



Galaxy-SynBioCAD: tools and automated pipelines for Synthetic Biology Design and Metabolic Engineering

Thomas Duigou, Joan Hérisson, Melchior Du Lac, Kenza Bazi-Kabbaj, Mahnaz Sabeti Azad, Gizem Buldum, Olivier Telle, Yorgo El-Moubayed, Pablo Carbonell, Neil Swainston, et al.

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Équipe BioRetroSynth



Galaxy-SynBioCAD: tools and automated pipelines for Synthetic Biology Design and Metabolic Engineering

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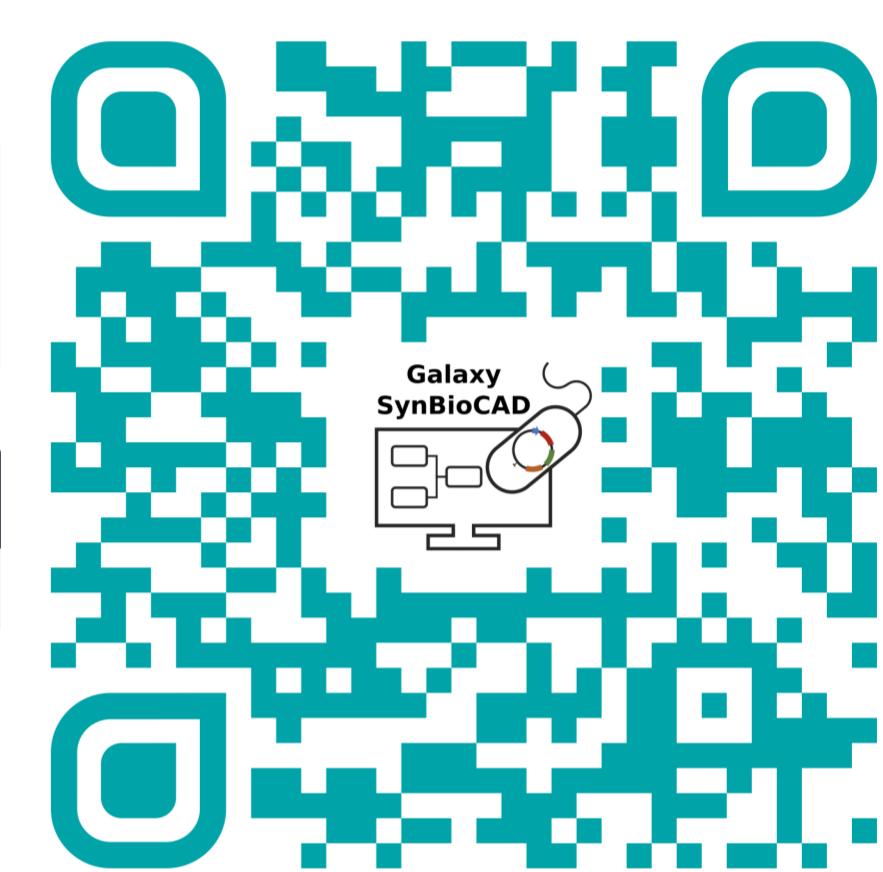
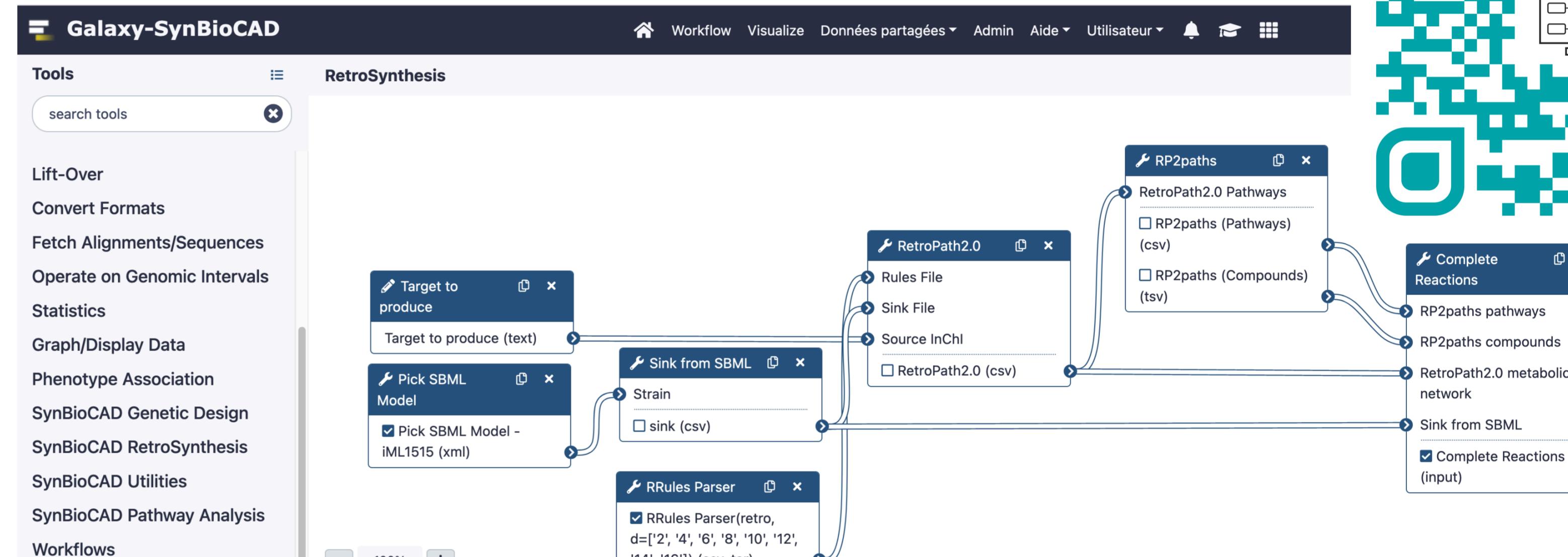
1 — Context

- Many tools, but few interoperability
- The (in-)accessibility of command line interface
- Not everyone owns a computing cluster “at home”

2 — The Galaxy-SynBioCAD portal

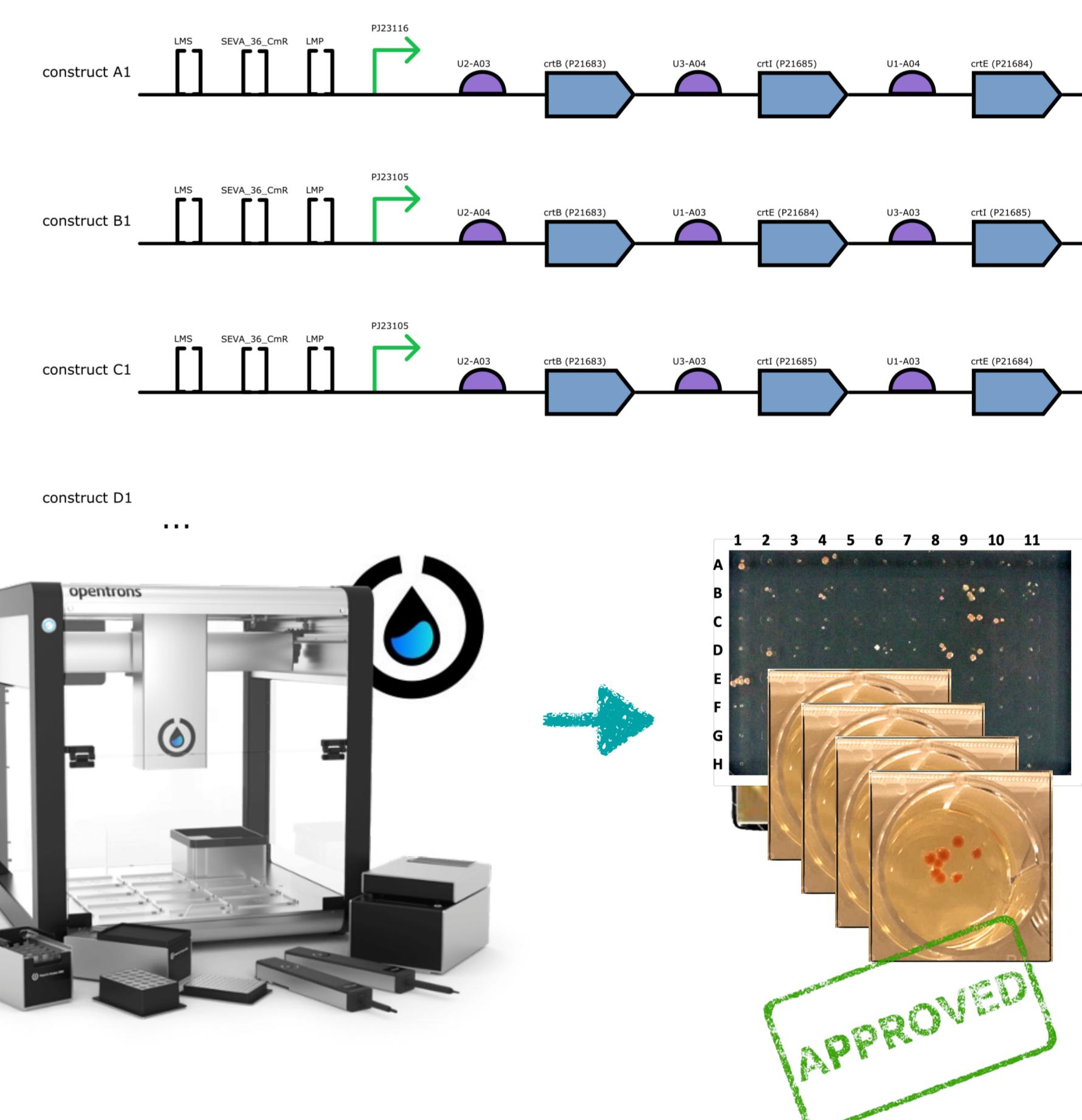
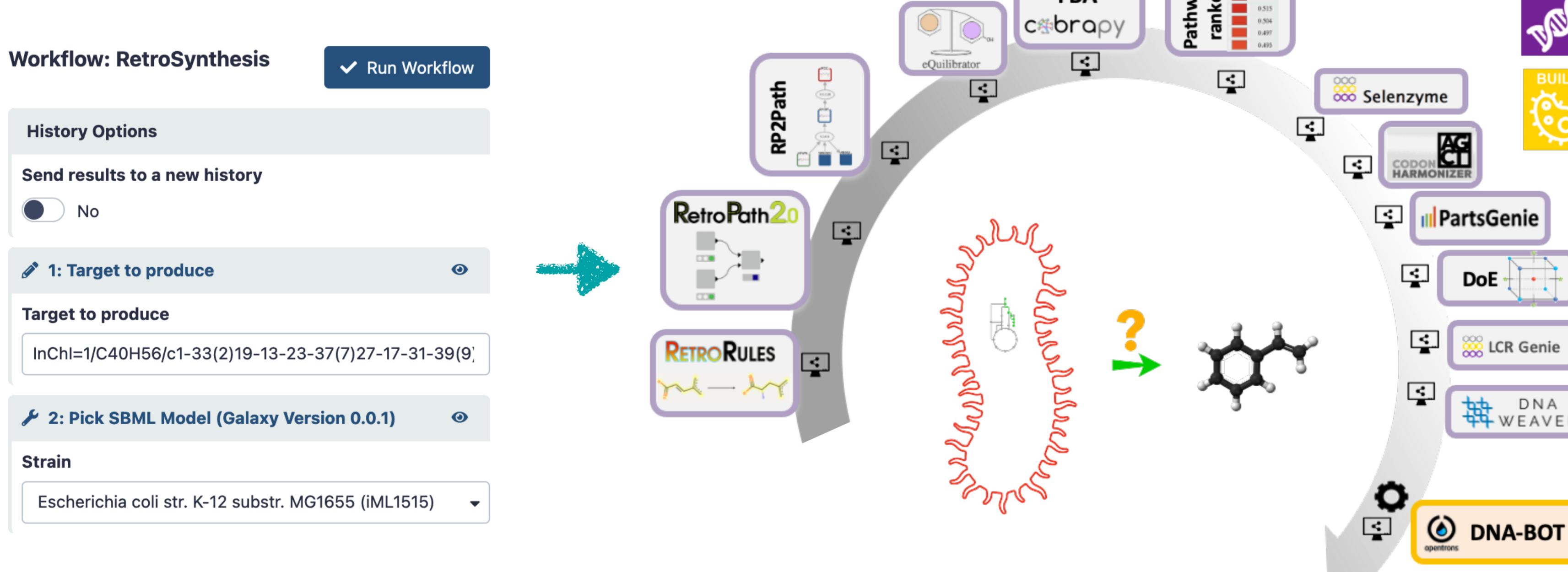
- Collection of Galaxy-ready tools and workflows
- Interoperable and standardized input / output:
 - SBML (metabolic pathways)
 - SBOL (genetic constructs)
- Use case workflows released so far:
 - biosynthesis** pathway design
 - pathway analysis** and scoring
 - genetic / plasmid design
 - sensing-enabling pathway design

<https://galaxy-synbiocad.org/>



3 — From specification to bio-producing strains

- Showcase: automate design and construction of lycopene-producing strains at the bench



4 — Under the hood: CI/CD integration process



- Git commits trigger GitHub actions
- Tools released as conda packages
- Wrappers validated with Planemo
- Tools available from the Galaxy ToolShed
- Integration with the IUC repo in progress

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