



**CoRC –  
Copasi R Connector**  
[jpahle.github.io/CoRC](https://github.com/jpahle/CoRC)

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<https://lab.pahle.org>

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# CoRC

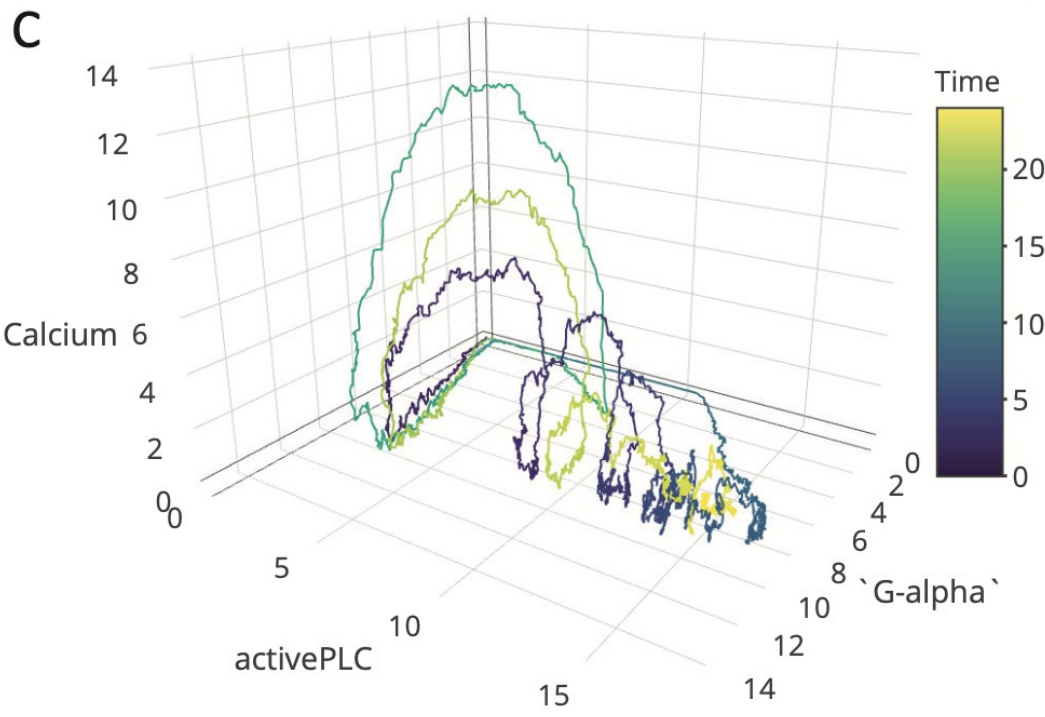
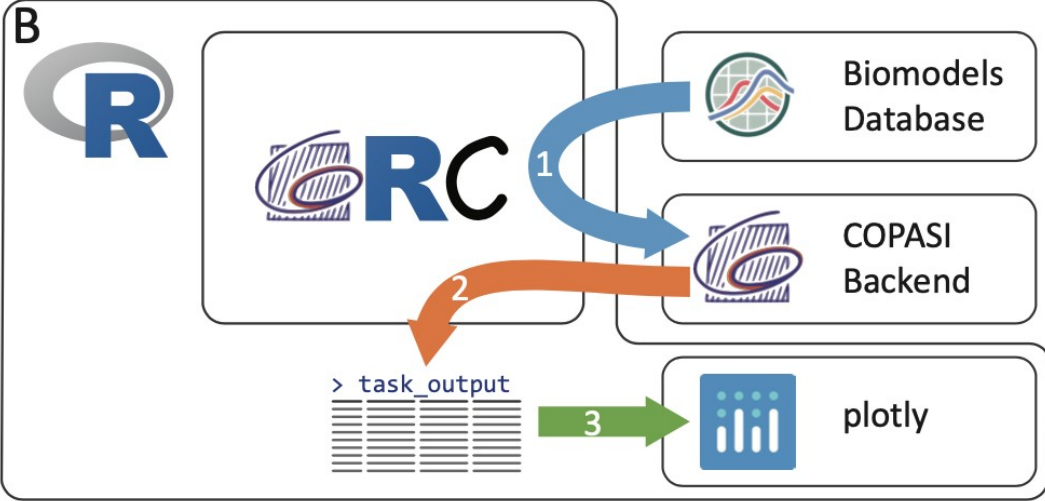
**CoRC** connects the

- Complex Pathway Simulator **COPASI**  
([copasi.org](http://copasi.org)) and the
- (statistical) programming environment **R**  
([r-project.org](http://r-project.org)).

```

A
library(CoRC)
library(plotly)
1 loadSBML(biomodels_url(id = 329, version = 2, format = "sbml"))
2 task_output <- runTimeCourse(dur = 24, interv = 10000, method = "directMethod")
3 plot_ly(data = task_output$result, type = "scatter3d", mode = "lines",
          x = ~`G-alpha`, y = ~activePLC, z = ~Calcium, color = ~Time)

```



- **High-level API** for COPASI in the R language. Uses COPASI's sophisticated computation backend.
- “Flat design”:
  - Functions for model creation/editing, tasks, etc.
  - Following the typical workflows with the GUI in a cognitive efficient way.

# CoRC features

- **Reproducible workflows** from data generation to analysis and plotting (R scripts and Markdown documents / notebooks).
- **Immediate access to R's** data analysis capabilities and publication-ready plotting.
- Systematic **modification of model structure** to test structural variations or **create large models**.
- **Parallelization** on multi-core machines or computing clusters.
- **Scaling up assays**, e.g. from 3 models to 3000.
- Handling of **multiple models** at once.

# Developer Team

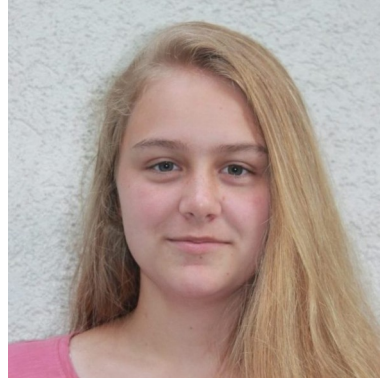
Jonas Förster  
(CoRC package)



Jürgen Pahle



Johanna Daas  
(CoRC workflows)



with help by Frank Bergmann and the rest of the Copasi developer team.

Systems biology

## CoRC: the COPASI R Connector

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J. Förster, F.T. Bergmann and J. Pahle (2021)  
CoRC: the COPASI R Connector.  
*Bioinformatics*, [doi:10.1093/bioinformatics/btab033](https://doi.org/10.1093/bioinformatics/btab033)

## Dynamic Publication Media with the COPASI R Connector (CoRC)

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J. Daas, J.D. Förster and J. Pahle (2022)  
Dynamic Publication Media with the  
COPASI R Connector (CoRC).  
*Mathematical Biosciences*, [doi:10.1016/j.mbs.2022.108822](https://doi.org/10.1016/j.mbs.2022.108822)

# CoRC website

[jpahle.github.io/CoRC](https://jpahle.github.io/CoRC)

- Downloads
- Installation instructions
- Examples
- Reference documentation

```
pip install copasi-basico
```

# basico: Python API for COPASI

You can load either COPASI, or SBML files directly using the `load_model()` command:

```
>>> load_model('brusselator.cps')
```

You can also load a model by providing

```
>>> load_model('https://fairdomhub.org')
```

We also provide a number of examples:

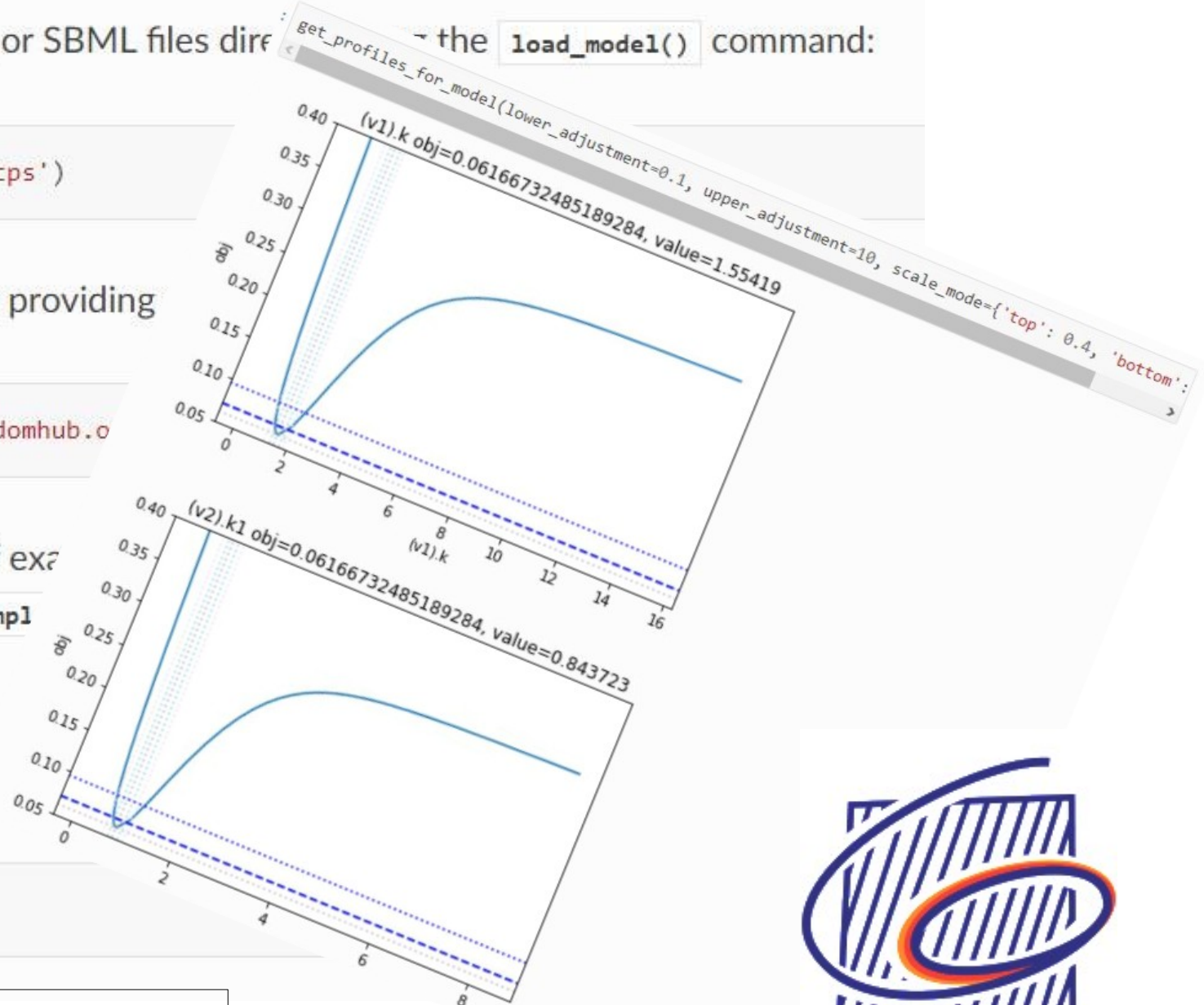
```
get_examples() and load_example()
```

Models from the BioModels database:

```
load_biomodel()
```

```
>>> load_biomodel(206)
```

<https://basico.rtf.d.io>





# Hands-on session...

Files:

<https://lab.pahle.org/ICSB2023-copasi-tutorial>