

Development of a demonstrator for web based community-resource on mathematical models in the field of plant protection



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Introduction

Mathematical models on properties and behavior of harmful organisms in the food chain are an increasingly important discipline in agriculture and food industry.

As a consequence, there are an increasing number of models published in the scientific literature which might be useful for business operators and risk assessors.

However there is a lack of international harmonized standards on model annotation and model formats, which would be necessary to set up efficient tools supporting broad model application and information exchange.

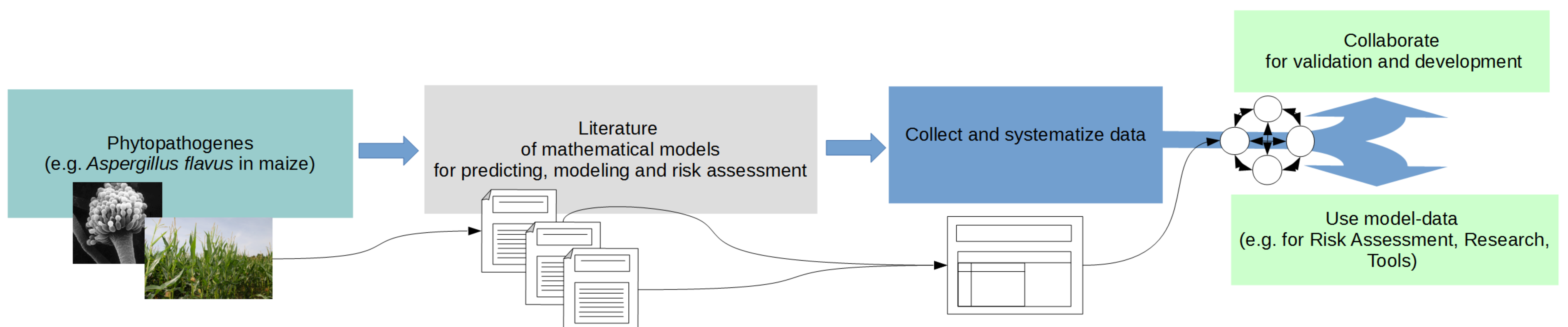
Fortunately, there are scientific disciplines where standards for model description are in place for years, specifically in the domain of Systems Biology, so there is the opportunity to transfer and adopt this knowledge into the area of plant protection.

Objectives

This work aimed at the development of an annotation scheme using domain-specific metadata that can serve as the basis for a web-based community-driven model repository.

This community resource currently contains models on the Aflatoxin producing fungus *Aspergillus flavus* in maize, as these models have a high relevance to food safety.

Specifically models describing biological processes like fungus growth and inactivation, Aflatoxin secretion as well as dose-response and carry-over models are included. Furthermore some phenological models for maize have been included.



Method to develop metadata-standard and the demonstrator

1. Categorization of mathematical models to phytopathogenes
2. Accumulation of literature on *Aspergillus flavus* in maize and Aflatoxin
3. Development of a classification scheme for the example models based on SBML
4. Choosing web-based resources for the demonstrator
5. Implement and test the demonstrator solution

Web-based resources for a community-driven web repository for phytopathogene models

Google Drive:

Cloud-based storage to save the data



Google Sheets

Spreadsheet-solution for the community-driven database



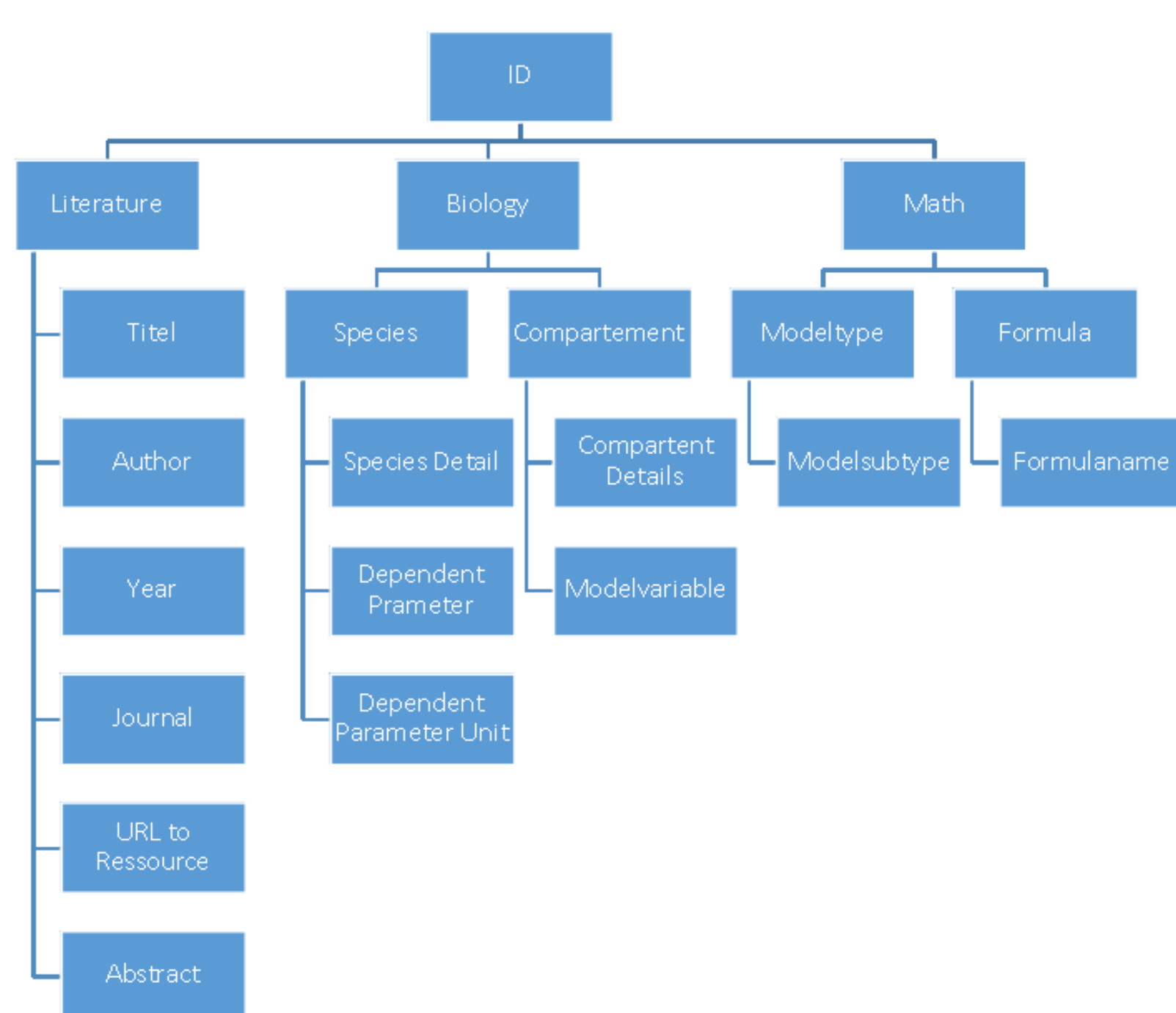
Google Sites

Web-based tool to build the website (PhyM-Database)



Results

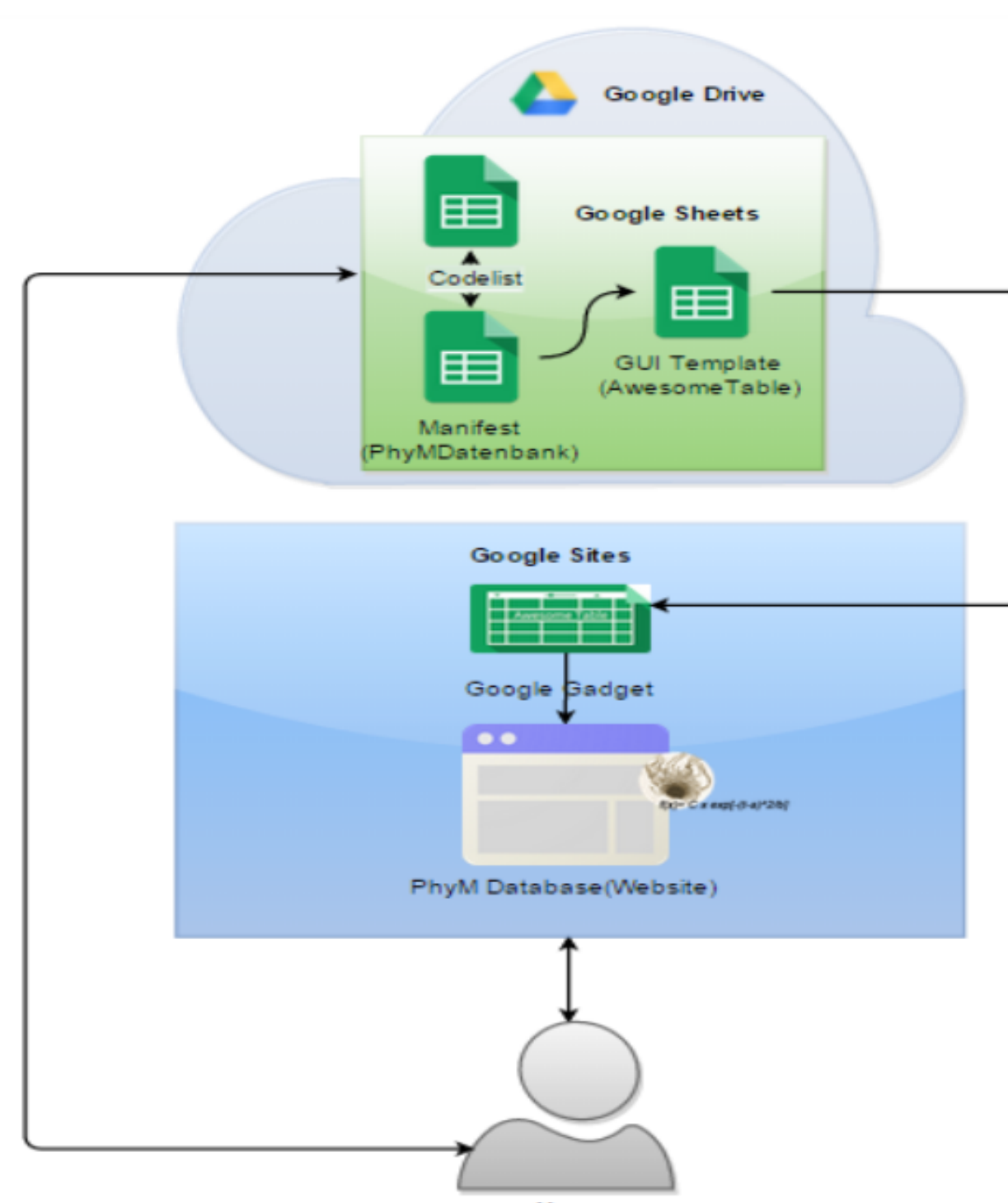
Systematic to collect model-metadata



System to collect phytopathogene metadata from literature is based on SBML (Systems Biological Markup Language) and modified different parts of it, to collect them in a minimal-standard.

The Systematic is variable and can be use for different domain specific datasets.

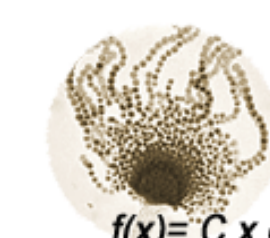
Framework



Google Drive is the storage for the Google Sheets data.

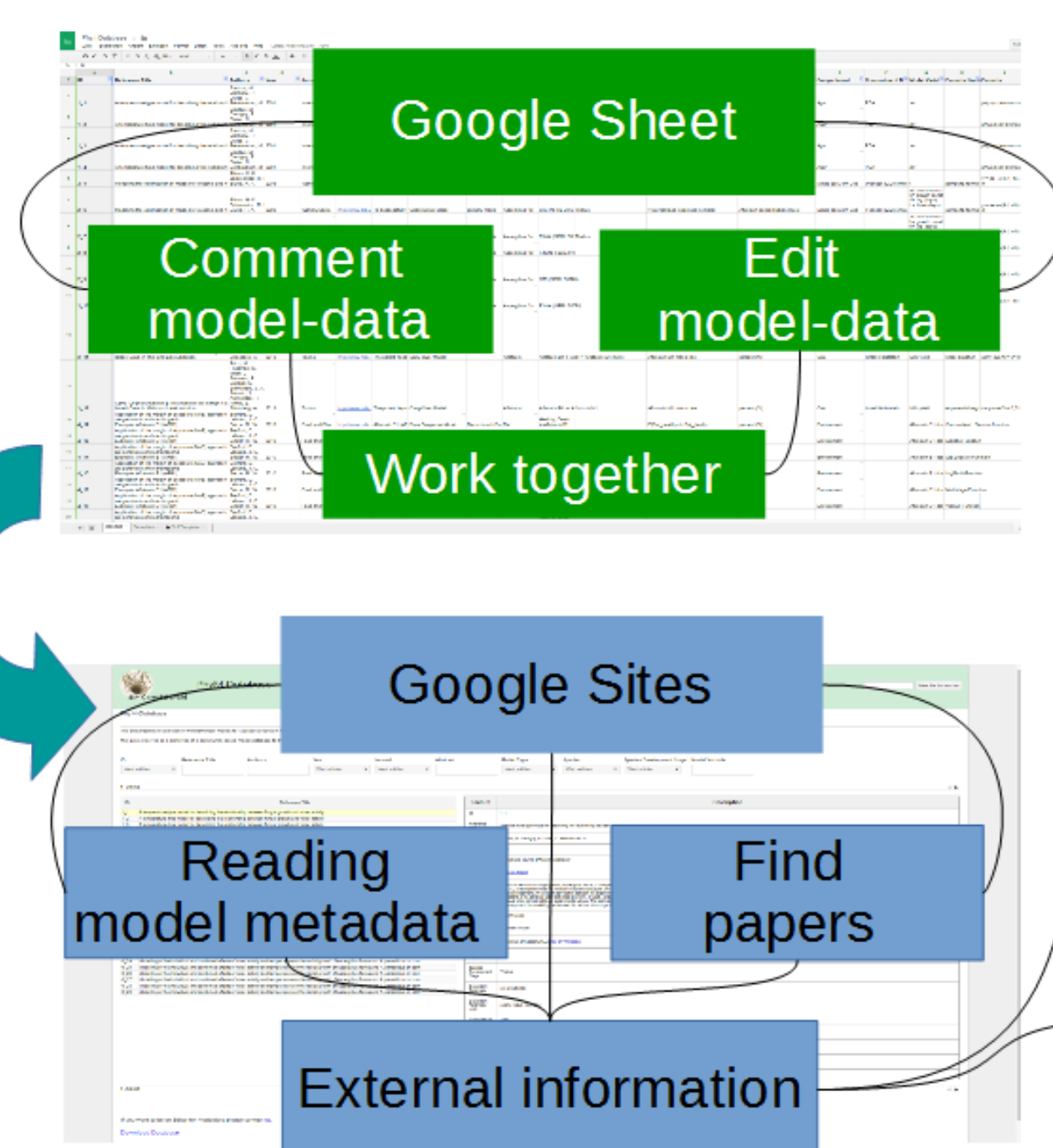
Google Sheet is a spreadsheets solution, the data for editing new models and the bridge to visualize the data on the website are there.

Google Sites use a template (Awesome-Table) to visualize the Data and bring it in a comfortable Format



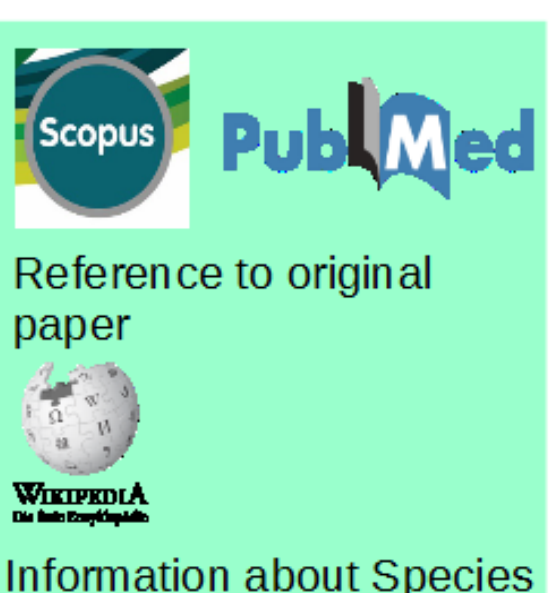
PhyM-Database

$$f(x) = C \times \exp[-(t-a)^2/b]$$



The PhyM-Database (Phytopathogene Model-Database) is the technical infrastructure of the community driven web-repository

It use Google Sheets as database (editing, commenting) and Google Sites to present the data.



Conclusions

By implementation of the model repository it could be demonstrated that the proposed annotation scheme is applicable for the description of models on plant pathogens.

A broad adoption of such annotation scheme within the scientific domain would thus promote communication and dissemination of mathematical models to interested end users.

Further this scheme supports modelers in their attempts to provide quality assured model descriptions. Even software developers will benefit from the proposed standard as this will help to establish harmonized interfaces between different software-tools. It has also been demonstrated that a community-driven model repository can easily be implemented with existing and freely available software resources.