





# Machine learning for pharmacometrics: examples of applications

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# Introduction to machine learning

- Machine learning (ML) is widely used in different aspects of our lives
  - Image recognition<sup>1</sup>
  - Text generation (ChatGPT or Gemini)
  - Big data analysis
  - Quantitative structure-activity relationship (QSAR)<sup>2</sup>
  - Discovery of a new antibiotic<sup>3</sup>
  - Alpha fold DeepMind<sup>4</sup>
  - Increase of data availability
  - Computational power + dedicated packages (R & Python)







<sup>1</sup> Shen, D., Wu, G. & Suk, H.-I. Deep Learning in Medical Image Analysis. Annu. Rev. Biomed. Eng. 19, 221–248 (2017).

<sup>2</sup> Chan, H. C. S., Shan, H., Dahoun, T., Vogel, H. & Yuan, S. Advancing Drug Discovery via Artificial Intelligence. *Trends Pharmacol. Sci.* **40**, 592–604 (2019)

<sup>3</sup> Stokes, J. M. et al. A Deep Learning Approach to Antibiotic Discovery. Cell 180, 688-702.e13 (2020)

<sup>4</sup> Jumper et al Highly accurate protein structure prediction with AlphaFold Nature 583–589 (2021)

# Introduction to machine learning

← Tweet



François Chollet 🤣 @fchollet

With tools like Colab, Keras, and TensorFlow, virtually anyone can solve in a day, with no initial investment, problems that would have required an engineering team working for a quarter and \$20k in hardware in 2014

Traduire le Tweet

10:03 PM  $\cdot$  20 nov. 2020  $\cdot$  Twitter for Android

facebook Artificial Intelligence





...

Big data : le volume de données créées va exploser Volume de données numériques créées dans le monde depuis 2010 (en zettaoctets) 2 142 1 2 12 2 100 2 142 1 2 12 2 142 1 2 15 2 142 1 2 15 1 2 12 1 2

<sup>1</sup> Shen, D., Wu, G. & Suk, H.-I. Deep Learning in Medical Image Analysis. Annu. Rev. Biomed. Eng. 19, 221–248 (2017).

<sup>2</sup> Chan, H. C. S., Shan, H., Dahoun, T., Vogel, H. & Yuan, S. Advancing Drug Discovery via Artificial Intelligence. *Trends Pharmacol. Sci.* **40**, 592–604 (2019)

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<sup>4</sup> Jumper et al Highly accurate protein structure prediction with AlphaFold Nature 583–589 (2021)



# Comparison of standard statistics vs ML

- Standard statistical approach (POPPK):
  - Based on understanding of biological processes, interpretable
  - but may be limited by current knowledge



- Machine Learning:
  - No explicitly defined physiological model (black box)
  - Complex algorithmic approach (e.g. Xgboost, neural network, SVM...)
  - Large numbers of free parameters and complex interactions

→ minimize errors between predicted and observed values (loss function)

# Comparison of standard statistics vs ML

- In simple words
  - Standard statistics: data are entered into a model to predict results
  - ML approaches, the data are fed with the results to an algorithm that constructs the model without a priori knowledge on the underlying associations (data driven).
- ML methods  $\rightarrow$  individual prediction
- ML methods particularly suited when there is a high degree of complexity/correlation between predictors (= "features").



Standard statistics



## Use of Machine Learning in Pharmacometrics





> Clin Pharmacokinet. 2021 Feb;60(2):223-233. doi: 10.1007/s40262-020-00927-6.

### A Machine Learning Approach to Estimate the Glomerular Filtration Rate in Intensive Care Unit Patients Based on Plasma Iohexol Concentrations and Covariates

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Jean-Baptiste Woillard <sup>1</sup> <sup>2</sup> <sup>3</sup>, Charlotte Salmon Gandonnière <sup>4</sup>, Alexandre Destere <sup>5</sup> <sup>6</sup> <sup>7</sup>,
Stephan Ehrmann <sup>4</sup> <sup>8</sup>, Hamid Merdji <sup>9</sup> <sup>10</sup>, Armelle Mathonnet <sup>11</sup>, Pierre Marquet <sup>5</sup> <sup>6</sup> <sup>7</sup>,
Chantal Barin-Le Guellec <sup>6</sup> <sup>12</sup> <sup>13</sup>
```

Affiliations + expand PMID: 32794122 DOI: 10.1007/s40262-020-00927-6

> Kidney Int Rep. 2023 Nov 3;9(1):134-144. doi: 10.1016/j.ekir.2023.10.023. eCollection 2024 Jan.

### Optimization of Rituximab Therapy in Adult Patients With PLA2R1-Associated Membranous Nephropathy With Artificial Intelligence

Alexandre Destere <sup>1 2</sup>, Maxime Teisseyre <sup>3 4 5</sup>, Diane Merino <sup>1</sup>, Marion Cremoni <sup>4 6</sup>, Alexandre O Gérard <sup>1 5</sup>, Thomas Crepin <sup>7</sup>, Noémie Jourde-Chiche <sup>8</sup>, Daisy Graça <sup>3 4 6</sup>, Kévin Zorzi <sup>3 4</sup>, Céline Fernandez <sup>3 4</sup>, Vesna Brglez <sup>3 4 6</sup>, Sylvia Benzaken <sup>6</sup>, Vincent L M Esnault <sup>3 5</sup>, Sylvain Benito <sup>9</sup>, Milou-Daniel Drici <sup>1</sup>, Barbara Seitz-Polski <sup>3 4 5 6</sup>

> Pharm Res. 2022 Oct;39(10):2497-2506. doi: 10.1007/s11095-022-03351-6. Epub 2022 Aug 3.

### Optimization of Vancomycin Initial Dose in Term and Preterm Neonates by Machine Learning

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Laure Ponthier <sup>1 2</sup>, Pauline Ensuque <sup>2</sup>, Alexandre Destere <sup>1 3</sup>, Pierre Marquet <sup>1 4</sup>,
Marc Labriffe <sup>1 4</sup>, Evelyne Jacqz-Aigrain <sup>5</sup>, Jean-Baptiste Woillard <sup>6 7</sup>
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Affiliations + expand

PMID: 35918452 DOI: 10.1007/s11095-022-03351-6

Epub 2024 Mar 19.

A machine learning approach to predict daptomycin exposure from two concentrations based on Monte Carlo simulations

Cyrielle Codde <sup>1</sup>, Florence Rivals <sup>2</sup>, Alexandre Destere <sup>3</sup>, Yeleen Fromage <sup>2</sup>, Marc Labriffe <sup>2</sup> <sup>4</sup>, Pierre Marquet <sup>2</sup> <sup>4</sup>, Clément Benoist <sup>4</sup>, Laure Ponthier <sup>4</sup>, Jean-François Faucher <sup>1</sup>, Jean-Baptiste Woillard <sup>2</sup> <sup>4</sup>

#### Epub 2024 Mar 16.

### Optimization of Ganciclovir and Valganciclovir Starting Dose in Children by Machine Learning

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Laure Ponthier <sup>1</sup> <sup>2</sup>, Julie Autmizguine <sup>3</sup> <sup>4</sup> <sup>5</sup>, Benedicte Franck <sup>6</sup> <sup>7</sup>, Anders Åsberg <sup>8</sup> <sup>9</sup>, Philippe Ovetchkine <sup>4</sup>, Alexandre Destere <sup>10</sup>, Pierre Marquet <sup>1</sup> <sup>11</sup>, Marc Labriffe <sup>1</sup> <sup>11</sup>, Jean-Baptiste Woillard <sup>12</sup> <sup>13</sup>
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Affiliations + expand

# Example: A posteriori TAC exposure

- Development of a ML model to predict the TAC AUC (TDM) based on ISBA data (https://abis.chu-limoges.fr/login):
   3 individual concentrations / a few covariates → ~5000 AUC/~2000 patients
- Excellent performances in external full PK profiles vs ref AUC (trapezoidal) based on 2 or 3 samples
- Bias/RMSE external data (e.g. in kidney transplant recipients) =
  - ML 3 samples: 2.1%/7.7%
  - ML 2 samples: -2.4%/8.8%
  - **POPPK** 3 samples: 5%/9.6%



Individual prediction vs reference AUC BID kidney

# In the case of a limited number of data $\rightarrow$ simulations to train ML algorithm?





External evaluation in 286 full PK profiles in kidney, heart and liver transplant recipients and comparison of predicted AUC<sub>0-12h</sub> to that of the MAP Bayesian estimation based on the 0, 1 and 3h limited sampling strategy





- 9000 tacrolimus Monte Carlo simulations performed from a population pharmacokinetic model in mrgsolve
- Application of filters to remove unrealistic simulated profiles



Iterations

http://tvas.me/articles/2019/08/26/Block-Distributed-Gradient-Boosted-Trees.html

Development of Xgboost machine learning algorithms :

Splitting into a training (75%) and a test (25%) set subsets.

 Ten-fold cross-validation applied to the training set to tune the hyperparameters and evaluate the model performance Estimation of drug exposure by machine learning based on simulations from published pharmacokinetic models: The example of tacrolimus

Jean-Baptiste Woillard<sup>a,b,c,\*,1</sup>, Marc Labriffe<sup>a,b,c</sup>, Aurélie Prémaud<sup>a,b</sup>, Pierre Marquet<sup>a,b,c</sup>

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 <sup>c</sup> Department of Pharmacology and Toxicology, CHU Limoges, F-87000 Limoges, France



		Traine simula	d from ations	Trained from ISBA*		
Organ transplanted	Method	Relative MPE (%)	relative RMSE (%)	Relative MPE (%)	relative RMSE (%)	
kidney 1 (n = 137)	Xgboost 2 concentrations	1.08	8.5	-0.6	9.0	
kidney 2 (n = 34)	Xgboost 2 concentrations	0.7	9.0	-1.0	9.1	
liver (n = 68)	Xgboost 2 concentrations	5.9	12.9	3.3	12.9	
heart (n = 47)	Xgboost 2 concentrations	3.2	11.4	-0.4	9.7	





Paves the way / development of ML algorithms for TDM in different therapeutic areas / importance to validate on "real" data.

\*https://abis.chu-limoges.fr/login / Woillard CPT 2021

# Ganciclovir in pediatrics: first dose prediction (PhD works L Ponthier)

- Monte Carlo simulations → 10800 patients from literature POPPK models (2 GCV IV, 3 GCV oral)
- Train of a classification ML model to predict AUC0-24h at SS in the target (40-60 mg\*h/L)
- Iterative search of the first dose that maximise the target attainment
- Comparison of theoretical target attainment after administration of the dose ML with POPPK literature formulae

Ponthier et al. ClinPK 2024



Clinical Pharmacokinetics https://doi.org/10.1007/s40262-024-01362-7

**ORIGINAL RESEARCH ARTICLE** 

### Check for updates

### Optimization of Ganciclovir and Valganciclovir Starting Dose in Children by Machine Learning

Laure Ponthier<sup>1,2</sup> · Julie Autmizguine<sup>3,4,5</sup> · Benedicte Franck<sup>6,7</sup> · Anders Åsberg<sup>8,9</sup> · Philippe Ovetchkine<sup>4</sup> · Alexandre Destere<sup>10</sup> · Pierre Marquet<sup>1,11</sup> · Marc Labriffe<sup>1,11</sup> · Jean-Baptiste Woillard<sup>1,11</sup>



### Rituximab in anti-PLA2R1 GEM

- Train of a classification ML model to predict underexposure at month-3
- Rationalization of features based on biological criteria

Association of Variables	Accuracy
Age + Gender + BSA	0.4559
Age + Gender + BSA + GFR on DO	0.5294
Age + Gender + BSA + GFR on DO + CD19 on DO	0.5
Age + Gender + BSA + GFR on DO + anti-PLA2R1 antibody titer on DO	0.5441
Age + Gender + BSA + GFR on DO + anti-PLA2R1 antibody titer on DO + weight	0.5417
Age + Gender + BSA + GFR on D0 + anti-PLA2R1 antibody titer on D0 + height	0.5441
Age + Gender + BSA + GFR on DO + anti-PLA2R1 antibody titer on DO + BMI	0.4559
Age + Gender + BSA + GFR on DO + anti-PLA2R1 antibody titer on DO + serum albumin on MO	0.6324
Age + Gender + BSA + anti-PLA2R1 antibody titer on D0 + serum albumin on D0	0.6471
Age + Gender + BSA + anti-PLA2R1 antibody titler on D0 + serum albumin on D0 + serum creatinine on D0	0.6618
Age + Gender + BSA + anti-PLA2R1 antibody titer on D0 + serum albumin on D0 + serum creatinine on D0 + use of angiotensin-converting enzyme inhibitors	0.6471
Age + Gender + BSA + anti-PLA2R1 antibody titer on D0 + serum albumin on D0 + serum creatinine on D0 + use of angiotensin II receptor blockers	0.6471
Age + Gender + BSA + anti-PLA2R1 antibody titer on D0 + serum albumin on D0 + serum creatinine on D0 + use of furosemide	0.6471
Age + Gender + BSA + anti-PLA2R1 antibody titer on D0 + serum albumin on D0 + serum creatinine on D0 + use of hydrochlorothiazide	0.6471
Age + Gender + BSA + anti-PLA2R1 antibody titer on D0 + serum albumin on D0 + serum creatinine on D0 + serum albumin on D15	0.72
Age + Gender + BSA + serum albumin on D0 + serum creatinine on D0 + serum albumin on D15 + serum creatinine on D15	0.72
Age + Gender + BSA + anti-PLA2R1 antibody titer on D0 + serum albumin on M0 + serum creatinine on D0 + serum albumin on D15 + serum creatinine on D15	0.794
Age + Gender + BSA + anti-PLA2R1 antibody titer on D0 + serum albumin on D0 + serum creatinine on D0 + serum albumin on D15 + serum creatinine on D15 + number of visits	0.748
Age + Gender + BSA + anti-PLA2R1 antibody titer on D0 + serum albumin on D0 + serum creatinine on D0 + serum albumin on D15 + proteinuria on D0	0.7647
Age + Gender + BSA + anti-PLA2R1 antibody titer on D0 + serum albumin on D0 + serum creatinine on D0 + serum albumin on D15 + proteinuria on D15	0.75
All predictors ( $N = 21$ )	0.7353

Performance Assessment Criteria	Training Data Set	Testing Data Set
Accuracy (%)	79.4	79.2
No information rate (%)	69.1	54.2
Sensitivity (%)	78.7	84.6
Specificity (%)	81.0	72.7
Positive predictive value (%)	90.2	78.6
Negative predictive value (%)	63.0	80.0
F-score (%)	84.1	81.5

# $\mathbf{Dose of tritrainable} \left( \mathbf{\hat{d}} \right)$

Probability of rituximab underdosing (%)

### Optimization of Rituximab Therapy in Adult Patients With PLA2R1-Associated Membranous Nephropathy With Artificial Intelligence

Alexandre Destere<sup>1,9,10</sup>, Maxime Teisseyre<sup>2,3,4,10</sup>, Diane Merino<sup>1</sup>, Marion Cremoni<sup>3,5</sup>, Alexandre O Gérard<sup>1,4</sup>, Thomas Crepin<sup>6</sup>, Noémie Jourde-Chiche<sup>7</sup>, Daisy Graça<sup>2,3,5</sup>, Kévin Zorzi<sup>2,3</sup>, Céline Fernandez<sup>2,3</sup>, Vesna Brglez<sup>2,3,5</sup>, Sylvia Benzaken<sup>5</sup>, Vincent L.M. Esnault<sup>2,4</sup>, Sylvain Benito<sup>8</sup>, Milou-Daniel Drici<sup>1,10</sup> and Barbara Seitz-Polski<sup>2,3,4,5,10</sup>

Destere et al. KIR 2023





# Rituximab in anti-PLA2R1 GEM (preliminary study of hospital clinical research program PHRC)

- Calculation of underexposure prediction and derivation of individualized dose
  - < 50 % : 1g x 2 (D0 and D15)
  - 50-75% : 1g x 3 (D0, D15 and M1)
  - > 75 % : 1g x 4 (D0, D15, M1 and M1.5)
- Reference : previous patient treated by RTX
- N = 11 patients
  - < 50 % : 7
  - 50-75% : 2
  - > 75 % : 2



### Artificial intelligence to guide rituximab therapy in patients with PLA2R1-associated membranous nephropathy

Maxime Teisseyre<sup>\*1,2,3,4</sup>, Alexandre Destere<sup>\*5,6</sup>, Marion Cremoni<sup>1,2,3,4</sup>, Sonia Boyer-Suavet<sup>7</sup>, Alexandre Karamé<sup>8</sup>, Léa Corlu<sup>9</sup>, Gabrielle Duneau<sup>10</sup>, Kévin Zorzi<sup>1,3</sup>, Céline Fernandez<sup>1,3</sup>, Vesna Brglez<sup>1,3,4</sup>, Sylvia Benzaken<sup>4</sup>, Guillaume Favre<sup>2</sup>, Vincent L. M. Esnault<sup>1,2</sup>, Sylvain Benito<sup>11</sup>, and Barbara Seitz-Polski<sup>1,2,3,4</sup>

Trials		Immunological remission*	Clinical remission
Algorithm-guided rituximab treatment	11	91 %	91%
GEMRITUX rituximab (23)	37	50%	35%
GEMRITUX NIAT (23)	38	12%	21%
RI-CYCLO rituximab (24)	37	63%	51%
RI-CYCLO cyclophosphamide-corticosteroid (24)	37	50%	65%
MENTOR rituximab (22)	65	52%	35%
MENTOR cyclosporin (22)	65	28%	49%
STARMEN tacrolimus-rituximab (32)	43	70%	44%
STARMEN cyclophosphamide-corticosteroid (32)	43	92%	74%
High-dose rituximab (15)	28	78%	64%

# Use of Machine Learning in Pharmacometrics



> Clin Pharmacokinet. 2022 Aug;61(8):1157-1165. doi: 10.1007/s40262-022-01138-x. Epub 2022 May 31.

Jean-Baptiste Woillard 4 5

**Isavuconazole Exposure Prediction** 

Alexandre Destere <sup>1 2</sup>, Pierre Marquet <sup>1 3</sup>, Marc Labriffe <sup>1 3</sup>, Milou-Daniel Drici <sup>2</sup>,

### A Hybrid Model Associating Population Pharmacokinetics with Machine Learning: A Case Study with Iohexol Clearance Estimation

Alexandre Destere <sup>1 2 3</sup>, Pierre Marquet <sup>1 2</sup>, Charlotte Salmon Gandonnière <sup>4</sup>, Anders Åsberg <sup>5 6</sup>, Véronique Loustaud-Ratti <sup>1 7</sup>, Paul Carrier <sup>7</sup>, Stephan Ehrmann <sup>4 8</sup>, Chantal Barin-Le Guellec <sup>1</sup>, Aurélie Premaud <sup>1</sup>, Jean-Baptiste Woillard <sup>9 10</sup>

### Hybrid model: combination of ML and POPPK to keep interpretability: iohexol (PhD works A Destere) (1)

- Simulation of 500 patients / iohexol for estimation of iohexol CL (GFR) from a literature POPPK model (2)
- MAP-BE on simulations
  - All samples (REF)
  - 3 samples (LSS)
  - Calculation of residual error (REF LSS)
- Train ML algorithm to learn residual error (from data obtained by MAP-BE: observed concentrations, PK parameters + featured engineering eg diff between observed concentrations)
- Evaluation in the train (10-fold CV), test and external real data



1-Destere A et al. A Hybrid Model Associating Population Pharmacokinetics with Machine Learning: A Case Study with Iohexol Clearance Estimation. *Clin Pharmacokinet*. 2022

2-Destere A et al. A single Bayesian estimator for iohexol clearance estimation in ICU, liver failure and renal transplant patients. *Br J Clin Pharmacol.* 2022;88:2793–801.

### Hybrid model: combination of ML and POPPK to keep interpretability: iohexol (PhD works A Destere) (1)

	Training		Testing		External	
	MAP-BE LSS	Hybrid model Xgboost	MAP-BE LSS	Hybrid model Xgboost	MAP-BE LSS	Hybrid model Xgboost
MPE%	-2.0	-0.3	-1.0	0.7	-3.7	-2.2
RMSE%	10.1	7.5	6.2	5.7	14.3	10.9
MPE out of ± 20% (%)	4.0	2.8	1.7	0.9	13.9	8.3

1-Destere A et al. A Hybrid Model Associating Population Pharmacokinetics with Machine Learning: A Case Study with Iohexol Clearance Estimation. *Clin Pharmacokinet*. 2022

2-Destere A et al. A single Bayesian estimator for iohexol clearance estimation in ICU, liver failure and renal transplant patients. *Br J Clin Pharmacol.* 2022;88:2793–801.

## Creation of synthetic patients by ML/DL

- Creation of virtual patients: continuous or categorical variables regardless of their distribution (e.g., GAN)
- Balance between utility and privacy
- Improvement of predictive model performances (limited data = often the case in Pharmacometrics)
- Alternative to federated learning: creation of virtual data twin of local data → sharing between centers (useful for multicentric projects)









Recent synthetic data approach privacy validated by CNIL (French National commission for informatics & privacy)



Fig. 5 The Avatar method uses local modeling to stochastically generate a synthetic individual, termed an avatar simulation. (1) Original pseudonymized sensitive data. (2) The core of the Avatar method consists of four steps: (a) individuals are projected in a multidimensional space; (b) pairwise distances are computed to find the k nearest neighbors (here k = 12) in a reduced space; (c) a synthetic individual is pseudo-randomly generated in the subspace defined by the neighbors; (d) privacy metrics are evaluated. (3) Output of the dataset of synthetic data. More details are provided online (https://docs.octopize.io/).

Guillaudeux et al Nature Digital Med 2023 Patient-centric synthetic data generation, no reason to risk reidentification in biomedical data analysis



Avatar k=10



Timo



# Benchmarking of different approaches

Algorithm	KL inverse	KS test	DCR* [5th-50th-95th]	NNDR* [5th-50th-95th]	AUC ROC#
Original data	NA	NA	NA	NA	NA
Avatar k=5	0.87	0.72	[0.28-0.57-1.00]	[0.14-0.33-0.75]	0.581
Avatar k=5 augmented	0.93	0.92	[0.09-0.42-1.51]	[0.05-0.27-0.94]	0.534
Avatar K k=10	0.79	0.90	[0.50-1.00-2.14]	[0.34-0.72-0.97]	0.550
Avatar k=10 augmented	0.89	0.91	[0.19-0.68-1.51]	[0.10-0.47-0.94]	0.518
Avatar k=20	0.77	0.89	[0 47-1 04-1 90]	[0.34-0.74-0.98]	0.503
Avatar k=20 augmented	0.76	0.88	[0.47.1.01.1.87]	[0.32-0.74-0.94]	0.474
CT-GAN	0.78	0.88	[0.83-1.78-3.39]	[0.52-0.87-0.99]	0.234
CT-GAN augmented	0.89	0.91	[0.81-1.87-3.62]	[0.52-0.87-0.99]	0.345
survVAE	0.84	0.89	[0.89-1.01-2.99]	[0.55-0.88-0.99]	0.298
survVAE augmented	0.86	0.90	[0.86-1.94-3.08]	[0.54-0.90-0.99]	0.367

Woillard et al. CPT PS, 2024

### Synthetic data in POPPK

Can synthetic data be the key to overcoming data sharing in pharmacometrics? A case study of tacrolimus in heart transplant patients

Alexandre Destere<sup>1,2</sup>, Adrien Paschier<sup>3,4</sup>, Marc Labriffe<sup>3,4</sup>, Clément Benoist<sup>3,4</sup>, Pierre Marquet<sup>3,4</sup>, Milou-Daniel Drici<sup>1</sup>, Charles Bouveyron<sup>2</sup>, Jean-Baptiste Woillard<sup>3,4</sup>

1.00 0.75 sensitivity 0.50 0.25 0.00 0.50 0.75 0.00 0.25 1.00 1 - specificity Avatar with K = 5

Under review CPT: PS

→ Evaluate the no-tracability of real data
 → Logistic regression to determine real or synthetic

data



Avatar with K = 15

### Synthetic data in POPPK

Can synthetic data be the key to overcoming data sharing in pharmacometrics? A case study of tacrolimus in heart transplant patients

Alexandre Destere<sup>1,2</sup>, Adrien Paschier<sup>3,4</sup>, Marc Labriffe<sup>3,4</sup>, Clément Benoist<sup>3,4</sup>, Pierre Marquet<sup>3,4</sup>, Milou-Daniel Drici<sup>1</sup>, Charles Bouveyron<sup>2</sup>, Jean-Baptiste Woillard<sup>3,4</sup>

Under review CPT: PS

- → Evaluate the abilities of tabular generative algorithms to create synthetic PK to develop POPPK model
- $\rightarrow$  Focus on structural model



### Tacrolimus population pharmacokinetics in adult heart transplant patients

	Paschier et al. Original development dataset	k=5	k=5 augmented	k=15	k=15 augmented	CTGAN	CTGAN augmented	TVAE	TVAE augmented
Best model	2cp ~ TrCp	2cp ~ TrCp	2cp ~ Tlag	2cp ~ TrCp	2cp ~ Tlag	2cp ∼ Tlag	2cp ~ Tlag	2cp ~ TrCp	2cp ~ Tlag
Tlag (RSE%)	-		0.3 (3.3)	-	0.3 (0.7)	0.3 (14.4)	0.4 (6.9)	-	0.3 (6.0)
Ktr (RSE%)	4.74 (Fixed)	8.7 (19.1)	-	23.8 (NE)	-	-	-	7.1 (13.8)	-
Mtt (RSE%)	0.5 (11.4)	0.4 (8.17)	-	0.3 (54.2)	-	-	-	0.6 (6.8)	-
Ka (RSE%)	1.0 (8.4)	0.6 (7.7)	0.7 (3.2)	13.7 (67.7)	8.5 (6.3)	0.6 (6.5)	0.4 (6.6)	1.2 (22.6)	0.9 (7.0)
CI (RSE%)	15.5 (10.9)	14.6 (8.7)	14.7 (4.6)	10.4 (NE)	0.2 (30.1)	14.7 (14.3)	14.7 (6.9)	11.5 (10.1)	10.2 (6.0)
V1 (RSE%)	21.2 (34.4)	10.5 (21.1)	23.8 (7.3)	146 (46.2)	175 (2.8)	29.4 (18.2)	19.2 (10.6)	0.0008 (NE)	27 (12.9)
Q (RSE%)	78.3 (11.2)	68.4 (8.4)	66.3 (4.8)	39.7 (97.3)	49.9 (5.2)	47.8 (21.1)	43.8 (8.8)	109 (16.7)	85.2 (6.7)
V2 (RSE%)	498.8 (16.7)	443 (15.5)	403 (6.4)	240 (NE)	2140 (3.5)	340 (54.7)	378 (13.2)	375 (17.8)	368 (9.9)
ωTlag (RSE%)	-	-	0.3 (12.6)	-	0.05 (13.5)	0.5 (19.1)	0.5 (9.0)	-	0.5 (10.1)
ωKtr (RSE%)	-	0.6 (26.6)	-	0.6 (105)	-	-	-	0.1 (109)	-
ωMtt (RSE%)	0.6 (16.0)	0.2 (31.7)	-	0.2 (135)	-	-	-	0.03 (143)	-
ωKa (RSE%)	0.2 (49.7)	0.2 (40.4)	0.2 (11.8)	0.8 (20.7)	0.5 (8.7)	0.1 (119.0)	0.2 (20.4)	0.3 (52.7)	0.2 3(23.5)
ωCl (RSE%)	0.7 (12.7)	0.4 (15.4)	0.5 (7.1)	0.6 (47.1)	0.7 (34.1)	0.6 (47.0)	0.6 (8.5)	0.4 (16.3)	0.5 (7.8)
ωV1 (RSE%)	2.5 (17.6)	0.3 (98.2)	0.6 (11.1)	0.2 (60.6)	0.3 (6.9)	0.2 (49.5)	0.3 (36.0)	3.2 (96.5)	0.4 (15.9)
ωQ (RSE%)	0.6 (16.4)	0.3 (17.8)	0.4 (8.2)	0.5 (78.4)	0.5 (7.0)	0.7 (18.4)	0.5 (12.0)	0.5 (17.7)	0.6 (9.8)
ωV2 (RSE%)	1.0 (16.2)	0.7 (17.5)	0.6 (8.3)	1.1 (69.9	0.4 (7.8)	0.5 (208)	0.8 (13.2)	0.8 (17.3)	0.9 (7.8)
a (mg/L) b (%)	- 0.12 (4.3)	- 0.06 (5.8)	- 0.07 (2.7)	- 0.05 (9.3)	- 0.06 (2.6)	- 0.22 (6.5)	- 0.23 (2.6)	- 0.13 (5.4)	- 0.14 (2.6)







# Thanks !





