

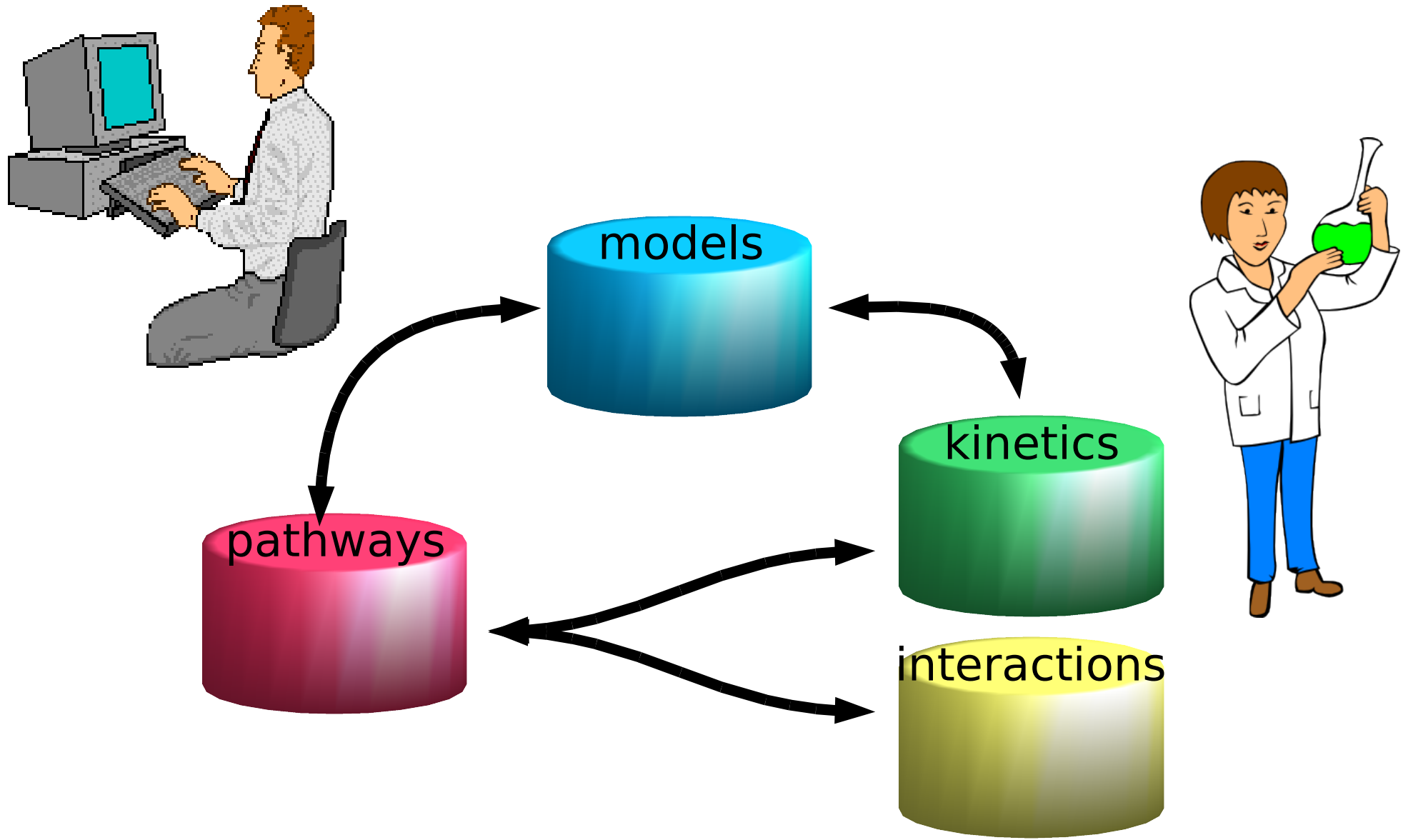
sbgn-level1.tex

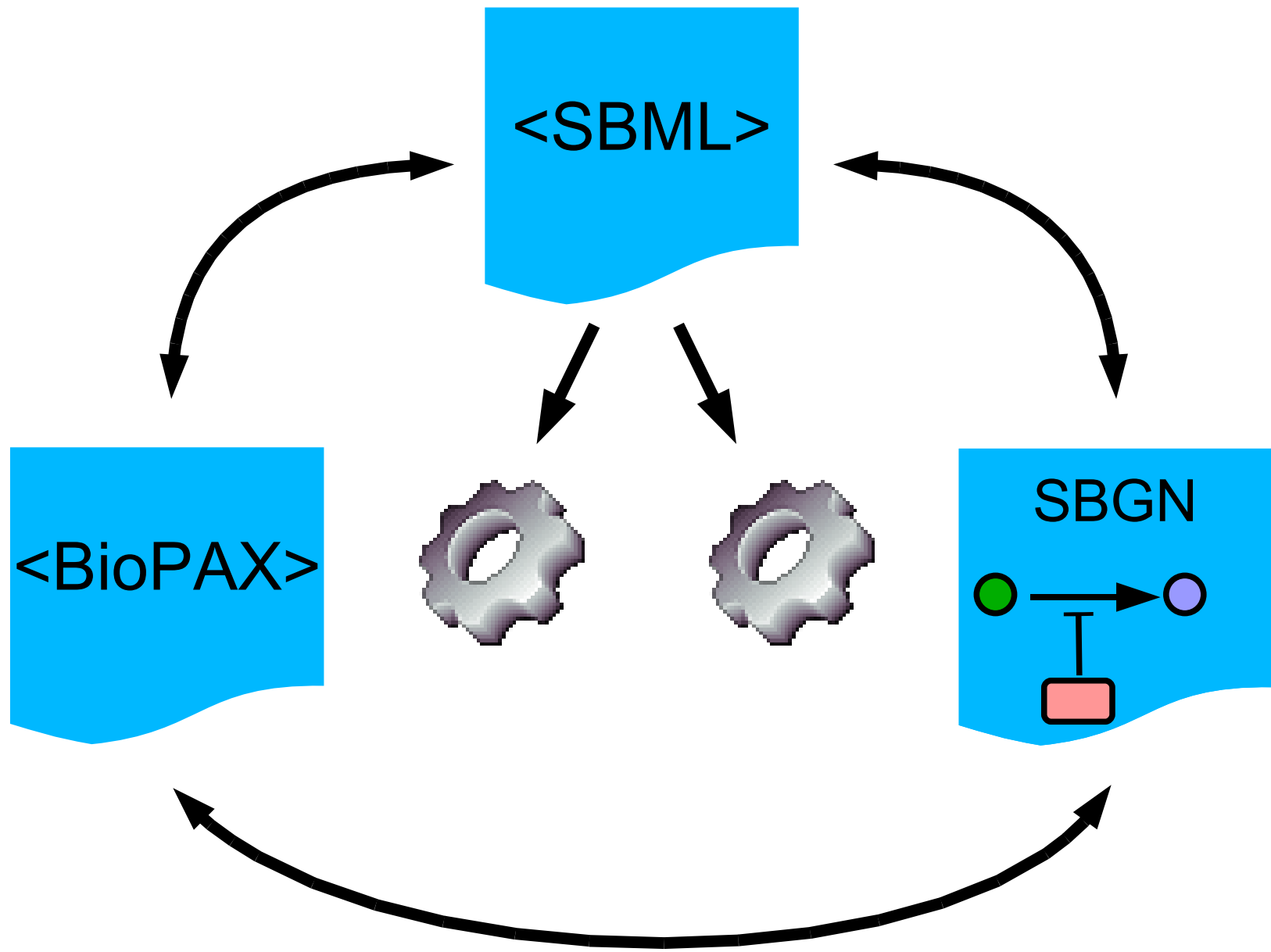
```
\include{sources/rationale}  
\include{sources/languages}  
\include{sources/STglyphs}  
\include{sources/st}  
\include{sources/AFglyphs}  
\include{sources/af}  
\include{sources/ERglyphs}  
\include{sources/er}  
\include{sources/layout}
```

sources/STglyphs.tex

```
\input{unitInformation.tex}  
\input{stateVariable.tex}  
\input{tag.tex}  
...
```

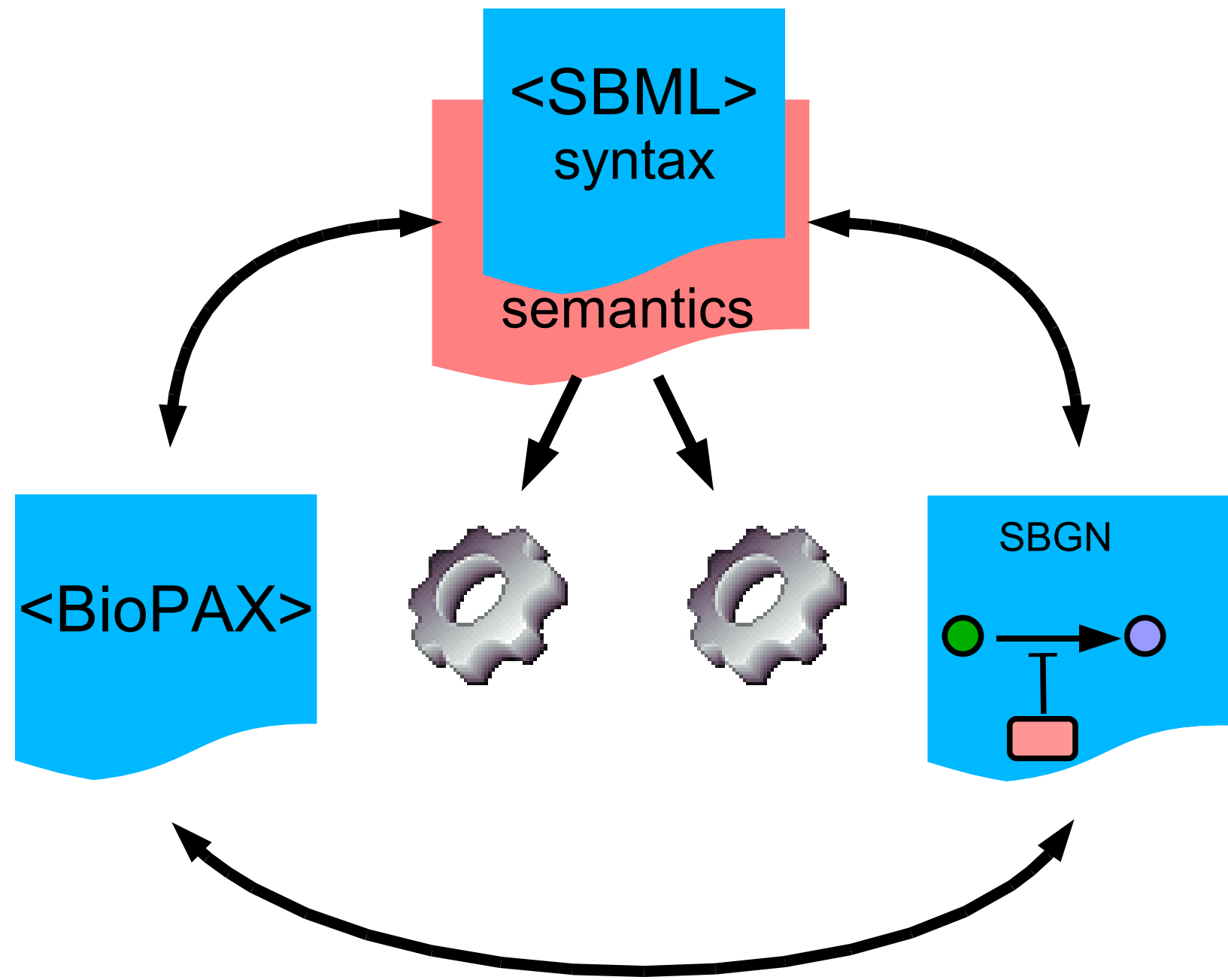
source/tag.tex





- Is a species a macromolecule, a simple chemical ...?
- Is a modifier a stimulator or an inhibitor?
- Is a reaction a catalysis, a dissociation ...?
- May-I use this model with a discrete simulator?
- Should-I get an oscillation with this model?
- How could-I “merge” models A and B and obtain something meaningful?





A community aiming to improve model annotation, interpretation, exchange and re-use. Not restricted to SBML (cf. CellML).



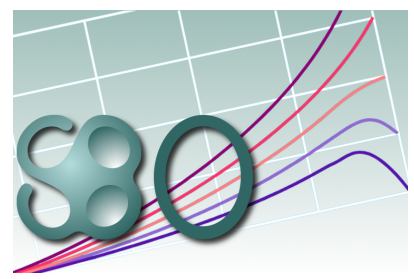
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Current projects:

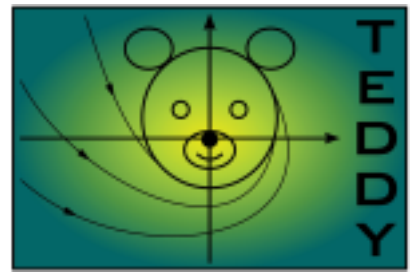
- A checklist for model annotation: MIRIAM (part of MIBBI)
- A set of relationships to link models and data
- An ontology to precise the semantics of models: SBO (part of OBO)
- A database of published models of biological interest: BioModels Database (now the reference resource for > 200 journals)



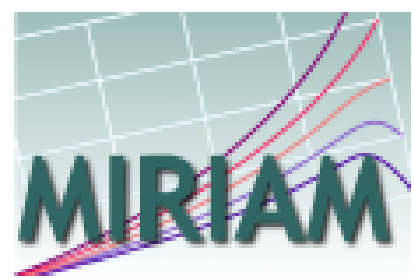
model semantics: Additional info on the model structure and meaning



behaviour semantics: Additional info on the model results



biological semantics: Additional info on the links between model and reality



simulation semantics: Additional info on the simulation process

