Jinkō: A Modern Collaborative Integrated and Scalable QSP Modeling Platform

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Build QSP models of any size with a modern interface combining core **modeling features** and powerful **AI accelerators**

Granularity, reusability and interoperability ⟷ Collaboration and review ⟷ Traceability and auditability

Import

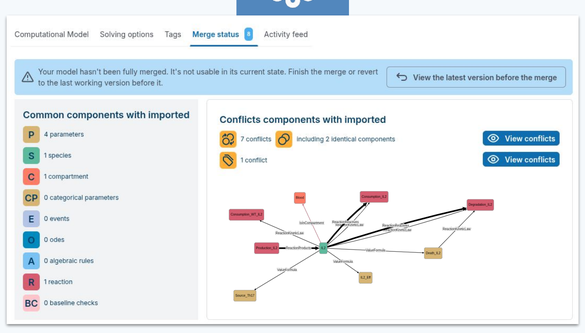
SBML Monolix SimBiology

Reuse existing templates

Create

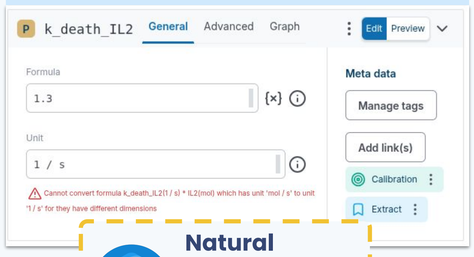
AI accelerated conversion from **scientific papers**

COMBINE



Connect **2 or more** models created in the platform or coming from the outside using a **git** inspired combination interface

Edit collaboratively

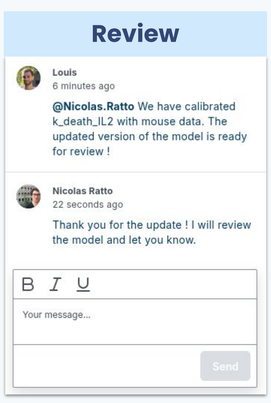


Natural language interactions with the model

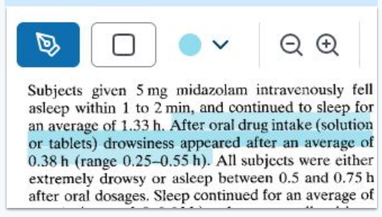
Model edition made easy thanks to auto-computed **sanity checks**

Persisted **discussion threads** facilitate traceable peer review and collaboration

Review



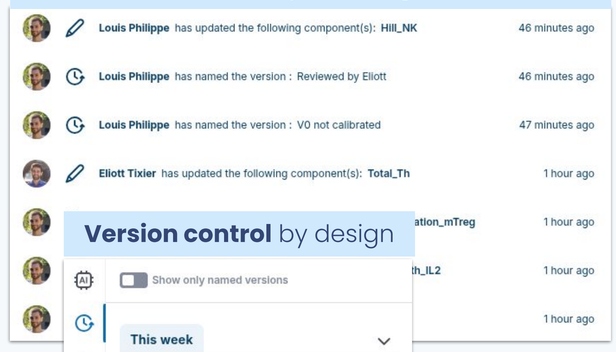
Document



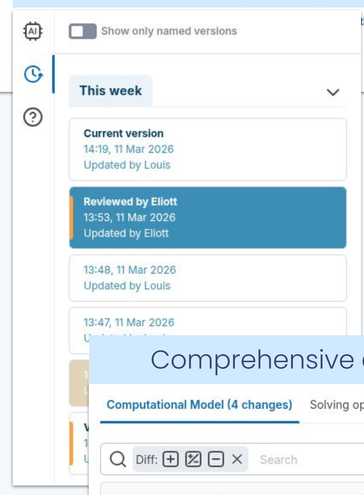
Subjects given 5 mg midazolam intravenously fell asleep within 1 to 2 min, and continued to sleep for an average of 1.33 h. After oral drug intake (solution or tablets) drowsiness appeared after an average of 0.38 h (range 0.25–0.55 h). All subjects were either extremely drowsy or asleep between 0.5 and 0.75 h after oral dosages. Sleep continued for an average of

Document model implementation with embedded **extracts** from scientific literature

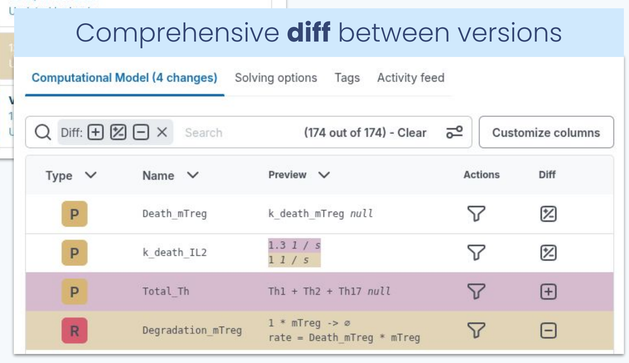
User friendly **activity feed**



Version control by design



Comprehensive **diff** between versions



BACKGROUND

Successful integration of QSP modeling into model-informed drug development is conditioned by high standards of **reusability**, **auditability** and long-term **maintainability** of the underlying implementations [1, 2]. As QSP models grow in size and complexity [3], consistent and reproducible model edition becomes increasingly challenging, especially when multiple contributors from interdisciplinary teams work with multi-scale models and inputs coming from heterogeneous sources.

To address these constraints, Jinkō is a modeling and clinical trial simulation platform supported by a scalable infrastructure. It provides a powerful QSP model edition module built on key principles and an intuitive user interface.

METHODS

Jinkō's model edition module is built on key principles inspired by the software engineering world:

- ➔ **Traceability and auditability**: Models are by design version-controlled ensuring full traceability of model evolution. A comprehensive diff tool allows for detailed inspection of structural and parametric changes between successive versions.
- ➔ **Collaboration and review**: The platform supports simultaneous contributions from several users on the same model, fostering team collaboration. Links to literature references and experimental data, along with persisted discussion threads enable transparent documentation of modeling decisions and structured scientific review.
- ➔ **Granularity**: Submodels can be implemented independently - as atomic modular bricks - and easily connected using a git-inspired combination tool. Changes to the submodels are automatically propagated to the overarching model.
- ➔ **Reusability** is facilitated by the creation of model templates, which allow consistent reuse across projects and therapeutic areas, and accelerate model development workflows.
- ➔ **Interdisciplinary** collaboration around model edition is further supported by AI-based accelerators, empowering non-modelers with adapted interfaces and natural language interactions, while enabling automated yet auditable workflows fully integrated with the platform's core features for modelers.
- ➔ **Interoperability**: Models can be imported from and exported to several industry standard formats including SBML, Monolix and SimBiology, to facilitate interoperability with other tools or softwares.

RESULTS

Thanks to a unique combination of core modeling features (native sanity checks, modular and reusable implementations) and AI accelerators (automated equation extraction from scientific publications, assisted model edition), Jinkō users have reported faster model development workflows. Internal benchmarks indicate an average **60%** time savings on the development of large QSP models (**1000+** parameters, **100+** equations, **20+** submodels). This acceleration is further supported by enhanced collaboration - with up to **10** simultaneous contributors on the same model - illustrating the platform's ability to scale model development workflows.

Users also reported improved auditability and maintainability of the models. With native traceability features and intuitive interfaces adapted to interdisciplinary environments, Jinkō provided an efficient tool for large teams (**15+** contributors, modelers and clinicians) to review and quality check QSP models, increasing their robustness as decision-making tools.

CONCLUSION

- ➔ By integrating established good software engineering practices as key principles of its core features, Jinkō is an efficient tool to accelerate the implementation of complex QSP models.
- ➔ In addition to improving model development efficiency, Jinkō also enhances model auditability, enabling faster iteration cycles and more robust decision-making in model-informed drug development.

REFERENCES

[1] Cucurull-Sanchez, Lourdes, et al. CPT: pharmacometrics & systems pharmacology 8.5 (2019): 259-272
[2] Musuamba, Flora T., et al. CPT: Pharmacometrics & Systems Pharmacology 10.8 (2021): 804-825
[3] Derbalah, Abdallah, et al. British journal of clinical pharmacology 88.4 (2022): 1430-1440.