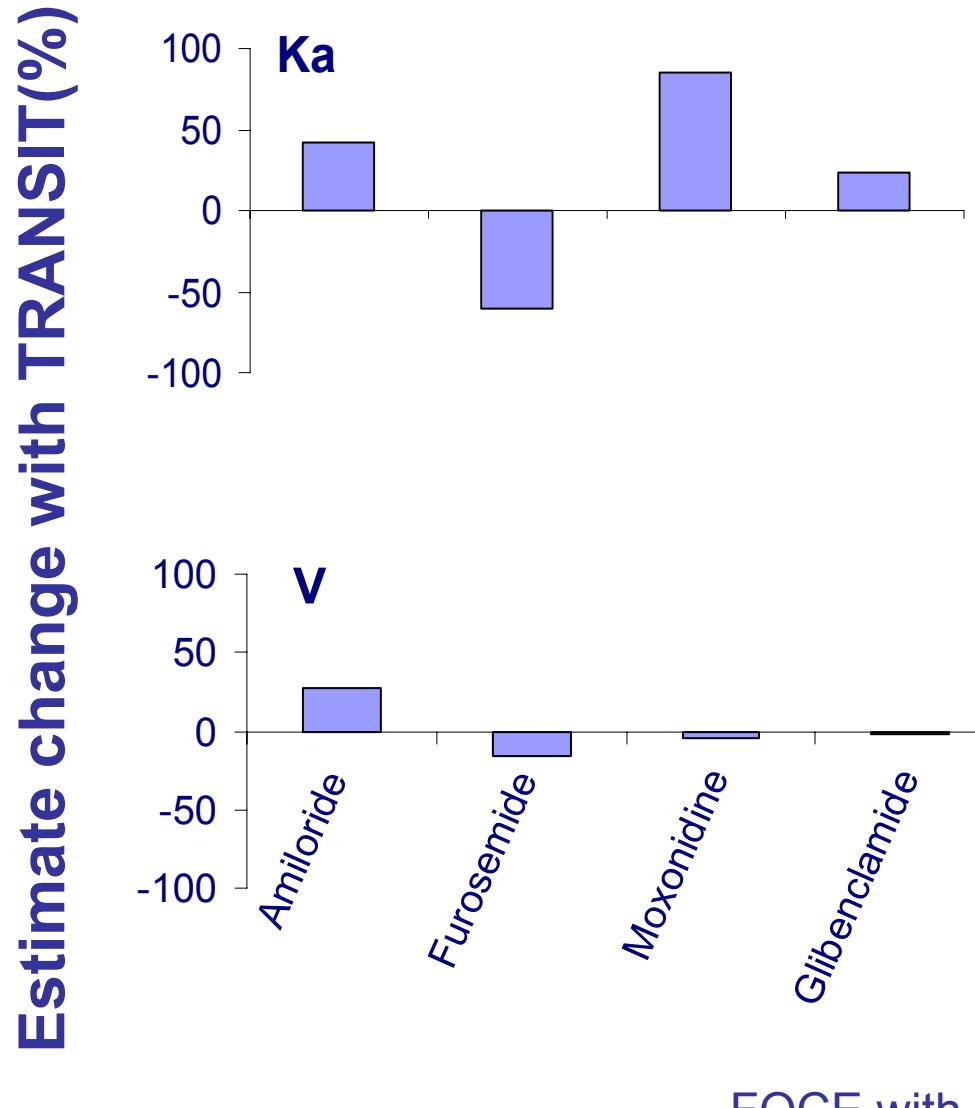


# *Improvement in GOF for all compounds*





# Estimates TRANSIT vs. LAG model





# Conclusion

***Compared to the LAG model, the TRANSIT model:***

1. Provided a significantly better model fit due to a more accurate description of the absorption phase
2. Is not a change-point model and was numerically more stable
3. Non-trivial differences in parameter estimates



*Finally...*

The implementation of the TRANSIT model in NONMEM can be obtained by contacting me:

[rada.savic@farmbio.uu.se](mailto:rada.savic@farmbio.uu.se)