

Run faster. Go further.

Why pharmacometricians are turning to the NLME engine from Certara Phoenix

The performance difference

The following table summarizes direct modeling experience across 14 challenging, real-world models evaluated between December 2025 and April 2026. Models were selected specifically because of known computational difficulty — these were not routine benchmarks.

Model description	NONMEM Outcome	NLME Outcome	Run time NONMEM vs NLME
CAR-T	SSE, SAEM, Issue = poor convergence	No issues (QRPEM)	288 min vs 244 min (example run only)
2-cpt, lots of covariates	Minimization termination error (rounding)	No issues	8.6s vs 5 s
PKPD, ODEs, complicated	Run failure (SAEM)	No issues (QRPEM)	NA vs 12.5 h (10 cores)
1-cpt, covariates	Minimization termination error	No issues	25s vs 167 s
P-M model + cov _ ADDL, SS, II, L2	Minimization termination error (\$COV never successful)	No issues (L2 excluded)	180 min vs 34 min (L2 excluded from both)
(L2 excluded from both)	Minimization termination error (\$COV never successful)	No issues	180 min vs 34 min
1-cpt PK + cov	No issues	No issues	453s vs 50.7 s
1-cpt PK + cov + BLQ (M4)	No issues	No issues (M4 changed to M3)	60s (10-core) vs 185s (1-core)
ODEs = cov + complicated absorption	Minimization termination error	Converged, but SE not estimated	108s vs 185 s
1-cpt KOKA + cov	No issues	No issues	14.7s vs 0.75 s
Nonlinear PK (ODEs)	Unstable (variable run or \$COV failure)	No issues	533s
PK-VK sequential	No issues	No issues	4886s vs 237 s
Time varying CL, ODEs + cov	Unstable	No issues	NA vs 7956 s (19 cores VDI)
Enzyme autoinhibition PK (ODEs)	Unstable (\$COV fails)	No issues	NA vs 221 min
PKPD turnover model aggregate and individual level data	Unstable (\$COV fails)	No issues	1743s vs 1246 s
P-M ODE model + BLQ	Unstable (run failure)	No issues	NA vs 153 min
ADC TMDD ODE model	Fine (\$COV fails sometimes)	No issues	1743s vs 1246 s

Across 14 challenging real-world models, Phoenix NLME resolved every convergence and stability issue encountered, often with faster runtimes and fewer manual adjustments.

Key abbreviations

cov = Covariates
P-M = Parent Metabolite
PKVK = PK-Viral Kinetics

SE = Standard Error
KOKA = Zero-Order +
First-Order Absorption

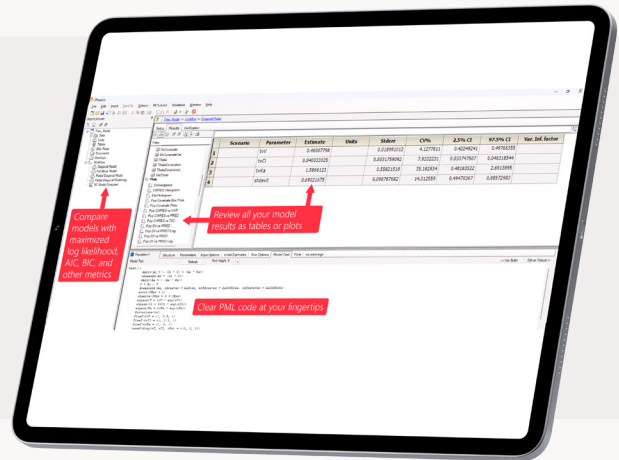
The experience difference

Speed counts, but so does ease of use. Phoenix NLME and RsNLME combine robust modeling with GUI- and R-based workflows that replace tool switching and file juggling.

- One project file for multiple models and outputs
- More stable model execution
- Simpler, more readable code
- Seamless integration with Phoenix or R workflows
- Support for initial estimates in NLME
- Uses intuitive parameter naming instead of numeric indexing
- Handles many modeling steps automatically
- Advanced built-in algorithms such as FOCE with automatic-differentiation-assisted parametric optimization and QRPEM improve model robustness while reducing the need for manual parameter tuning
- Cleaner, more transparent workflows

One-stop modeling

With Phoenix NLME, build, run, and compare all your models, with their output, in one versatile interface.



Code, without the cracks

RsNLME offers an analogous “all-in-one session” organization of files and outputs.

The Real-World impact

You know the frustration of slow, fragile runs that terminate without warning. With Phoenix NLME and RsNLME, you can iterate faster, diagnose more clearly, and stay focused on the model, not the machinery. Cleaner, more transparent workflows.

Bring us your toughest population models and talk with our team about your most challenging modeling workflows.

Learn more about Phoenix NLME and RsNLME



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