

DOI: doi.org/10.21009/03.1401.FA04

# THE EFFECTS OF INTRA-INDIVIDUAL VARIABILITY SETTING ON THE ACCURACY OF TIME-INTEGRATED ACTIVITY CALCULATIONS USING NONLINEAR MIXED-EFFECTS MODELING

Fira Dwi Ananda<sup>1</sup>, Assyifa Rahman Hakim<sup>1</sup>, Indra Budiansah<sup>1</sup>, Rien Ritawidya<sup>2</sup>, Deni Hardiansyah<sup>1, a)</sup>

<sup>1</sup>*Medical Physics and Biophysics, Physics Department, Faculty of Mathematics and Natural Sciences, Universitas Indonesia, Depok, Indonesia.*

<sup>2</sup>*Research Center for Radioisotope Technology, Radiopharmaceuticals, and Biodosimetry, Nuclear Power Research Organization, National Research and Innovation Agency, South Tangerang, Indonesia*

Email: <sup>a)</sup>denihardiansyah@ui.ac.id

## Abstrak

Estimasi yang akurat terhadap *time-integrated activity* (TIA) penting untuk perencanaan pengobatan pada *peptide receptor radionuclide therapy* (PRRT). Dalam konteks pemodelan farmakokinetik, *intra-individual variability* (IAV) — yang berkaitan dengan ketidakpastian pengukuran — dapat memengaruhi estimasi nilai TIA. Penelitian ini bertujuan untuk meneliti dampak variasi pengaturan IAV terhadap perhitungan TIA. Data biokinetik ginjal (PMID: 33443063) dari 10 pasien tumor neuroendokrin setelah pemberian [<sup>177</sup>Lu]Lu-DOTATATE dianalisis menggunakan SPECT/CT. Estimasi TIA dilakukan menggunakan *Nonlinear Mixed-Effects Modeling* (NLMEM) dengan *error model* proporsional. Metode 1: TIA referensi (rTIA) dihitung dengan mengestimasi *inter-individual variability* (IIV) and IAV. Metode 2: Nilai IAV kemudian ditetapkan menjadi setengah (hTIA) dan dua kali lipat (tTIA) dari nilai yang diperoleh pada Metode 1. Pengaruh perubahan IAV terhadap akurasi TIA dievaluasi dengan membandingkan hTIA dan tTIA terhadap rTIA menggunakan *relative deviation* (RD), *root-mean-square error* (RMSE), dan *mean absolute percentage error* (MAPE). Hasil menunjukkan bahwa penetapan IAV menjadi setengah dari nilai referensi menghasilkan RMSE sebesar 5% dan MAPE sebesar 3%. Sementara itu, perubahan dua kali nilai IAV menghasilkan RMSE sebesar 7% dan MAPE sebesar 6%. Secara keseluruhan, perubahan pengaturan IAV memberikan dampak yang sangat kecil, karena perhitungan TIA tetap stabil dan tidak sensitif terhadap variasi IAV, baik ketika nilainya dikurangi setengah maupun digandakan dalam data biokinetik populasi ini.

**Keywords:** PRRT, NLMEM, Intra-individual variability (IAV)

## Abstract

Accurate estimation of kidney time-integrated activity (TIA) is essential for treatment planning in peptide receptor radionuclide therapy (PRRT). In the context of pharmacokinetic modeling, the intra-individual variability (IAV) setting—associated with measurement uncertainty—may influence TIA estimates. This study investigates the impact of varying IAV settings on TIA calculation. Kidney biokinetic data (PMID: 33443063) from 10 neuroendocrine tumor patients after [<sup>177</sup>Lu]Lu-DOTATATE administration were analyzed using SPECT/CT. A Nonlinear Mixed-Effects Modeling (NLMEM) with proportional error model was used for TIA estimation. Method 1: reference TIA (rTIA) was calculated by estimating both inter-individual variability (IIV) and IAV. Method 2: IAV was fixed at half (hTIA) and twice (tTIA) the value obtained in Method 1. The influence of altered IAV on TIA accuracy was evaluated by comparing hTIA and tTIA against rTIA using relative deviation (RD), root-mean-square error (RMSE), and mean

absolute percentage error (MAPE). Fixing IAV at half the reference value resulted in RMSE and MAPE of 5% and 3%, respectively. Furthermore, doubling the IAV led to an RMSE of 7% and MAPE of 6%. Modifying the IAV setting had a negligible impact as TIA calculation remained robust and insensitive to IAV variations when doubled and halved in our population biokinetic data.

**Keywords:** PRRT, NLMEM, Intra-individual variability (IAV)

## INTRODUCTION

Peptide receptor radionuclide therapy (PRRT) with [<sup>177</sup>Lu]Lu-DOTATATE has become a standard treatment for advanced neuroendocrine tumors (NETs), demonstrating significant improvements in progression-free survival and symptom control [1]. Patient-specific calculation of time-integrated activity (TIA) for radiopharmaceuticals in kidney as organs at risk (OAR) is desirable in molecular radiotherapy [2], [3], [4], [5], as it enables personalized dosimetry, minimizes toxicity, and optimizes therapeutic efficacy. The TIA represents the total accumulated activity in tissues over time that is required for determining absorbed dose [6].

Recent studies have highlighted the critical role of pharmacokinetic modeling in TIA calculation, particularly through Nonlinear Mixed-Effects Modeling (NLMEM) approaches that account for interindividual variability (IIV) and intra-individual variability (IAV) [7], [8], [9], [10]. The findings suggest that data type (sparse or rich data) may influence the estimation of IAV, while IIV is less affected in pharmaceutical drug research [11]. In the context of pharmacokinetic modeling, the IAV setting—associated with measurement uncertainty—may influence TIA estimates. Therefore, this study investigates how variations in IAV settings influence kidney TIA estimates in patients receiving [<sup>177</sup>Lu]Lu-DOTATATE. By elucidating the impact of IAV on the accuracy of TIA calculation, the findings could be used for clinical dosimetry practices.

## MATERIALS AND METHODS

### Biokinetic Data

This study utilized secondary data of Devasia et al. (PMID: 33443063) [9] from a retrospective clinical analysis of 10 patients who underwent multi-time-point SPECT/CT imaging following one cycle of standard [<sup>177</sup>Lu]Lu-DOTATATE PRRT for NETs at the University of Michigan Medical Center (August 2018–March 2020). Sequential SPECT/CT imaging (up to 4 time points per patient) was performed on a Siemens Intevo Bold system, with the first scan acquired pre-discharge on the treatment day and subsequent scans at 1–7 days post-therapy, including a targeted ~96-hour time point based on prior dosimetry optimization studies. SPECT reconstruction used Siemens xSPECT Quant software with voxel values in Bq/mL [8], [9], [12]. Kidneys were manually segmented on baseline CT by an experienced technologist, and VOIs were propagated to later time points via contour intensity-based alignment for time-activity data extraction. The pharmacokinetic data of the right kidney and left kidney of 10 patients were treated as distinct, the total dataset comprised 20 pharmacokinetic measurements.

### Standard Biexponential Time-Activity Fit for Clinical Patients

The biexponential models (Equation 1) that was used in the original paper analyzing the biokinetic data [9] in describing uptake and clearance of the radiopharmaceuticals, the model was described as follows:

$$A(t_{ij}) = \frac{ke * ka}{c(ka - ke)} \times \left[ \exp(-ke * t_{ij}) - \exp(-ka * t_{ij}) \right] + \epsilon(t_{ij}) \quad (1)$$

$$TIA = \int_0^{\infty} A(t) dt = \frac{1}{c} \quad (2)$$

$i = 1, \dots, n = \text{kidney index}$

$j = 1, \dots, n_j = \text{time index}$

Parameter  $c$  scales the curve up or down, while  $ka$  (uptake/absorption rate) and  $ke$  (elimination rate) govern its shape. The term  $\epsilon$  represents measurement error, assumed measurement error with variance of  $\sigma_{err}^2$ .

### Nonlinear mixed effects modelling (NLMEM)

NLMEM provides a framework for assessing both IIV and IAV [13], [14], [15], [16]. The NLMEM parameterizes fixed and random effects. Fixed effects describe the mean values of the estimated parameters in the population, while random effects describe the IIV of the estimated parameters between subjects in the population [17].

$$P_j = TVP_j \times \exp(ETA_j) \quad (3)$$

$$ETA_j = N(0, \sigma_j^2) \quad (4)$$

Where  $P_j$  is the estimated parameter  $j$  in a function,  $TVP_j$  is the fixed effect of the estimated parameter  $j$ , and  $ETA_j$  is the random effect.  $ETA_j$  is a random number following a Gaussian distribution with mean zero and variance  $\sigma_j^2$ . The proportional error model was used for the NLMEM model fitting [18] account for IAV in the observed kidney time–activity data. NLMEM model fittings and simulations were performed using NONMEM software (version 7.6.0; ICON Development Solutions, Ellicott City, MD).

### Variation of IAV parameter settings in TIA calculation

**Figure 1** shows the workflow of this study. Kidney biokinetic data from 10 NET after [<sup>177</sup>Lu]Lu-DOTATATE administration were fitted both IIV and IAV. In method 1, the TIA derived from fitting by estimating both IIV and IAV as the reference TIA (rTIA). Furthermore, in Method 2, the IAV value is varied by fixed at half (hTIA) and and twice (tTIA) the value obtained in Method 1.

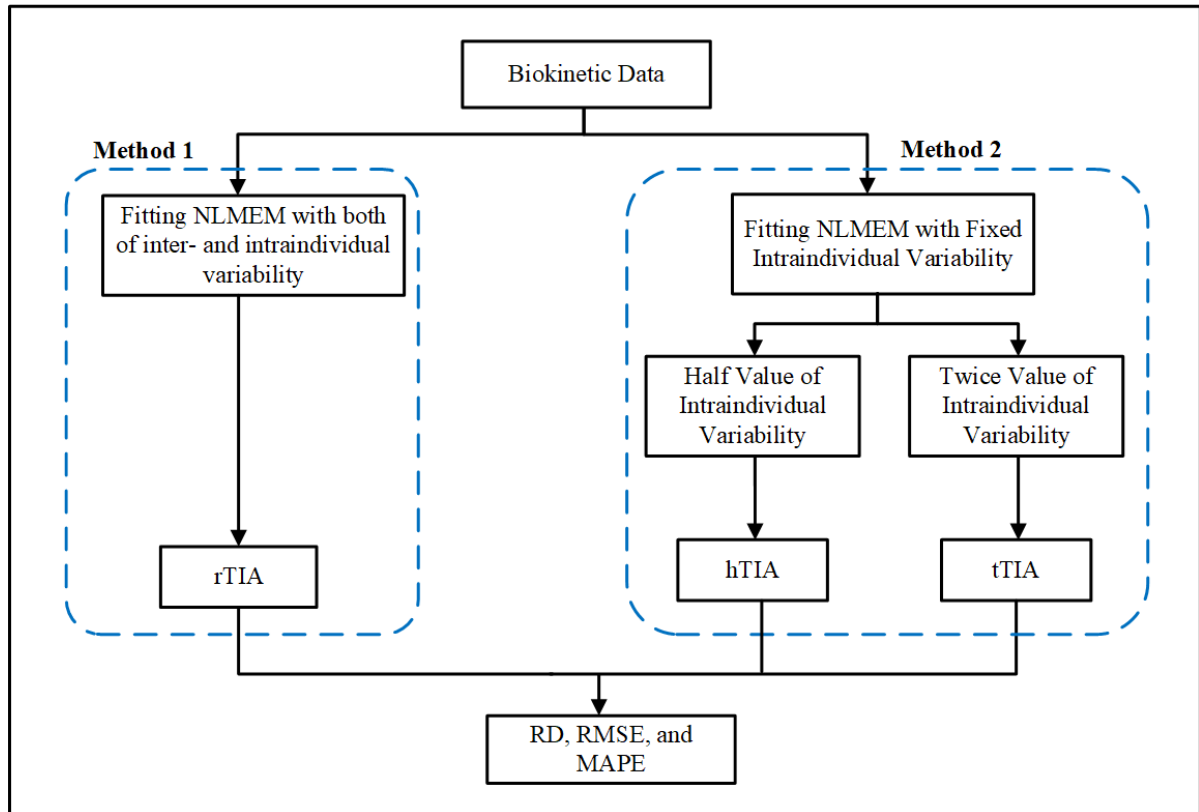


FIGURE 1. Workflow of this study

The influence of altered IAV on TIA accuracy was evaluated by comparing hTIA and tTIA against rTIA using relative deviation (RD), root-mean-square error (RMSE), and mean absolute percentage error (MAPE). The relative deviation RD and the RMSE were calculated according to:

$$RD_k = \frac{kTIA - rTIA}{rTIA} \tag{5}$$

$$RMSE_k = \sqrt{(SDRD_k)^2 + (Mean RD_k)^2} \tag{6}$$

where  $kTIA$  is TIA from each method ( $k$  represents a method where  $h$ =half original IAV ( $hTIA$ ) or  $t$ =twice original IAV ( $tTIA$ )),  $rTIA$  is reference TIA,  $RD_k$  is the RD of the each method at  $k$ ,  $RMSE_k$  is the root-mean square of  $RD_k$  over all patients, and  $SDRD_k$  is the SD of  $RD_k$ .

Mean Absolute Percentage Error (MAPE) represents the average of the absolute percentage differences between the TIA estimated from hTIA and tTIA with the rTIA obtained from fitted both IIV and IAV as the reference:

$$MAPE = \frac{1}{n} \sum_{i=1}^n \left| \frac{kTIA - rTIA}{rTIA} \right| \times 100\% \tag{7}$$

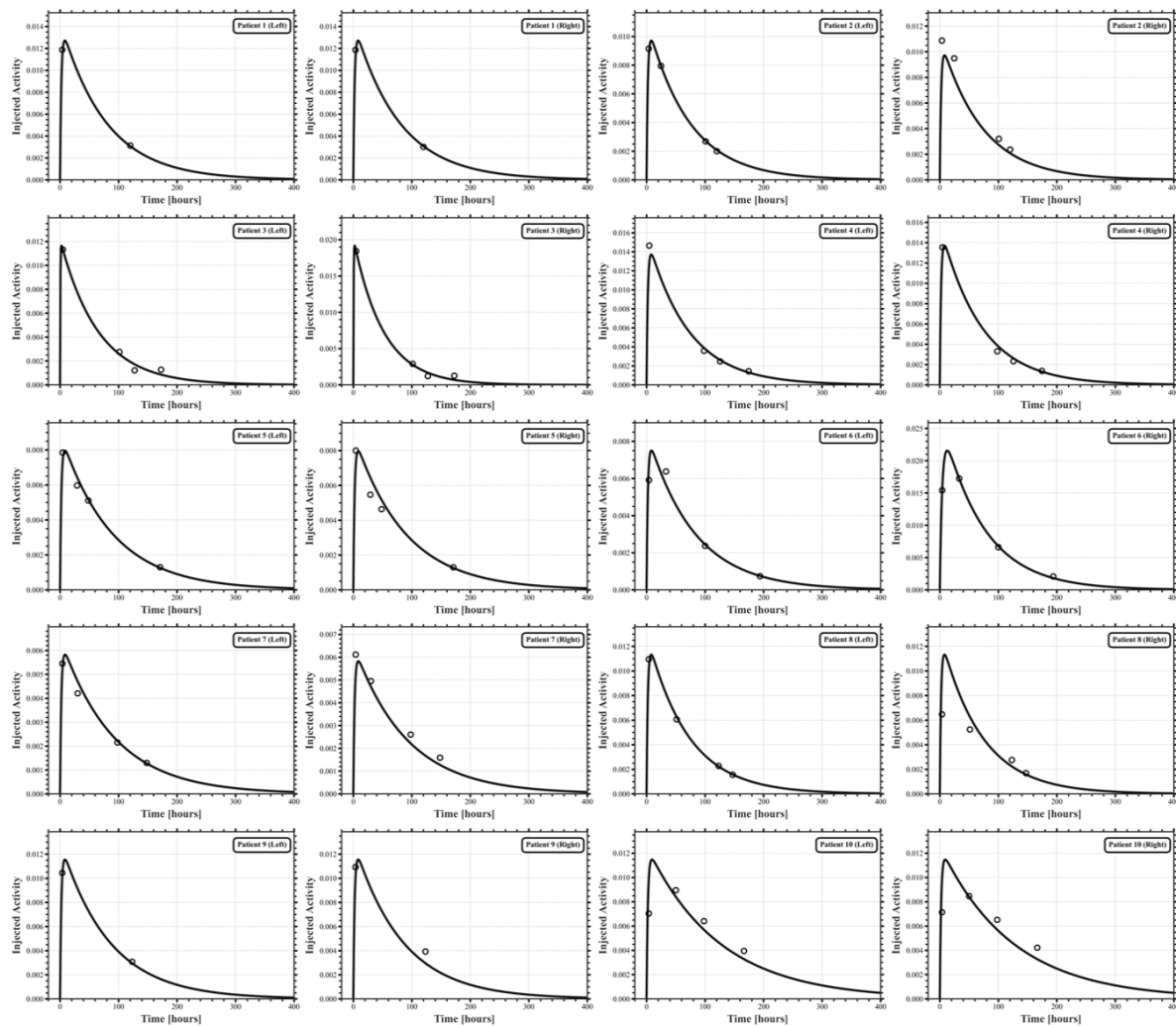
### RESULT AND DISCUSSION

In method 1, the NLMEM fitting incorporating both IIV and IAV yielded an initial estimate of the IAV parameter at 17%, along with the corresponding fitting curve (Figure 2) and the estimation result

of the IIV obtained a relative standard error (RSE) of less than 50%. In the fitting process, the  $k_a$  parameter remained fixed as it was not estimated. Devasia et al. [9] previously demonstrated that all parameters in their bi-exponential model incorporated random effects indicating IIV across each parameter. However, the current study observed no random effects for the parameter  $k_a$ , as its variability was negligible (variance  $< 10^{-6}$ ).

These differences may stem from differences in computational tools and estimation methodologies. Specifically, the present analysis utilized NONMEM version 7.6.0, which implements stochastic approximation expectation maximization (SAEM) coupled with importance sampling (IMP) for objective function computation [19], whereas the prior study employed the Statistical Analysis System (SAS), typically reliant on generalized NLMEM techniques. Discrepancies in estimation algorithms, convergence thresholds, and optimization strategies between software platforms may contribute to minor variations in parameter estimates, as also reported in the literature [20].

For the value of IAV serves as a crucial baseline for evaluating how deviations in fixed IAV can influence model performance. The half and twice multiples of the estimated IAV were 8.5% and 34%, respectively. These values were subsequently used as fixed parameters in method 2.



**FIGURE 2.** Time activity curves of the relationship between injected activity and time from Equation 1 by estimating the IAV value (reference).

For method 2, the fitting results for half and twice the IAV were evaluated to assess their influence on TIA estimation, based on the analysis of RD, RMSE, and MAPE (**Figure 3** and **Table 1**). The

RMSE and MAPE values obtained with half the IAV were 4.92% and 3.10%, respectively, while the RMSE and MAPE values with twice the IAV were 6.80% and 5.52%.

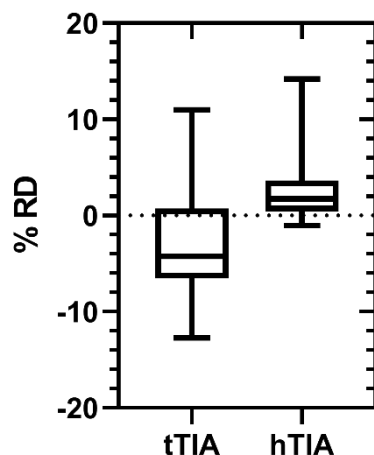


FIGURE 3. RD of TIA obtained using fixation IAV

TABEL 1. RD value of TIA obtained using fixation IAV

Intra-individual variability (IAV) Fixed	RD%		RMSE of the RD(%)	MAPE(%)
	Mean (SD)	Median [Min, Max]		
8.5%	2.94 (3.95)	1.76 [-1.06,14.19]	4.92	8.5%
34%	-3.22 (5.93)	-4.25 [-12.72,10.99]	6.80	34%

As shown in **Figure 3** and **Table 1**, the TIA obtained with twice the fixed IAV showed marginally higher deviations compared to the reference, while deviations with half the IAV remained minimal. However, despite the slightly elevated errors with doubled IAV, both scenarios maintained sufficiently low RD, RMSE, and MAPE values to be considered negligible in practice. This confirms that fixing the IAV value—whether halved or doubled—has minimal impact on TIA accuracy, suggesting that the TIA calculation is robust and insensitive to variations in predefined IAV values. Thus, while careful assessment of IAV levels is advisable, the method remains reliable even when fixed values are applied.

This study has several limitations. First, the analysis relied on a single dataset, and second, only a narrow range of fixed IAV values (8.5% and 34%) was examined. These constraints may limit the ability to capture the full variability observed in broader clinical settings. Consequently, the generalizability of the findings remains uncertain. Future studies should validate these results using larger, more diverse datasets and a wider range of fixed IAV values.

### CONCLUSION

This study demonstrates that fixed IAV values whether halved (RMSE: 4.92%, MAPE: 3.10%) or doubled (RMSE: 6.80%, MAPE: 5.52%) yield clinically acceptable TIA accuracy. TIA calculation remains robust and insensitive to IAV variations, even when the parameter is fixed at predefined values in our population biokinetic data.

### ACKNOWLEDGMENT

This research was funded by the Ministry of Education, Culture, Research, and Technology of the Republic of Indonesia through the Master Thesis Research Grant in 2025, under the main contract number 070/C3/DT.05.00/PL/2025 and derivative contract number PKS-589/UN2.RST/HKP05.00/2025. FDA and ARH studies were supported by the Degree by Research Scholarship Program of the National Research and Innovation Agency (BRIN) with contract number 118/II/HK/2024. No other potential conflict of interest relevant to this article was reported

### REFERENCES

- [1] J. Strosberg *et al.*, “Phase 3 Trial of  $^{177}\text{Lu}$ -DOTATATE for Midgut Neuroendocrine Tumors,” *New England Journal of Medicine*, vol. 376, no. 2, pp. 125–135, 2017, doi: 10.1056/nejmoa1607427.
- [2] G. Glatting, M. Bardiès, and M. Lassmann, “Treatment planning in molecular radiotherapy,” *Z Med Phys*, vol. 23, no. 4, pp. 262–269, 2013, doi: 10.1016/j.zemedi.2013.03.005.
- [3] D. Hardiansyah *et al.*, “The role of patient-based treatment planning in peptide receptor radionuclide therapy,” *Eur J Nucl Med Mol Imaging*, vol. 43, no. 5, pp. 871–880, 2016, doi: 10.1007/s00259-015-3248-6.
- [4] M. Lassmann, C. Chiesa, G. Flux, and M. Bardiès, “EANM Dosimetry Committee guidance document: Good practice of clinical dosimetry reporting,” *Eur J Nucl Med Mol Imaging*, vol. 38, no. 1, pp. 192–200, Jan. 2011, doi: 10.1007/s00259-010-1549-3.
- [5] G. Chen *et al.*, “Lu-177-PSMA dosimetry for kidneys and tumors based on SPECT images at two imaging time points,” *Front Med (Lausanne)*, vol. 10, no. 1, Nov. 2023, doi: 10.3389/fmed.2023.1246881.
- [6] W. E. Bolch *et al.*, “MIRD pamphlet No. 21: A generalized schema for radiopharmaceutical dosimetry-standardization of nomenclature,” *Journal of Nuclear Medicine*, vol. 50, no. 3, pp. 477–484, 2009, doi: 10.2967/jnumed.108.056036.
- [7] D. Hardiansyah, A. Riana, A. J. Beer, and G. Glatting, “Single-time-point estimation of absorbed doses in PRRT using a non-linear mixed-effects model,” *Z Med Phys*, 2022, doi: 10.1016/j.zemedi.2022.06.004.
- [8] D. Hardiansyah, A. Riana, A. J. Beer, and G. Glatting, “Single - time - point dosimetry using model selection and nonlinear mixed - effects modelling : a proof of concept,” *EJNMMI Phys*, pp. 1–12, 2023, doi: 10.1186/s40658-023-00530-1.
- [9] T. P. Devasia, Y. K. Dewaraja, K. A. Frey, K. K. Wong, and M. J. Schipper, “A Novel Time-Activity Information-Sharing Approach Using Nonlinear Mixed Models for Patient-Specific Dosimetry with Reduced Imaging Time Points: Application in SPECT/CT After  $^{177}\text{Lu}$ -DOTATATE,” *J Nucl Med*, vol. 62, no. 8, pp. 1118–1125, 2021, doi: 10.2967/jnumed.120.256255.

- [10] A. Jadidan, F. D. Ananda, Z. Muhammad, and D. Hardiansyah, "Mathematical model to calculate the total number of decays in Peptide Receptor Radionuclide Therapy using nonlinear mixed effect modelling," *J Phys Conf Ser*, vol. 2596, no. 1, 2023, doi: 10.1088/1742-6596/2596/1/012033.
- [11] W. Sukarnjanaset, T. Wattanavijitkul, and S. Jarurattanasirikul, "Evaluation of FOCEI and SAEM Estimation Methods in Population Pharmacokinetic Analysis Using NONMEM ® Across Rich, Medium, and Sparse Sampling Data," *Eur J Drug Metab Pharmacokinet*, vol. 43, no. 6, pp. 729–736, 2018, doi: 10.1007/s13318-018-0484-8.
- [12] J. Tran-Gia and M. Lassmann, "Characterization of Noise and Resolution for Quantitative <sup>177</sup>Lu SPECT/CT with xSPECT Quant," *Journal of Nuclear Medicine*, vol. 60, no. 1, pp. 50–59, Jan. 2019, doi: 10.2967/jnumed.118.211094.
- [13] C. W. Tornøe, H. Agersø, E. N. Jonsson, H. Madsen, and H. A. Nielsen, "Non-linear mixed-effects pharmacokinetic/pharmacodynamic modelling in NLME using differential equations," *Comput Methods Programs Biomed*, vol. 76, no. 1, pp. 31–40, 2004, doi: 10.1016/j.cmpb.2004.01.001.
- [14] M. Davidian and D. M. Giltinan, "Nonlinear models for repeated measurement data," *Nonlinear Models for Repeated Measurement Data*, vol. 27695, pp. 1–360, 2017, doi: 10.1201/9780203745502.
- [15] J. S. Owen and J. Fiedler-Kelly, *Introduction to Population Pharmacokinetic / Pharmacodynamic Analysis with Nonlinear Mixed Effects Models*. Wiley, 2014. doi: 10.1002/9781118784860.
- [16] P. L. Bonate, *Pharmacokinetic-Pharmacodynamic Modeling and Simulation*. Boston, MA: Springer US, 2011. doi: 10.1007/978-1-4419-9485-1.
- [17] D. R. Mould and R. N. Upton, "Basic concepts in population modeling, simulation, and model-based drug development," *CPT Pharmacometrics Syst Pharmacol*, vol. 1, no. 1, pp. 1–14, 2012, doi: 10.1038/psp.2012.4.
- [18] D. Hardiansyah *et al.*, "Single-Time-Point Renal Dosimetry Using Nonlinear Mixed-Effects Modeling and Population-Based Model Selection in [<sup>177</sup>Lu]Lu-PSMA-617 Therapy," *Journal of Nuclear Medicine*, vol. 65, no. 4, pp. 566–572, Apr. 2024, doi: 10.2967/jnumed.123.266268.
- [19] R. J. Bauer, "NONMEM Tutorial Part II: Estimation Methods and Advanced Examples," *CPT Pharmacometrics Syst Pharmacol*, vol. 8, no. 8, pp. 538–556, 2019, doi: 10.1002/psp4.12422.
- [20] V. Vasić *et al.*, "A PBPK model for PRRT with [<sup>177</sup>Lu]Lu-DOTA-TATE: Comparison of model implementations in SAAM II and MATLAB/SimBiology," *Physica Medica*, vol. 119, Mar. 2024, doi: 10.1016/j.ejmp.2024.103299.