



COSBI



**SANOFI**

Global QSP meeting

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# Quantitative System Pharmacology compiler collection (QSP<sup>cc</sup>)

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# Challenges in Model-based drug development

- A recognized and frequent choice
- Predictions\*
- Helps policy making

1. Programming platforms used by different people / groups



2. Computational power demands

- Intractable optimization problems



Source: <https://www.webart.com/>

3. Licensing schemes for commercial platforms

- Difficult to scale at cluster level (license on each node)



Source: <https://www.spkaa.com/>

4. Non-standard dialects different from the main language

- Considerable manual effort pre- & post- run

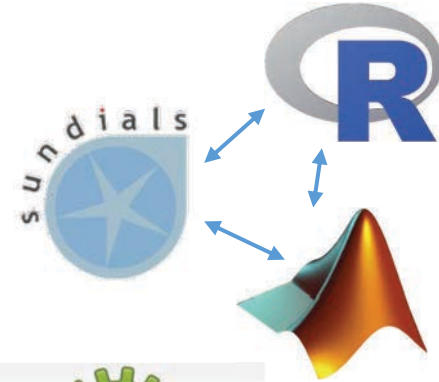


Source: <https://www.audiencebloom.com/>

# QSPcc can save your day

- A recognized and frequent choice
- Predictions\*
- Helps policy making

- ✓ Extensible number of supported languages
- ✓ Automatically translate heavy computations into highly efficient machine-code
- ✓ Execute in standalone mode and on clusters without relying anymore on MATLAB
- ✓ Works out-of-the-box: Integrate in MATLAB optimization code using the automatically generated MEX bindings

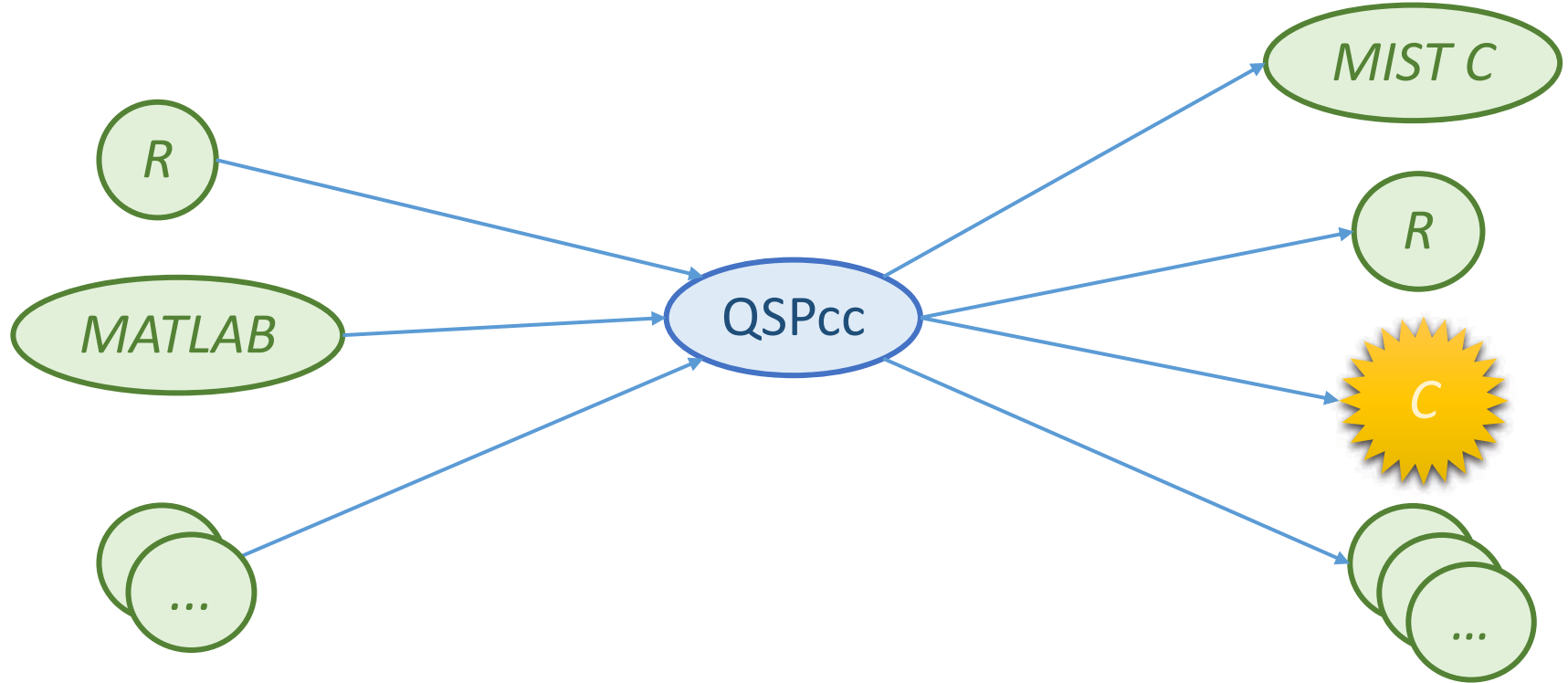


Source: <https://www.spkaa.com/>



Source: <https://www.audiencebloom.com/>

## QSPcc can save your day (cont.)

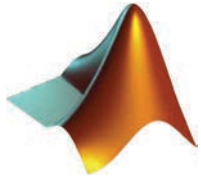


- Sundials v2.7, v3.x ... v5
- Intel Math Kernel Library (MKL): **on user's choice**
- .mat files loading; optimized load as csv
- automatic MEX interface generation

Tested on Linux, MACOS (**Windows ongoing**)



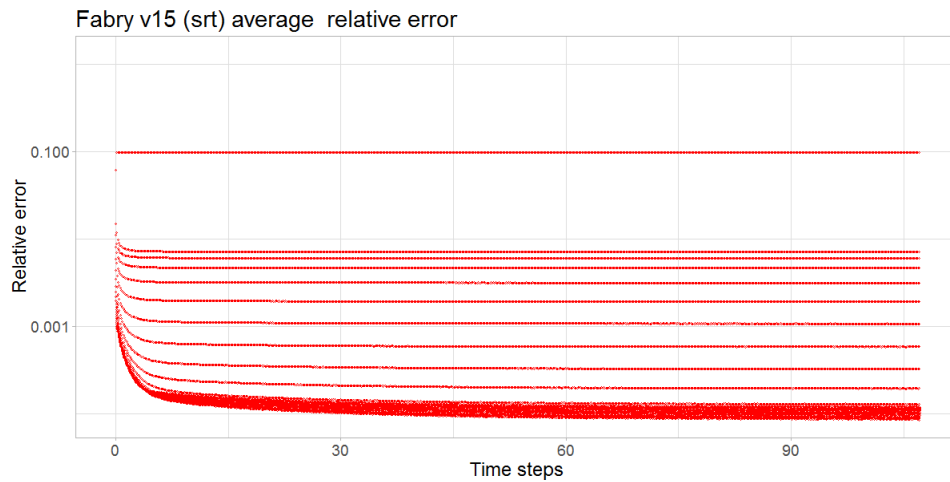
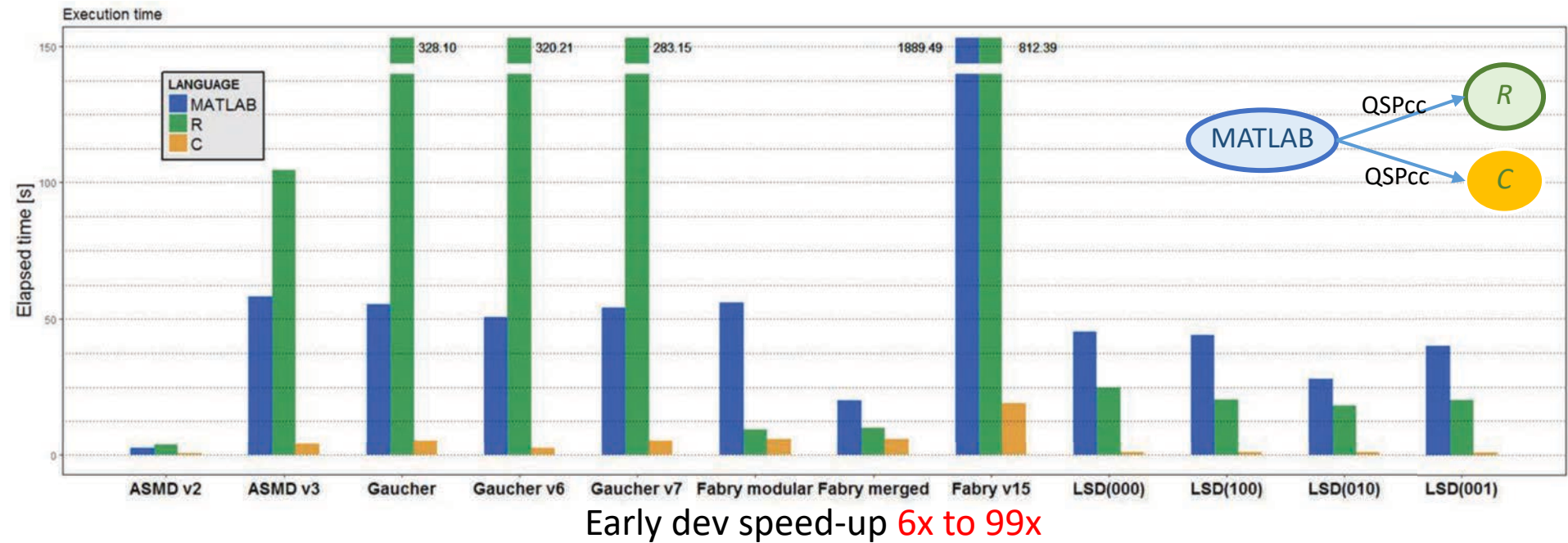
# Semantic equivalence



```
1  
2 for i = 1:numel(a)  
3     b = f(a,b+i)  
4 end  
5  
6 b = f(a,b+i)
```

```
/*  
 * for i = 1:numel(a)  
 *     b = f(a,b+i)  
 * end at line 4  
 */  
for(int i=1;i<=max(a.dim1, a.dim2);i=i+1)  
{  
    /*  
     * b = f(a,b+i) at line 6  
     */  
    b = f(a, (double )b + (double )i);  
}
```

# Performances

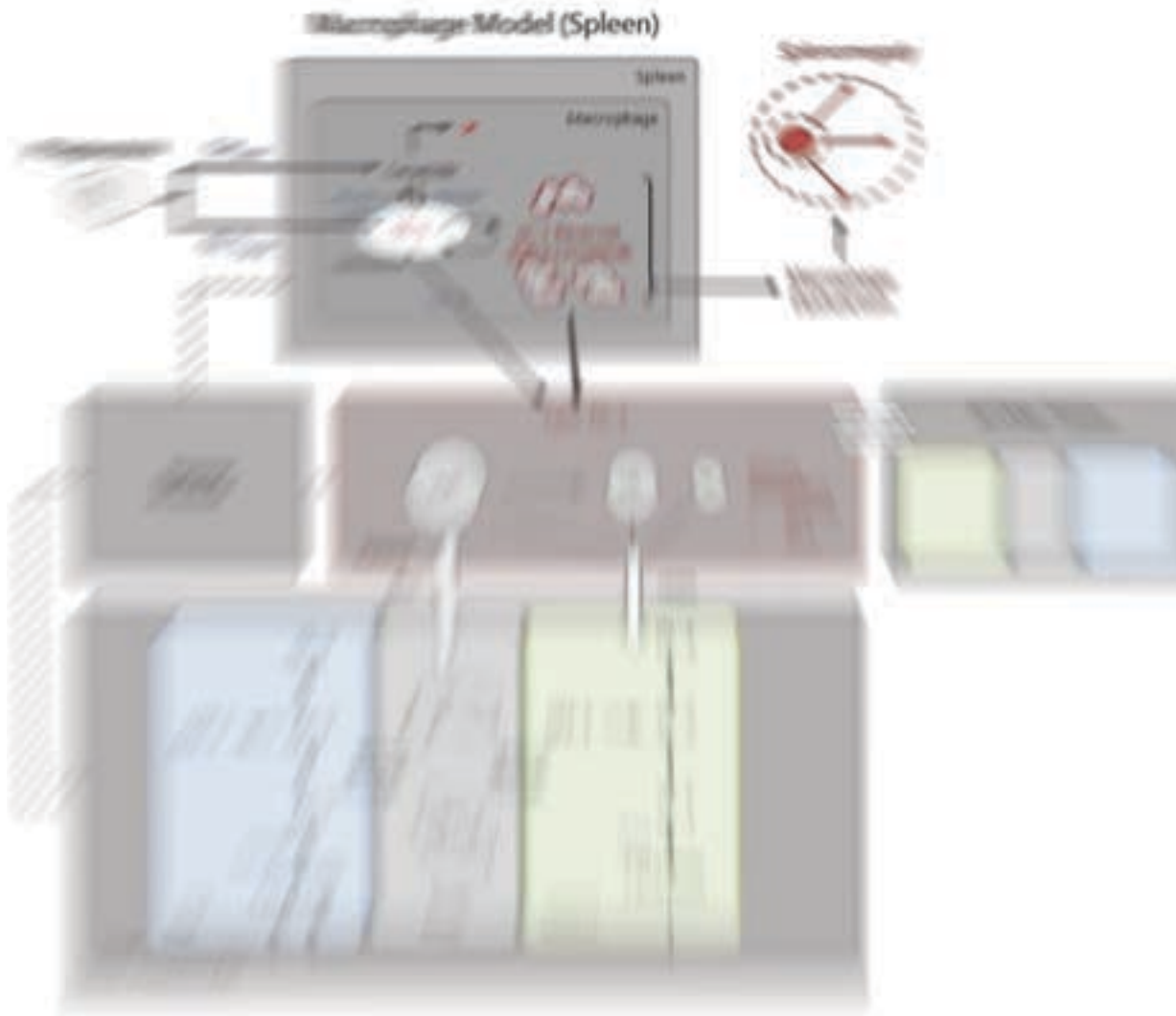


All Sanofi models have excellent simulated equivalences.





# The GD1 model



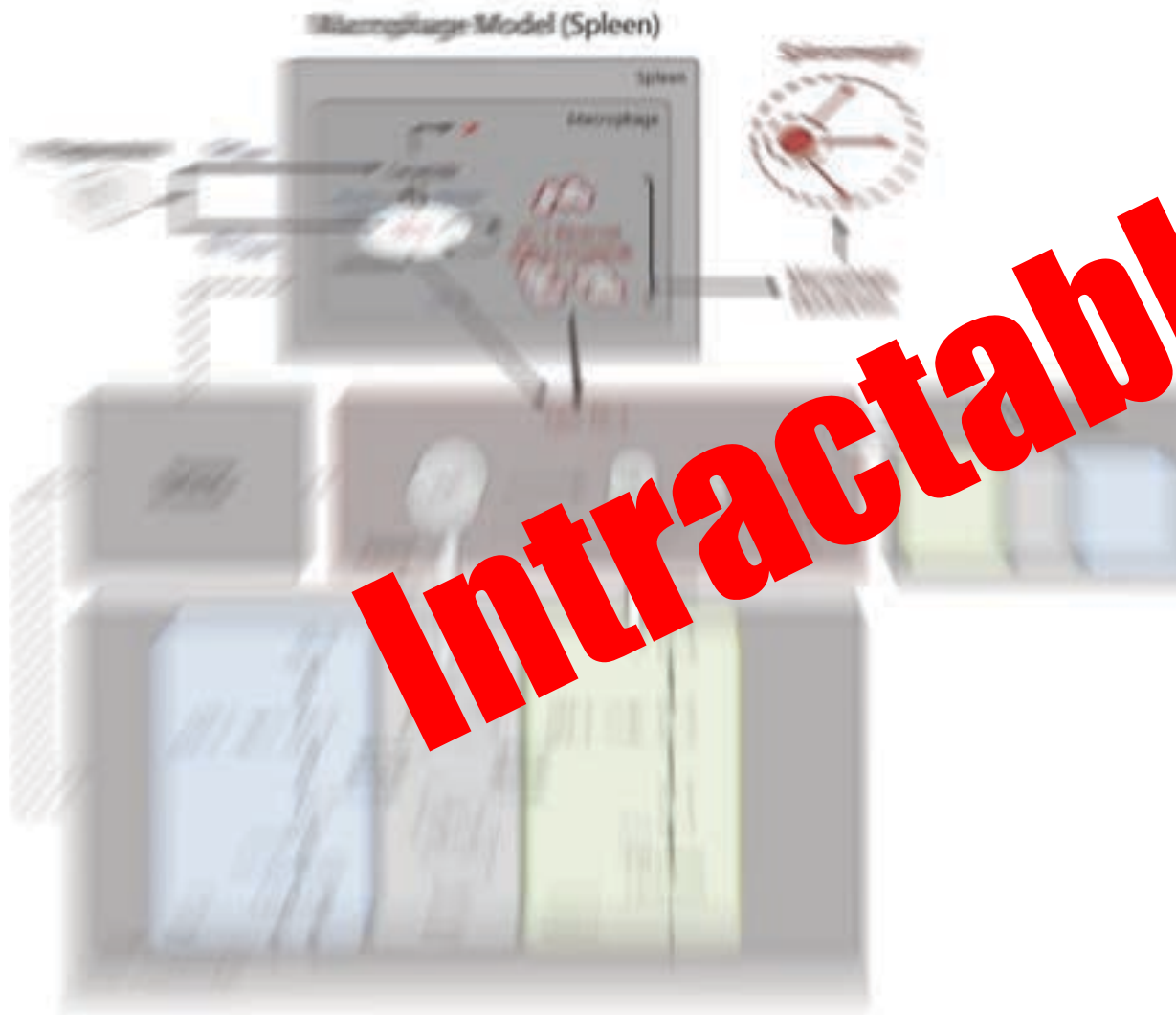
The complete model:  
82 differential equations  
175 parameters

For the model calibrations  
we fit 23 parameters using  
5 observed variables

We use an evolutionary  
algorithm for which about  
10000 simulations must  
be done for each patient



# The GD1 model



The complete model:  
2 differential equations  
7 parameters

For the model calibrations  
we fit 23 parameters using  
5 observed variables

We use an evolutionary  
algorithm for which about  
10000 simulations must  
be done for each patient





# The GD3 model

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The complete model:  
**180 differential equations**  
**~ 230 parameters**

For the model calibrations  
we **fit ~30 parameters**  
using 5 observed variables

We use an evolutionary  
algorithm for which about  
**10000 simulations** must  
be done for each patient



# The GD3 model

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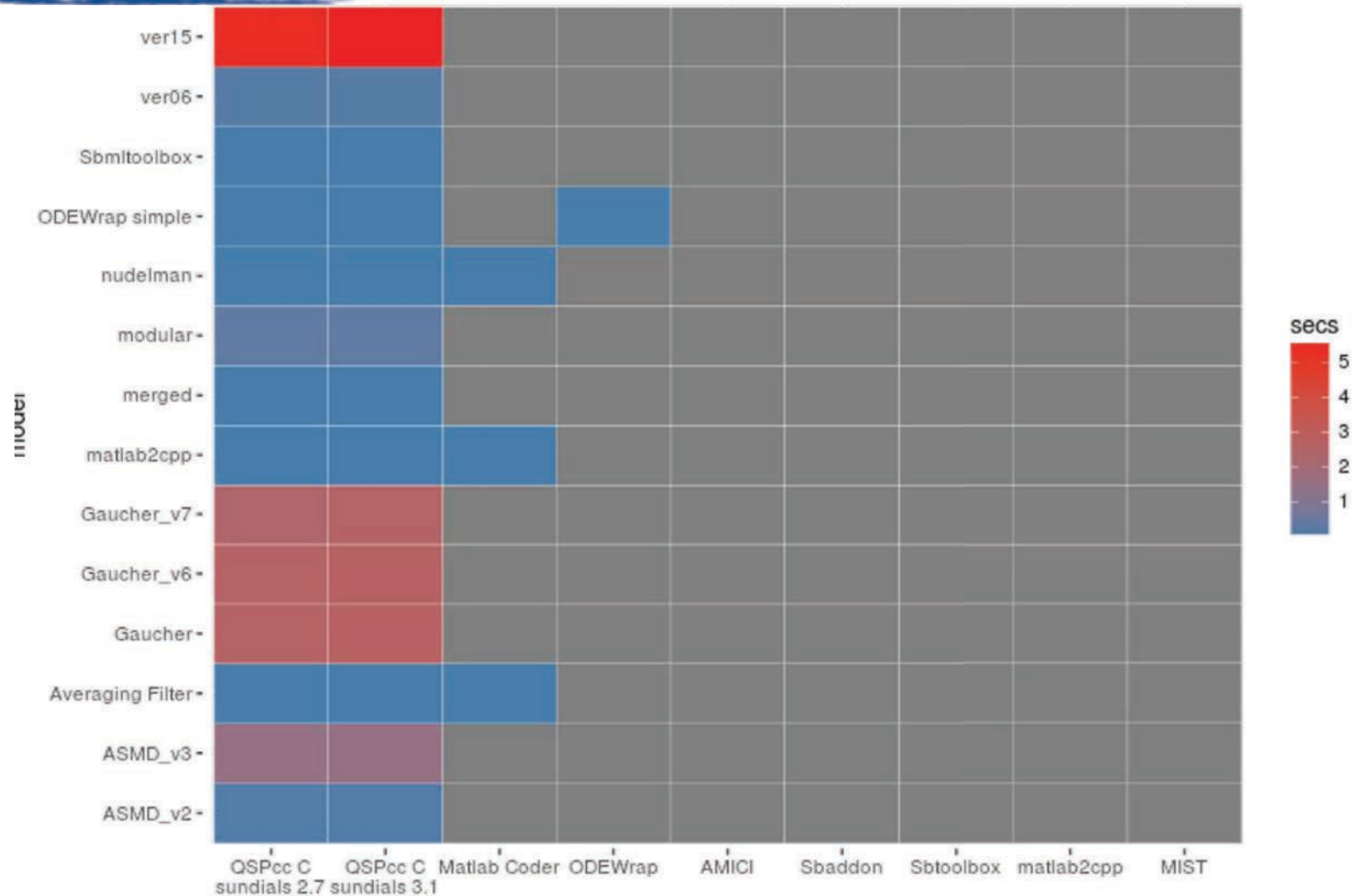
The complete model:  
119 differential equations  
500 parameters

For the model calibrations  
we fit ~30 parameters  
using 5 observed variables

We use an evolutionary  
algorithm for which about  
10000 simulations must  
be done for each patient



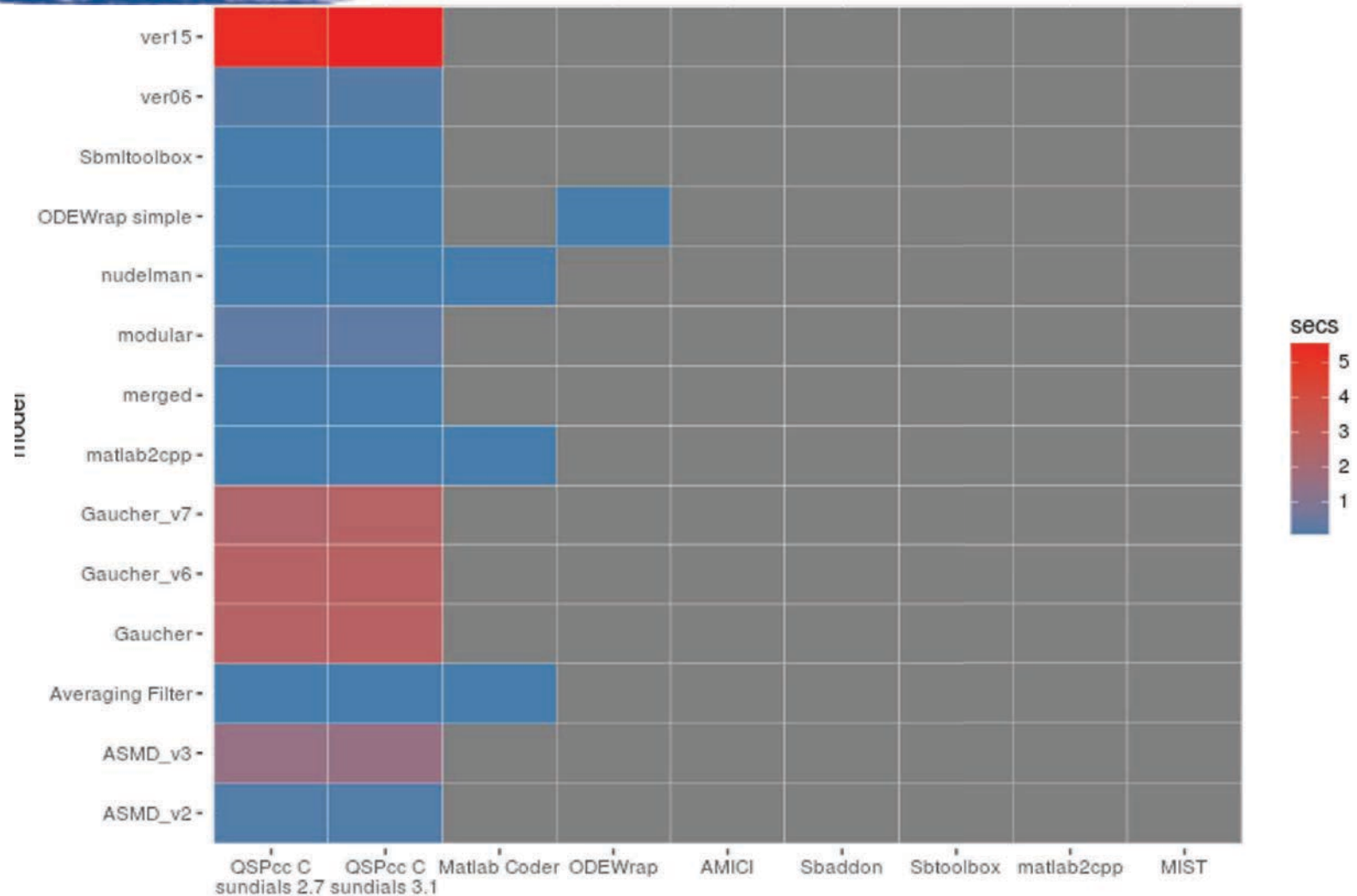
# Competitors



- AMICI (custom models, doesn't work on pure matlab)
- SBaddon (custom models, doesn't work on pure matlab)
- SBToolbox (custom models, doesn't work on pure matlab)
- matlab2cpp (requires manual intervention)
- MIST (custom models, requires manual intervention)



# Competitors (?)



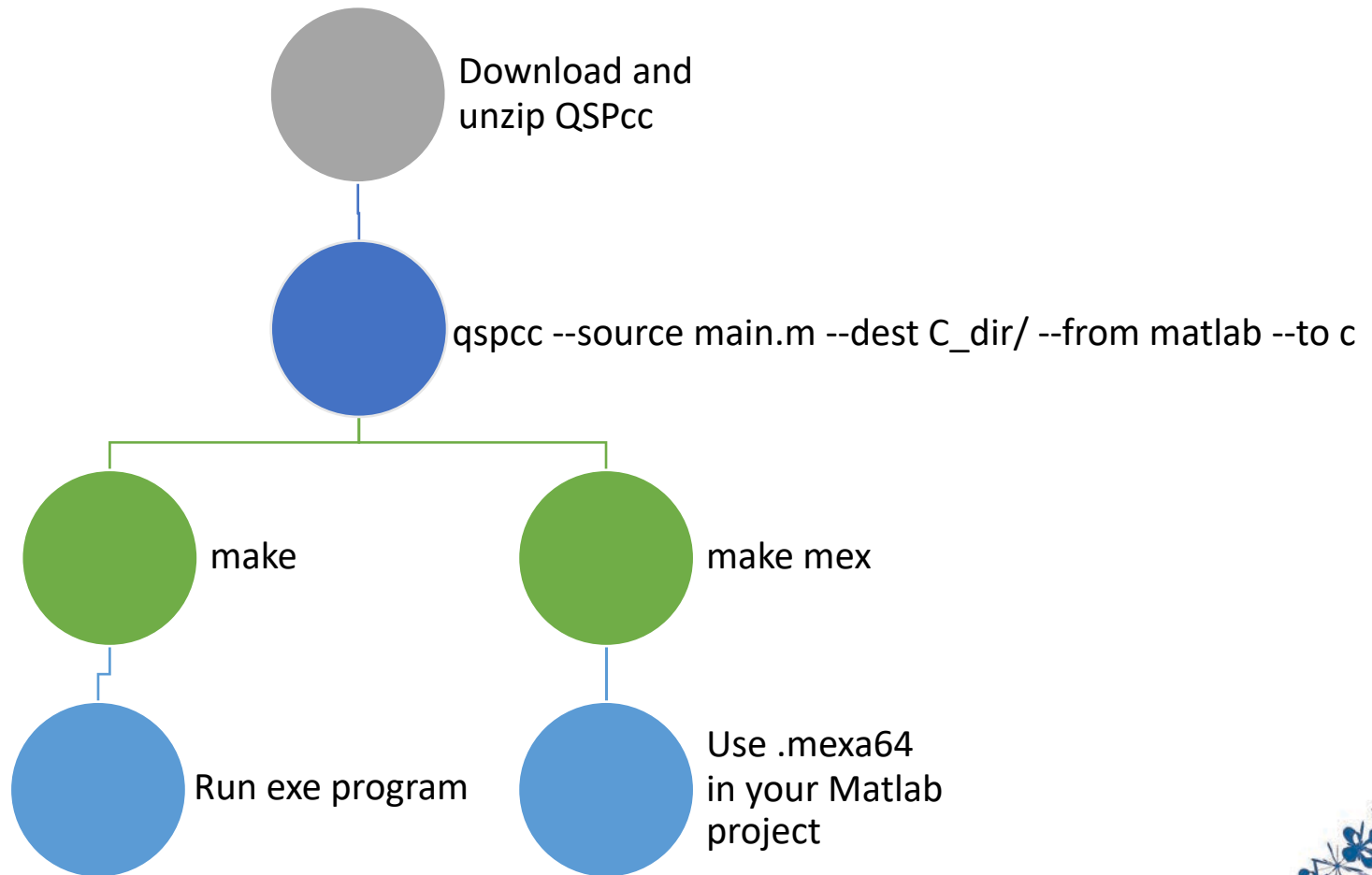
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Learn non-standard dialects  
different from the main language



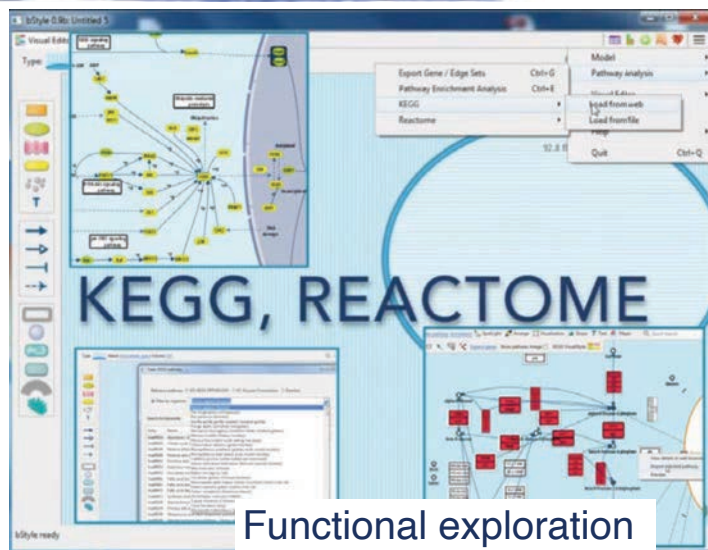
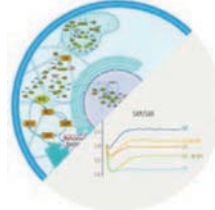
# How-To

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# QSPcc and visual modeling



Functional exploration  
and pathways

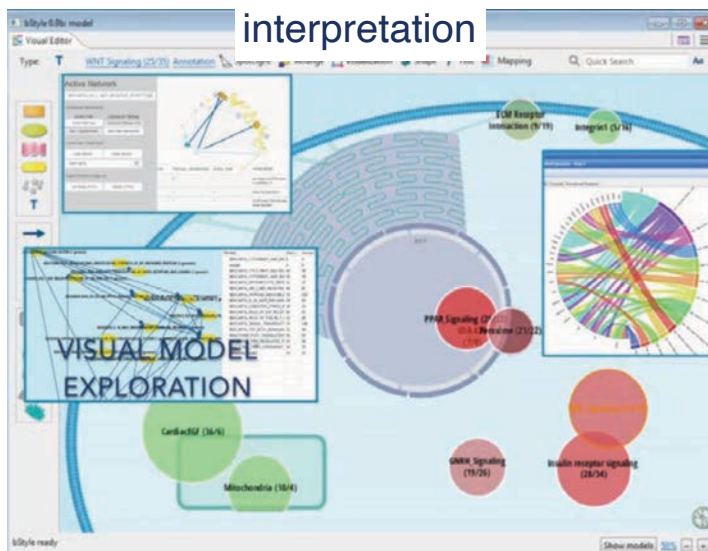


advanced yet intuitive  
visual modeling

bStyle video

<https://youtu.be/OYRrcByM2wI>

interactive  
interpretation



user-centered  
simulations and optimizations

