

<sup>1</sup> **pharmsol: A high-performance Rust library for pharmacokinetic/pharmacodynamic modeling and simulation**

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**Software**

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<sup>8</sup> **Summary**

<sup>9</sup> **pharmsol** is a library for pharmacokinetic/pharmacodynamic (PK/PD) simulation written in <sup>10</sup> Rust. It provides the necessary tools and frameworks for defining, solving, and analyzing <sup>11</sup> compartmental models, with support for differential equations, their analytical solutions, and <sup>12</sup> experimental support for stochastic differential equations. Written in Rust, the library aims <sup>13</sup> to provide researchers and developers with a framework for pharmacokinetic simulation in a <sup>14</sup> memory-safe and performant language. The library is distributed via crates.io with <sup>15</sup> comprehensive API documentation, usage examples, and a test suite validated through continuous <sup>16</sup> integration.

**Statement of Need**

<sup>18</sup> Pharmacokinetic and pharmacodynamic modeling and simulation are computationally intense <sup>19</sup> when applied to modern, complex, and sophisticated dosing regimens, mechanistic models, <sup>20</sup> and individualized approaches. Unlike comprehensive pharmacometric platforms such as <sup>21</sup> NONMEM ([Beal & Sheiner, 1992](#)), Phoenix NLME ([Certara USA, Inc., 2024](#)), or Monolix <sup>22</sup> ([Simulations Plus \(United States\), 2024](#)), **pharmsol** is purpose-built as a simulation engine that <sup>23</sup> pharmacometrists can leverage to rapidly execute simulations for individuals or populations <sup>24</sup> with pre- and user-defined models.

<sup>25</sup> As a fully open-source solution, **pharmsol** empowers users to inspect, modify, and extend <sup>26</sup> the simulation capabilities without licensing constraints. Users can define custom models by <sup>27</sup> specifying their own differential equations as closures, or use the provided analytical solutions <sup>28</sup> for standard compartmental models. Additionally, **pharmsol** can be integrated in more user-<sup>29</sup> friendly languages such as R using `extendr` ([Reimert et al., 2024](#)), making it accessible to <sup>30</sup> pharmacometrists who may prefer higher-level interfaces.

<sup>31</sup> **Data format**

<sup>32</sup> **pharmsol** is designed around a hierarchical data structure that models the typical organization <sup>33</sup> of pharmacometric data. The primary data struct, `Data`, is a collection of `Subjects`, which <sup>34</sup> may have one or more `Occasions`, i.e. separate pharmacokinetic investigations. Each occasion <sup>35</sup> consists of one or more `Events`, e.g. an instantaneous dose (`bolus`), infusions of drug, or <sup>36</sup> observed concentrations at given times.

`Data` → `Subject` → `Occasion` → `Event` (`Bolus`, `Infusion`, `Observation`)

<sup>37</sup> Currently, pharmsol provides methods to parse the Pmetrics ([Neely et al., 2012](#)) data format.  
<sup>38</sup> In the future, we aim to also support additional formats, such as those used by NONMEM,  
<sup>39</sup> Monolix ([Simulations Plus \(United States\), 2024](#)), and more.

## <sup>40</sup> Supported equation formats

<sup>41</sup> The equation module provides the mathematical foundation for simulating PK/PD output  
<sup>42</sup> with three model equation solver types: analytical solutions, ordinary differential equations,  
<sup>43</sup> and experimental support for stochastic differential equations.

### <sup>44</sup> Analytical Solutions

<sup>45</sup> For standard compartmental models, pharmsol provides closed-form solutions for one- and  
<sup>46</sup> two-compartment models, with and without oral absorption. These have been verified against  
<sup>47</sup> their differential equation counterparts. Benchmarks demonstrate 20-33 $\times$  speedups compared  
<sup>48</sup> to equivalent ODE formulations without loss of precision (see repository benchmarks for details).  
<sup>49</sup> Additional analytical solutions will be added in future versions.

### <sup>50</sup> Ordinary Differential Equations

<sup>51</sup> For more complex or non-standard models, pharmsol supports user-defined ordinary differential  
<sup>52</sup> equations (ODEs). The numerical integration is performed using the diffsol library ([Robinson,](#)  
<sup>53</sup> [2024](#)), which provides efficient BDF solvers suitable for the stiff systems often encountered in  
<sup>54</sup> pharmacometric modeling.

### <sup>55</sup> Stochastic Differential Equations

<sup>56</sup> Experimental support for stochastic differential equations (SDEs) is available using the Euler-  
<sup>57</sup> Maruyama method. SDEs allow modeling of within-subject variability as a continuous stochastic  
<sup>58</sup> process. However, particular care should be taken if applying SDEs in a non-parametric approach  
<sup>59</sup> to population pharmacokinetic modeling, such as when using the non-parametric adaptive grid  
<sup>60</sup> algorithm (NPAG) ([Yamada et al., 2020](#)) for parameter estimation.

## <sup>61</sup> Conclusion and Future Work

<sup>62</sup> pharmsol aims to support the evolving needs of pharmacometric research by providing a modern,  
<sup>63</sup> efficient platform that can adapt to the increasing complexity of pharmaceutical development  
<sup>64</sup> while remaining accessible through its open-source licensing model. Future development will  
<sup>65</sup> focus on additional analytical model implementations, support for common data formats used  
<sup>66</sup> by other pharmacometric software, non-compartmental analysis and continued performance  
<sup>67</sup> improvements.

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