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Model-based diagnostics post-processing for fast automated model building; show-cased with residual error models and CWRES Moustafa M.A. Ibrahim, Rikard Nordgren, Maria C. Kjellsson, Mats O. Karlsson Pharmacometric Research Group, Department of Pharmaceutical Biosciences, Uppsala University

Eq.1

Eq.2

Eq.6

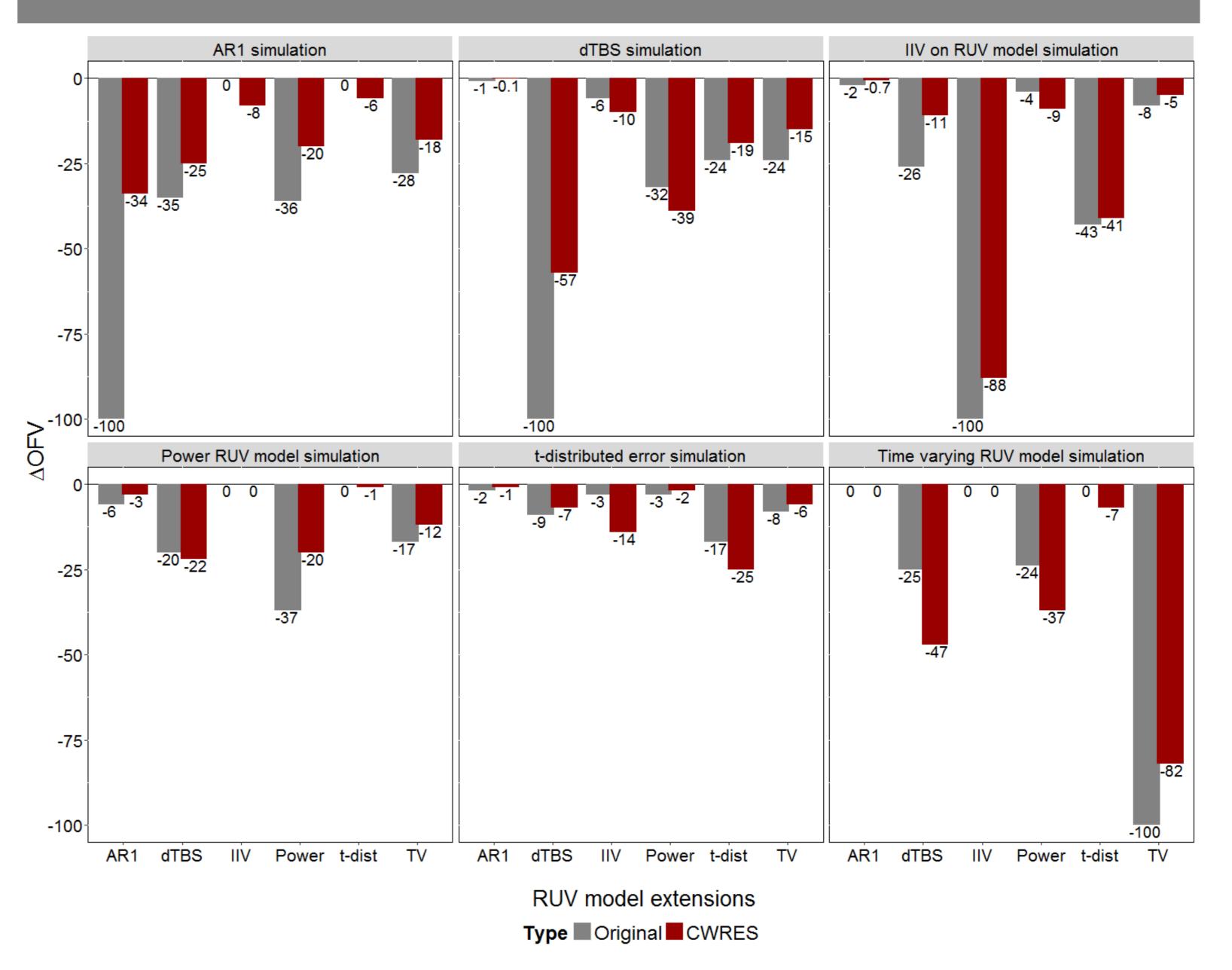
Eq.7

Objective

We propose a new diagnostic tool based on conditional weighted residuals CWRES [1], that scan extended residual variability RUV models and assess in a fast and robust way quantitively whether extensions are needed to implement

The extended RUV models evaluated were [2-4] :

- 1) Autocorrelated errors AR1 (Eq.2)
- 2) Dynamic transform both sides dTBS (Eq.3)
- 3) Interindividual variability IIV on RUV (Eq.4)
- 4) Power model (Eq.5)
- 5) T-distributed errors (Eq.6)
- 6) Time varying error magnitude (Eq.7)



Results

Methods

CWRES are expected to be distributed N(0,1) for a correct model.[1]

CWRES data outputted from the original model execution, were treated as dependent variable DV and modelled by a base model:

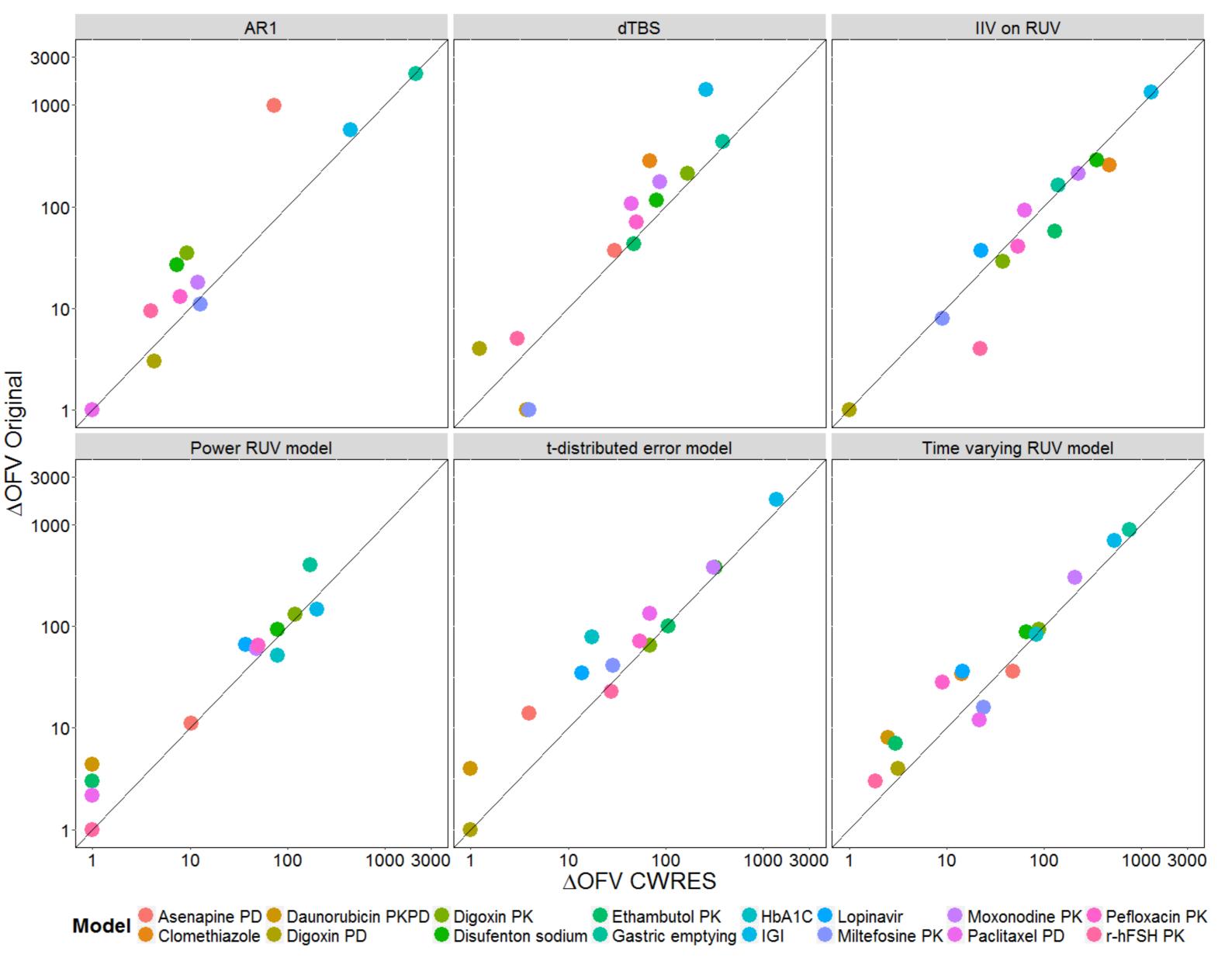
 $y_i = \Theta_1 + \eta_{1i} + \varepsilon_{1i}$

The base model (Eq.1) was then extended with the different RUV models, and used to model CWRES:

 $Corr(\varepsilon_{1ij},\varepsilon_{1ik}) = \exp((-0.693/\Theta_2) * (Time_j - Time_k))$ $y_i = \Theta_1 + \eta_{1i} + \varepsilon_{1i}$

 $y_i = \exp(y_i)$ $ln(y_i) = ln(IPRED) + \varepsilon_{1i} * IPRED^{\zeta}$ if $\lambda = 0$ $\frac{y_i^{\lambda} - 1}{\lambda} = \frac{IPRED^{\lambda} - 1}{\lambda} + \varepsilon_{1i} * IPRED^{\zeta}$ Eq.3 Otherwise Eq.4 $y_i = \Theta_1 + \eta_{1i} + \varepsilon_{1i} * \exp(\eta_{2i})$ $y_i = \Theta_1 + \eta_{1i} + \varepsilon_{1i} * IPRED^{\zeta}$ Eq.5 $L_{base} = \left(\sqrt{2\pi\sigma^2}\right) \exp\left(-\frac{IWRES^2}{2}\right)$





$L_{t-dist} = \frac{\Gamma(\frac{v+1}{2})}{\Gamma(\frac{v}{2}\sqrt{v\pi\sigma^2})} \left(1 + \frac{IWRES^2}{v}\right)^{-(\frac{v+1}{2})}$

 $y_i = \Theta_1 + \eta_{1i} + \varepsilon_{1i}$ IF (Time > break point time) $y_i = \Theta_1 + \eta_{1i} + \varepsilon_{2i}$

Different base models were needed for different transformations (Eq.3 & 6).

 ΔOFV_{CWRES} was calculated for each extended RUV model as the difference between CWRES base model (Eq.1) objective function value OFV and extended RUV model OFV. $\Delta OFV_{original}$ was calculated by implementing these extended RUV models on the original model (conventional analysis).

The agreement between $\Delta OFV_{original}$ and ΔOFV_{CWRES} was evaluated in both simulated and real data examples.

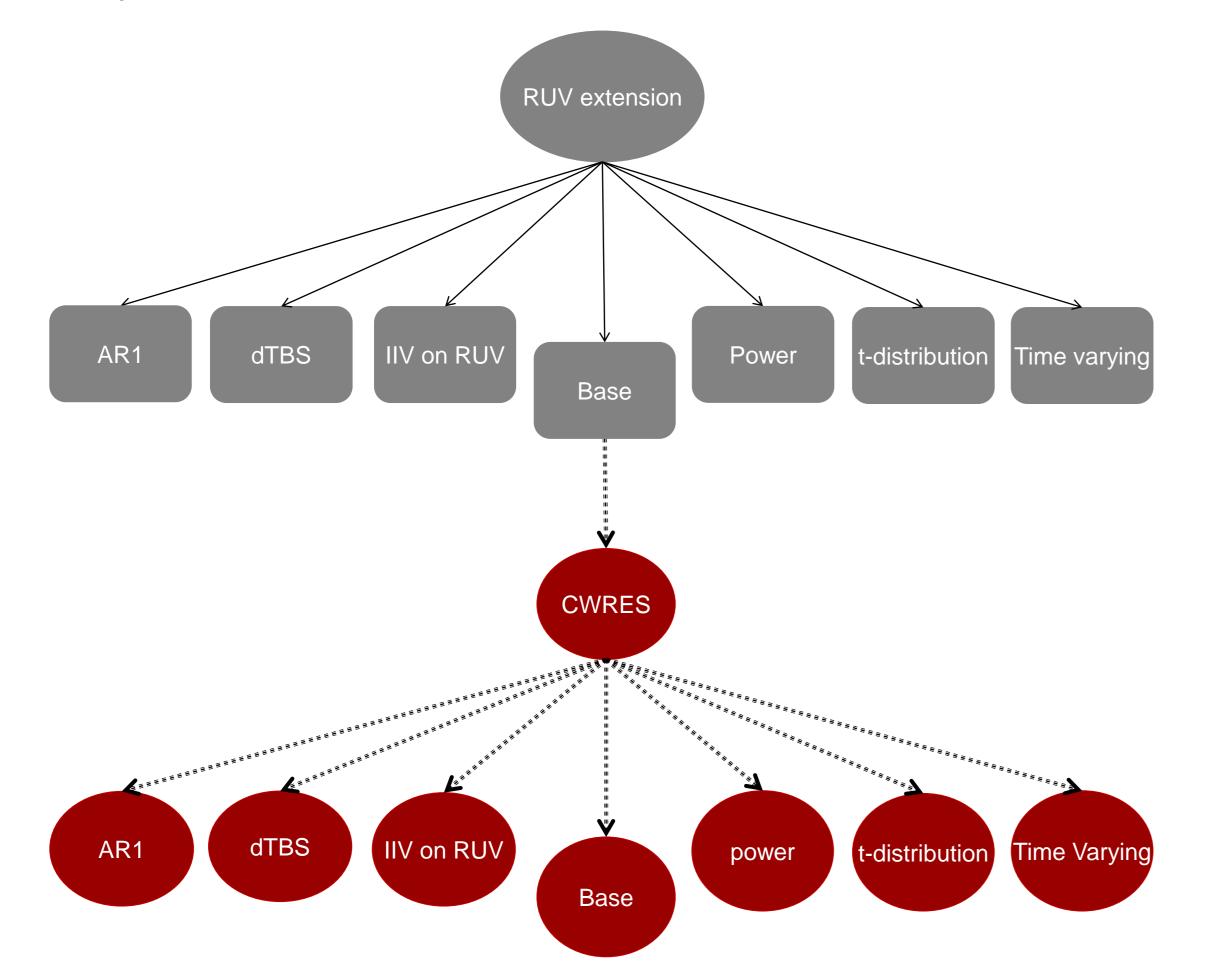


Figure 3: Real data results.

The agreement between $\Delta OFV_{original}$ and ΔOFV_{CWRES} was high for all 6 RUV extensions (r across all models = 0.88 with an average ratio of $\Delta OFVs$ of 0.92).

The typical improvement $\Delta OFV_{original}$ was substantial across all models with average of -220. The parameters governing the extended RUV showed good concordance between the estimates obtained in the CWRES and original models, except for dTBS as they are on different scale.

Figure 1: Setup for both simulated and real data examples

When t-distribution was the most important improvement, IIV on RUV showed inflated ΔOFV_{CWRES} .

Conclusion

- CWRES modelling is a promising easily automated diagnostic tool for model development/evaluation process, as it provides guidance for the nature and magnitude of potential model misspecification/improvements.
- It is extremely fast compared to conventional analysis. •
- It can be easily implemented in analysis software and is already implemented as **resmod** \bullet tool in **PsN**.

References

[1] Hooker, A. C., Staatz, C. E., & Karlsson, M. O. (2007). Conditional Weighted Residuals (CWRES): A Model Diagnostic for the FOCE Method. Pharmaceutical Research, 24(12), 2187-2197 [2] Karlsson, M. O., Beal, S. L., & Sheiner, L. B. (1995). Three new residual error models for population PK/PD analyses. Journal of Pharmacokinetics and Biopharmaceutics, 23(6), 651-672. [3] Karlsson, M.O., Jonsson, E. N., Wiltse, C.G & Wade, J.R. (1998). Assumption Testing in Population Pharmacokinetic Models: Illustrated with an Analysis of Moxonidine Data from Congestive Heart Failure Patients. Journal of Pharmacokinetics and Biopharmaceutics, 26(2),207-246.

[4] Dosne, A., Bergstrand, M., & Karlsson, M. O. (2015). A strategy for residual error modeling incorporating scedasticity of variance and distribution shape. Journal of Pharmacokinetics and Pharmacodynamics, 43(2), 137-151.