

Physiologically-based demographic modelling

A compositional modelling approach

George Simmons, IDEMS

Today's structure

IDEMS

- IDEMS (Innovation and Development in Education and Mathematical Sciences) is a UK-based not for profit
- We employ a diverse range of mathematical scientists, anthropologists and social impact scientists in Europe and Africa
- We deliver education, capacity building and research methods support in socially impactful projects with a focus on low-resource environments
- We work across public health, climate, agroecology and education



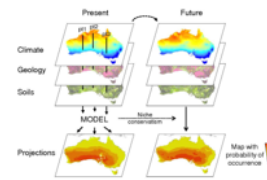
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PBDH

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Invasive species modelling

- Classically modelled using species distribution models (SDMs)
- SDMs are correlative models, predicting invasive species occurrence from climatic and environmental variables
- They are derived from species occurrence data and climatic/environmental observations
- Reflective models can be constructed with fewer than 10 variables



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Agroecosystem modelling

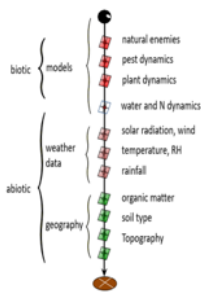
- Focuses on the interactions between insects, plants and environment
- The goal is to optimise yield, profit per harvest or farming sustainability (soil or ecosystem health)
- Classic models are qualitative, first-order, or are climate-independent
- Even with good approaches, tertiary effects are hard to model



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PBDM

- Physiologically-based demographic models (PBDMs) consist of mechanistic population dynamics components, driven by climate and environmental data
- They do not require observational data to parametrise, so maintain predictive capability in new environments and regions
- They strike a balance between fully mechanistic modelling and relatively small parametrisation sets of correlative modelling
- They allow layers of intricacy to be built in depending on knowledge and data availability

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Our implementation

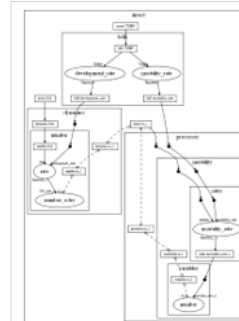
- IDEMS and CASAS Global are developing the python package **psymple** (Python **S**YMBOLic PopuLation Ecology)
- Goal is to create an environment for diagrammatic modelling of PBDM features and wider complex dynamic systems
- Inspired by the category-theoretic approach used in Topos' *AlgebraicDynamics.jl*



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Physiologically-based demographic modelling

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Capturing PBDM

- Every organism or sub-organism of a population is captured as a **functional population** with:
 - Bidermographic functions (rates for growth, development, reproduction, predation, etc.)
 - Population dynamics (age and stage structure models)
 - Processes (variable or resource creation, e.g. mortality, photosynthesis)
 - Metabolic pool (supply-demand resource allocation)

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CASAS Global

- CASAS (**Center for Analysis of Sustainable Agroecological Systems**) is a nonprofit organisation of collaborating scientists founded by Prof. Andrew Gutierrez (UC Berkeley)
- Their mission is dedicated to analysing issues in diverse crops, rangelands and medical and veterinary vectors to benefit populations and governments in developing countries worldwide



Collaboration aims

- Produce an open-source codebase implementing a general, reusable and modular of CASAS Global's physiologically-based demographic modelling (PBDM) framework
- Build an accessible platform of tools for general users to build, parametrise and simulate PBDMs
- Allow for third-party solutions and expertise to integrate with the platform
- Build scalability through internship programmes, education, training, and outreach schemes
- Maximise the impact of these modelling ideas by building the right solutions, interfaces and integrations for stakeholders

What we're currently doing

Software

- A python-based, open-source compositional modelling package implementing population dynamics and functional responses
- An open-source, general and reusable PBDM implementation

Scaling & outreach

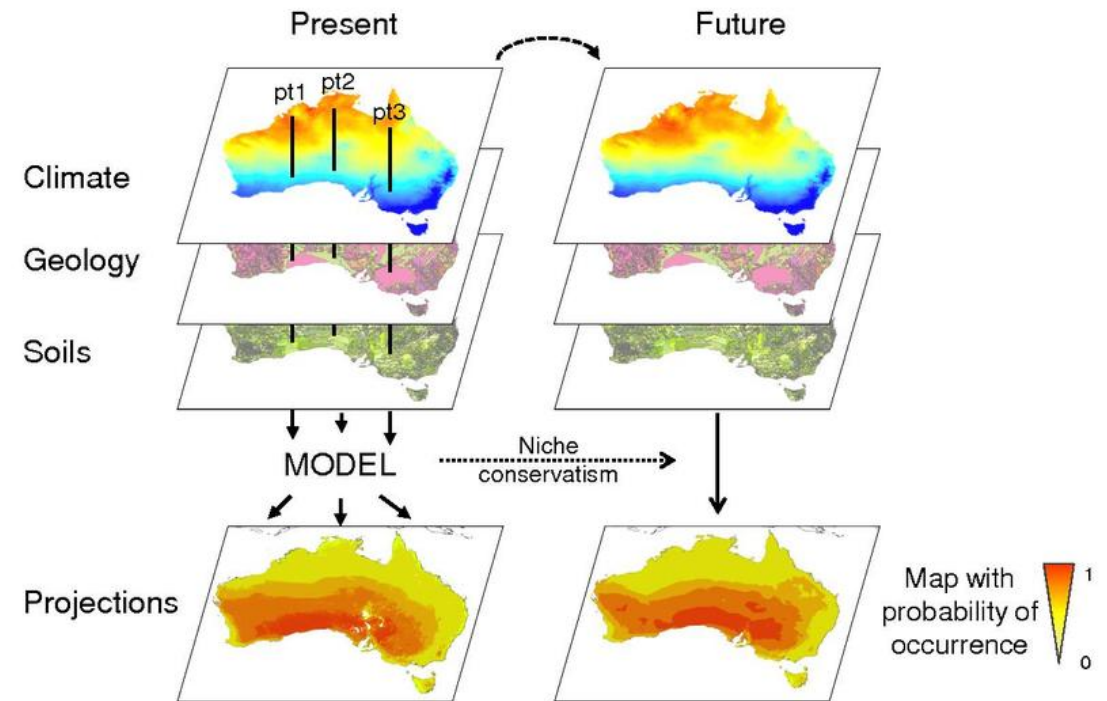
- An internship programme in Kenya to teach PBDM, driving local knowledge and creating collaborations
- Support for locally-relevant Master's projects around insect and crop modelling

Accessibility & impact

- Building for interoperability, i.e. allowing different crop modelling systems or climate data sources to integrate with the platform
- An emphasis on building the right solutions for different users (academic, government, local/regional policy, industry)

Invasive species modelling

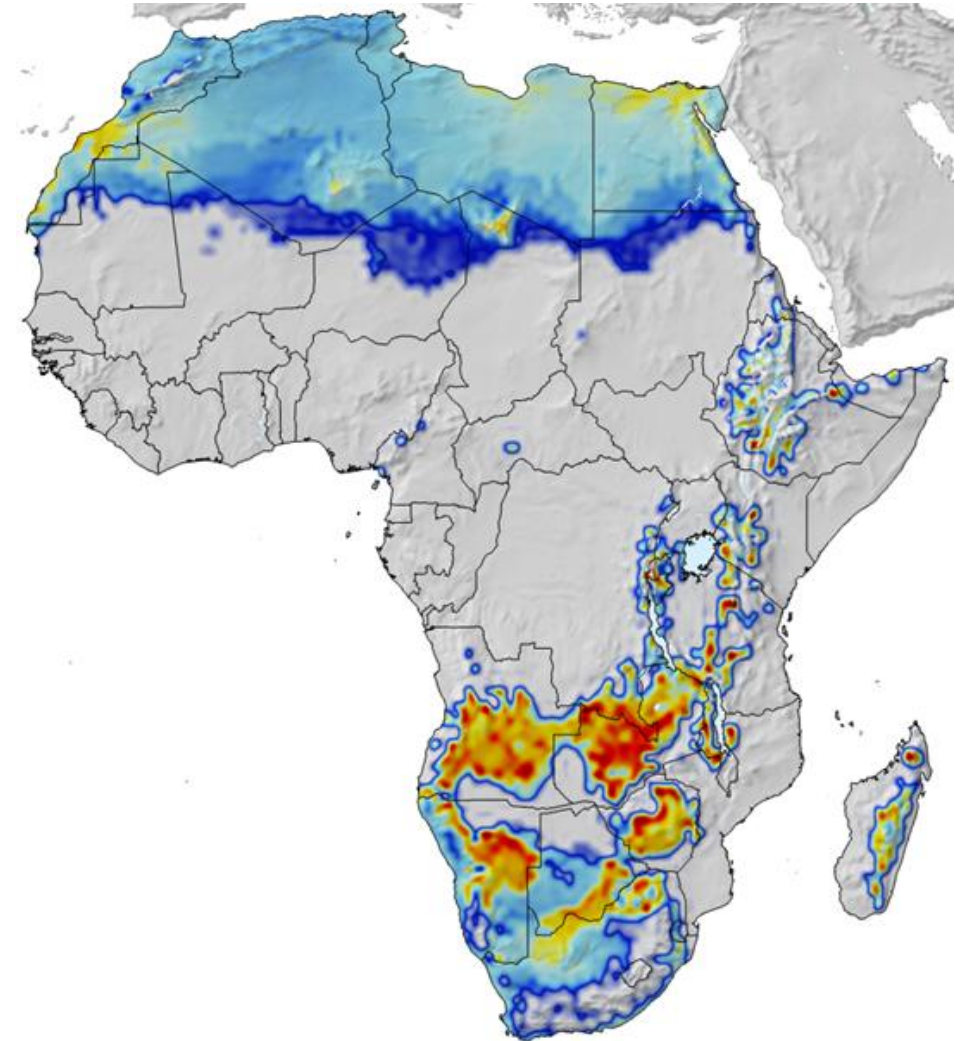
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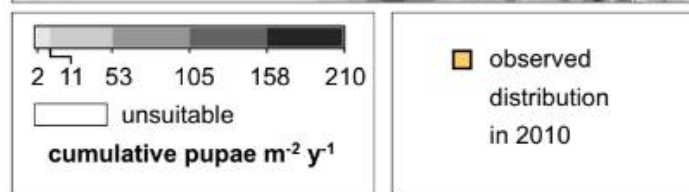
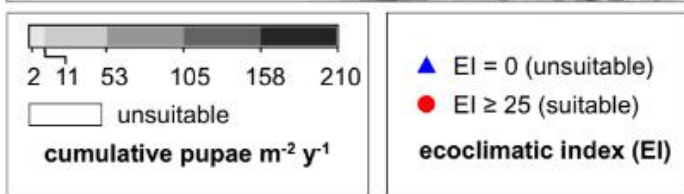
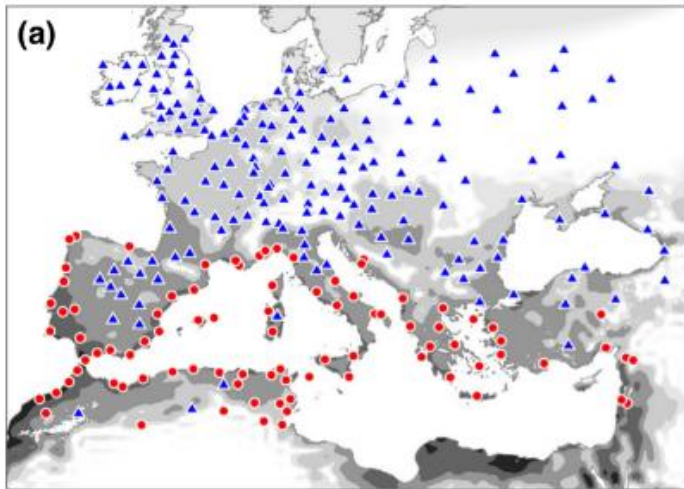


Regional modelling

Possible questions:

- What potential invasive species have to thrive in different regions
- Predicting disease vectors, agricultural impacts and economic costs
- How to use regional policy to have the biggest impact potential
- How these factors change with climate change



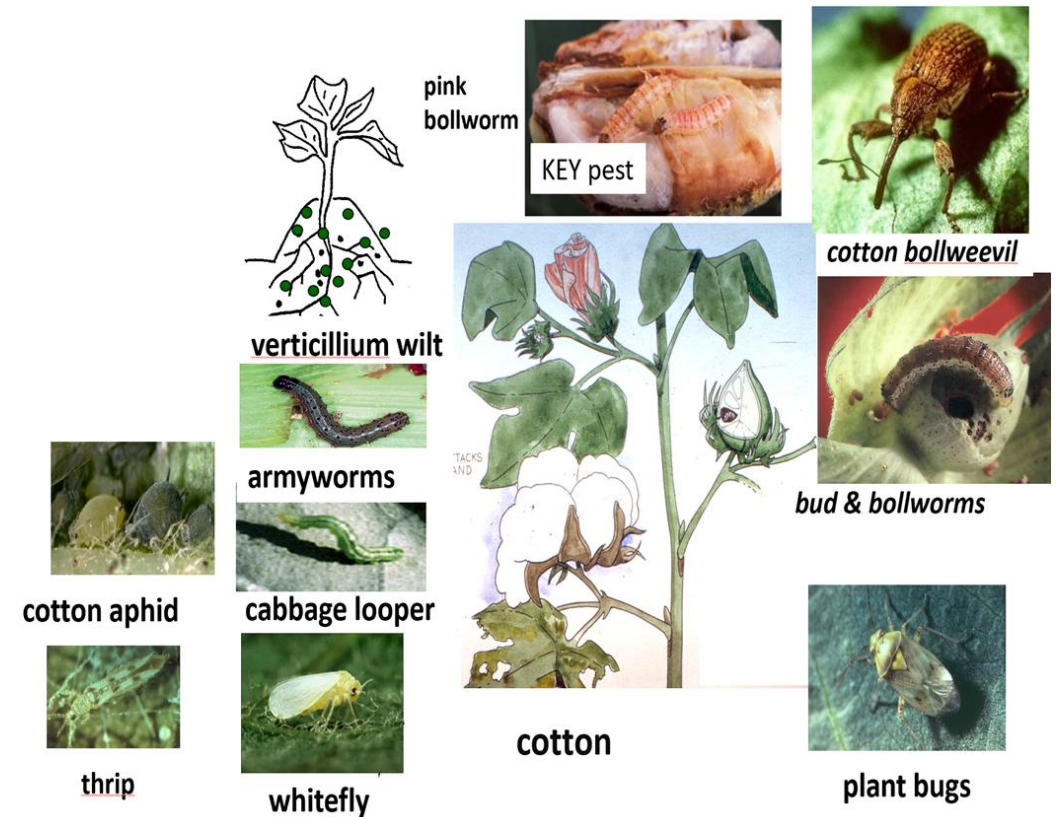


Case study: tomato pinworm (part 1)

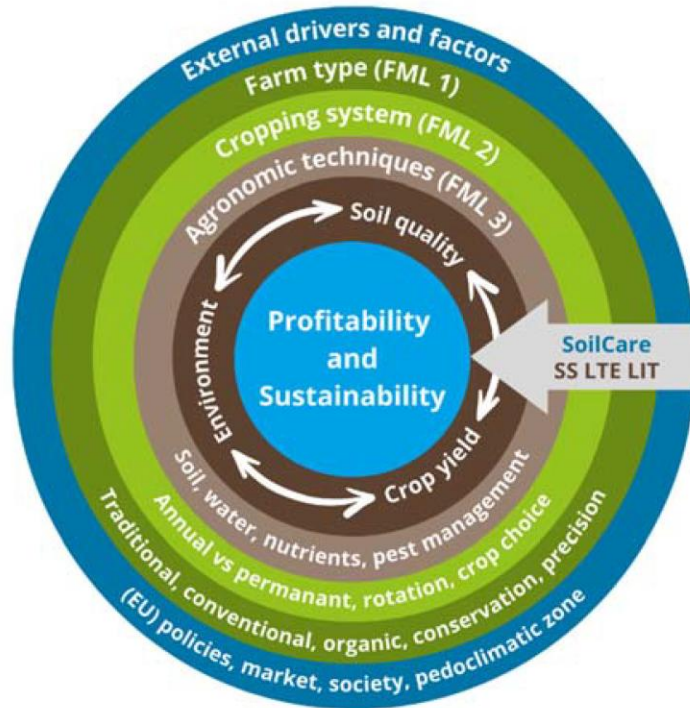
- Correlative models predicted tomato pinworm distribution in Europe in 2010 to be limited to Mediterranean boundary
- Based on occurrence data from South America
- Observations in 2010 were recorded around the Black Sea, Baltics, France and UK

Agroecosystem modelling

- Focuses on the interactions between insects, plants and environment
- The goal is to optimise yield, profit per harvest or farming sustainability (soil or ecosystem health)
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Agronomic modelling



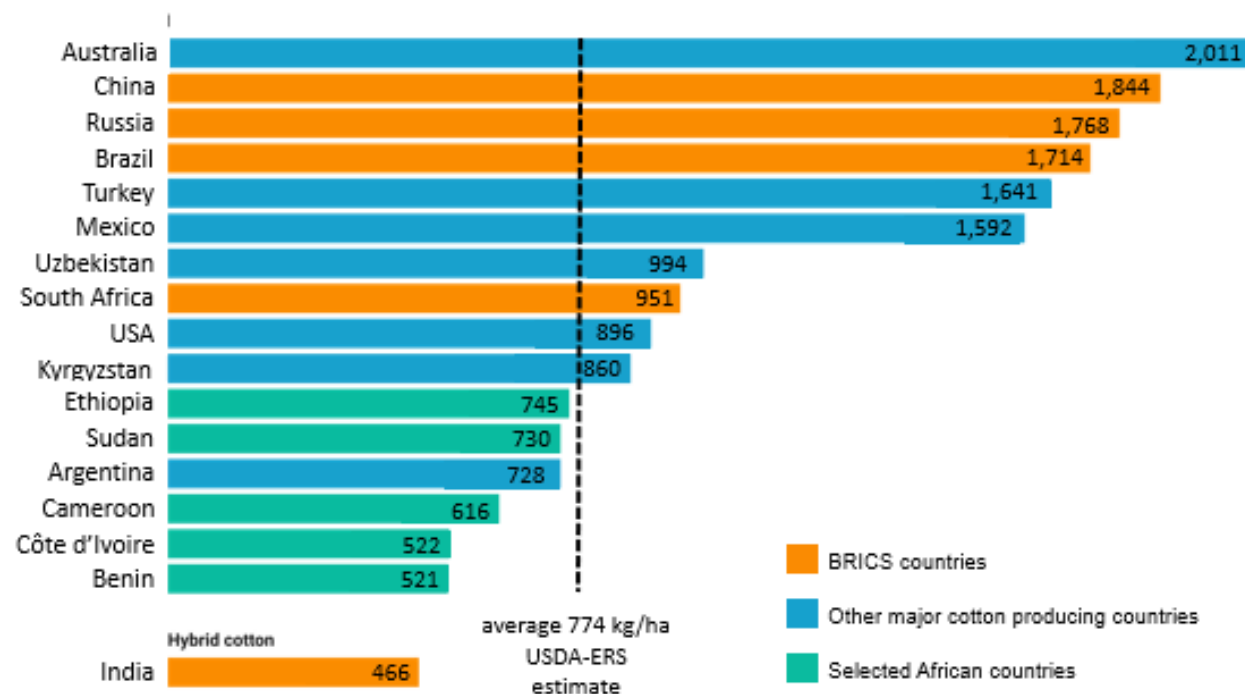
Possible questions:

- Optimal planting methods and farming techniques
- How to control pests (biocontrol, traps, pesticides, crop hygiene)
- Understand soil health or wider environmental impacts
- The impacts of weather and climate change
- The impact of government regulations or subsidies

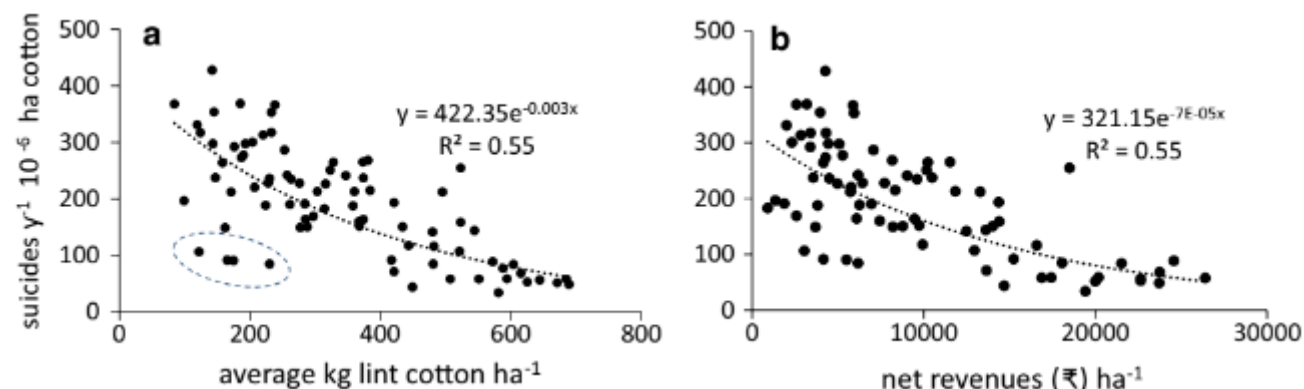
Case study: cotton in India (part 1)

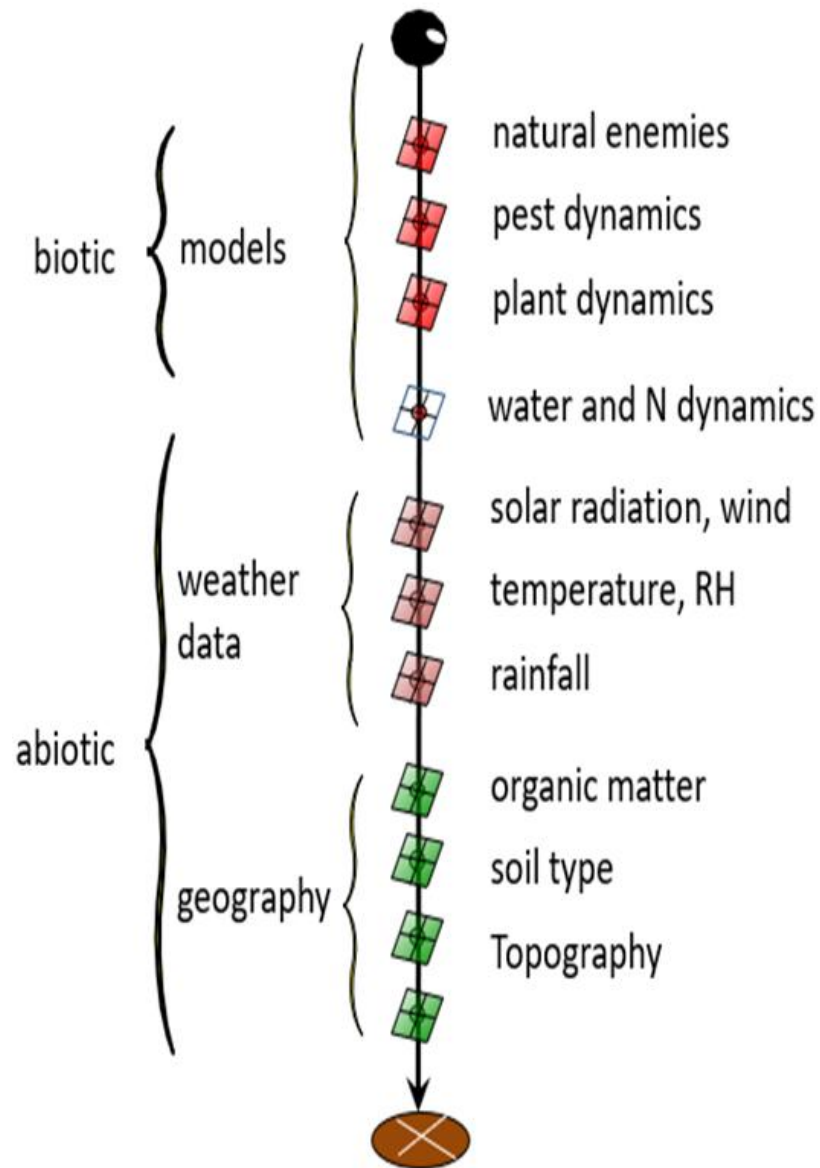
- Hybrid genetically-modified cotton was introduced in India, producing a toxin to control pink bollworm
- After initially good results, yields stagnated and declined
- More than 100,000 suicides attributed to low cotton yields and failures

Average national seed cotton yields (kg/ha) 2020-2021



2021 data - International Cotton Advisory Committee, Washington DC





PBDM

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Three key features of PBDM

Demand-driven evolution

Supply and demand

- Each organism acquires and allocates resources towards survival, reproduction and growth
- PBDMs balance between biological realism and mathematical homogeneity
- Interactions can be thought of as resource flows
- Bioeconomic issues can be thought of in the same language

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Weather and climate dependency

Environmental response

- The effects of climate (temperature, humidity, day length) or other factors (age, density) are captured by functions parametrised from **field or laboratory data**
- Responses to other variables are captured by scalar multipliers $0 \leq \phi_g \leq 1$:

$$rate(t) = \prod_g \phi_g(t) \times rate_{opt}(t)$$

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Age and stage-structured dynamics

Population dynamics

- Age-structure dynamics to enhance realism, e.g.

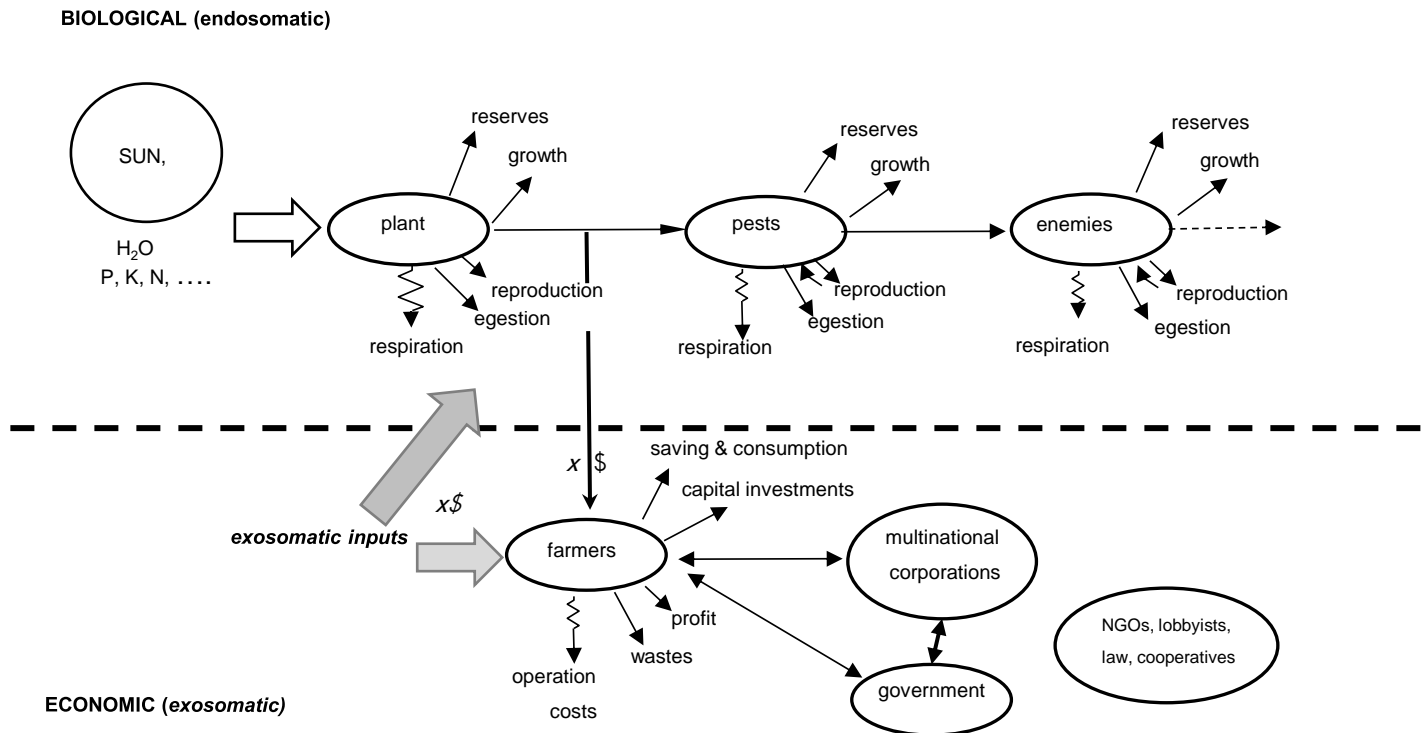
$$\frac{\partial N(t, a)}{\partial t} + v \frac{\partial N(t, a)}{\partial a} - D \frac{\partial^2 N(t, a)}{\partial a^2} = -\mu(t, a)N(t, a)$$

- Stage-structure (nested populations) to reflect reality:
 - Adult females attack young fruit developmental stage
 - Parasitic adults attack other insect larvae

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Supply and demand

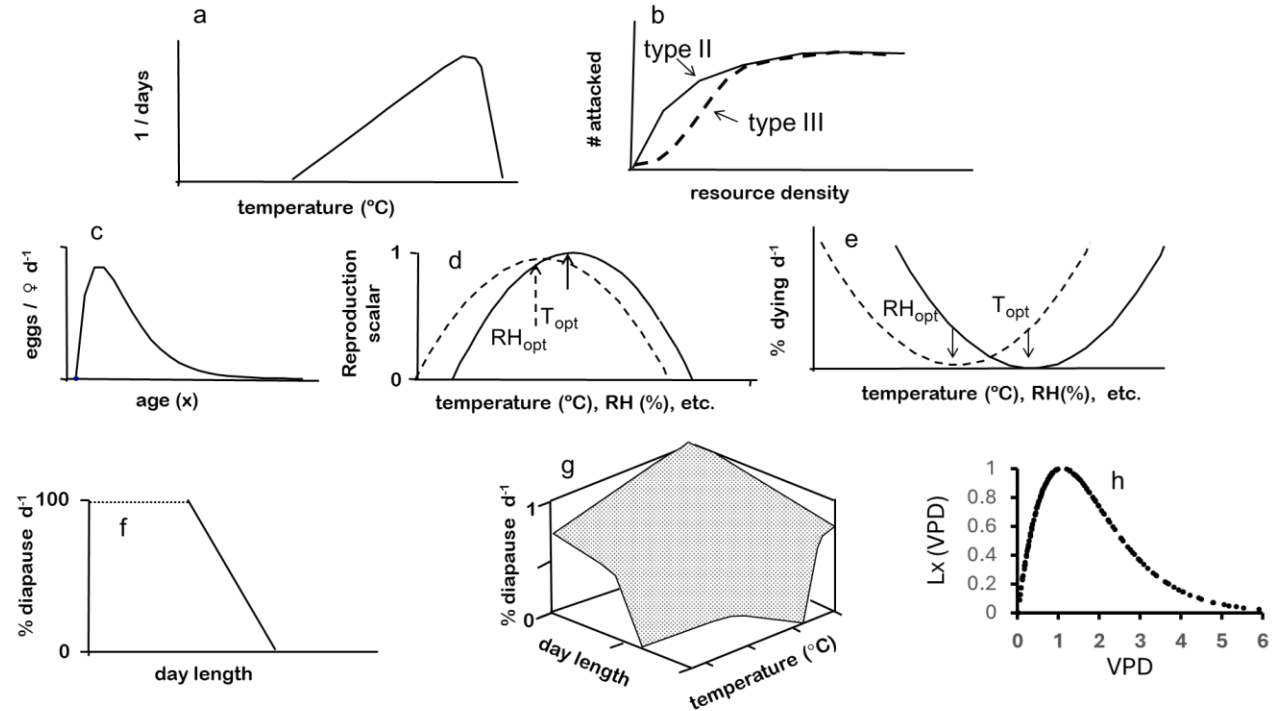
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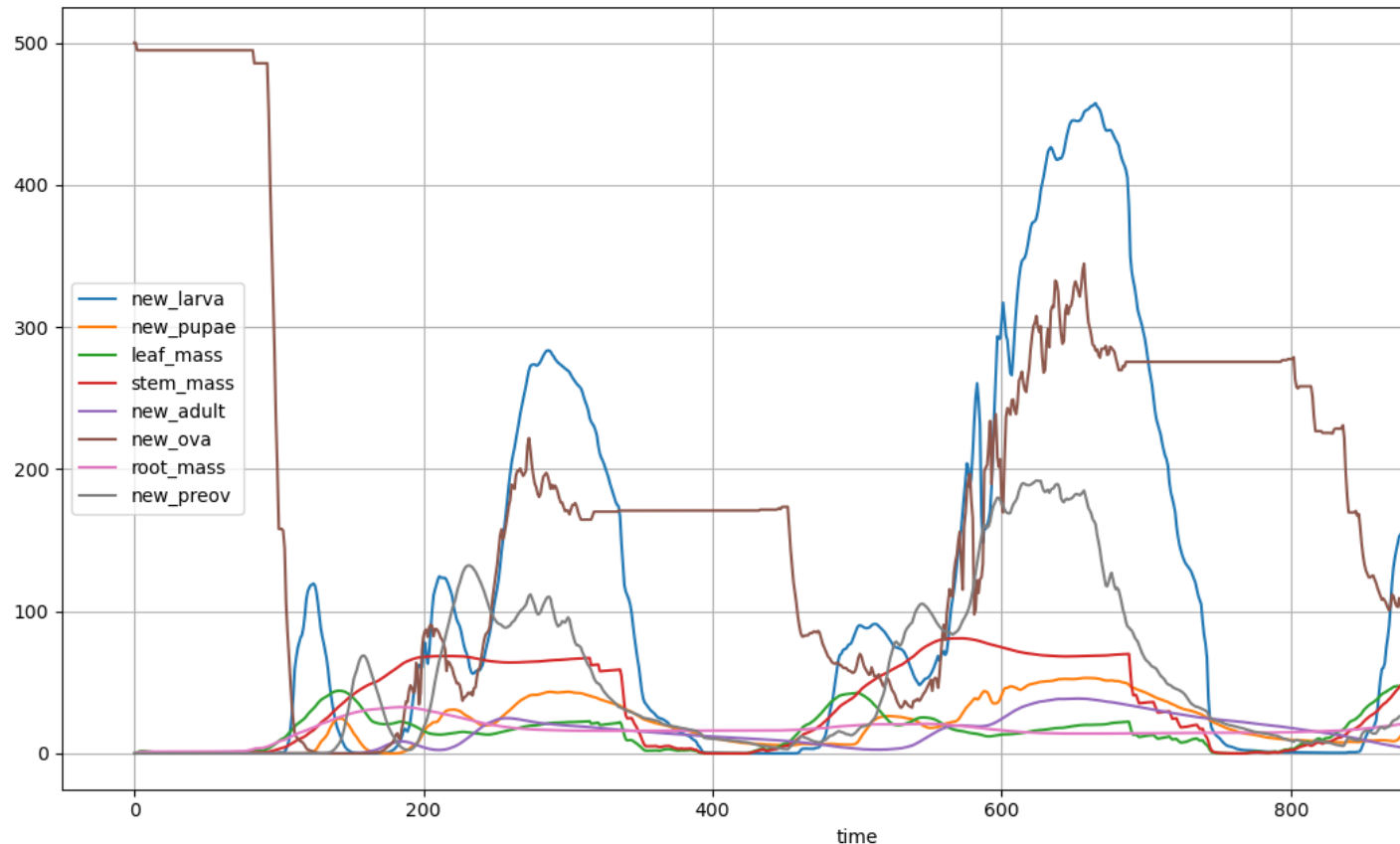


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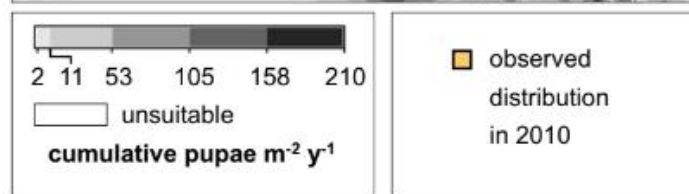
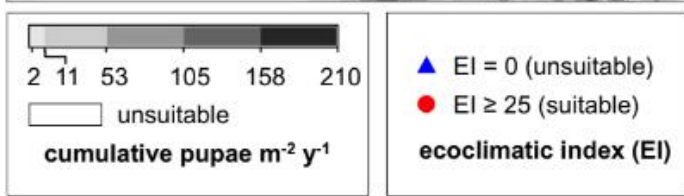
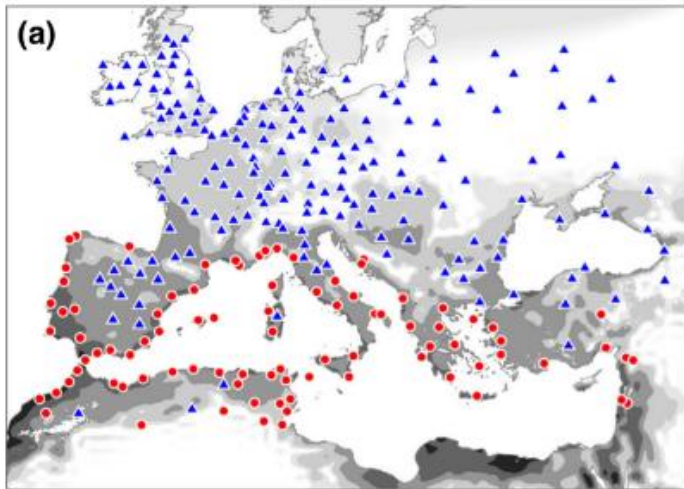


Population dynamics

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- Stage-structure (nested populations) to reflect reality:
 - **Adult females** attack **young fruit** developmental stage
 - Parasitic **adults** attack other insect **larvae**



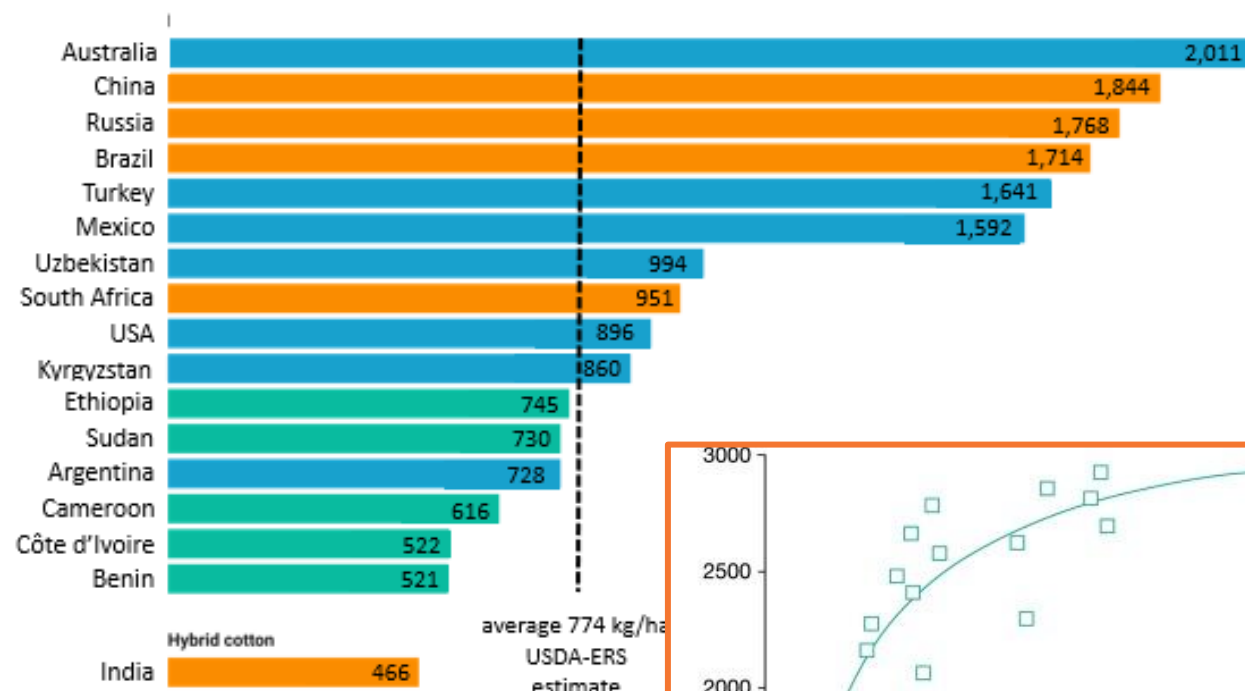
Case study: tomato pinworm (part 2)

- PBDM analysis (greyscale) predicts the observational data much more closely than the correlative data based on South American observations
- Since PBDM does not require the occurrence data to parametrise, they would have predicted the 2010 outbreak of *T. absoluta* in the EU

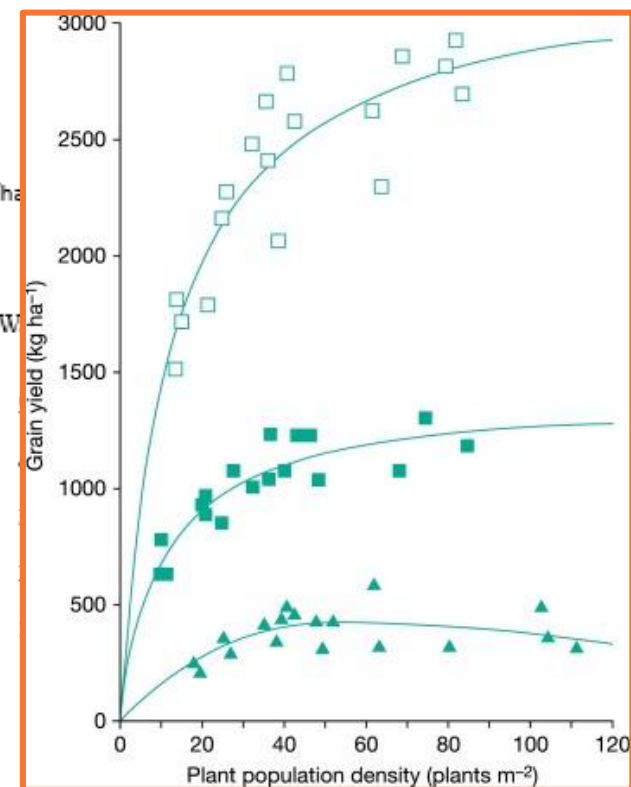
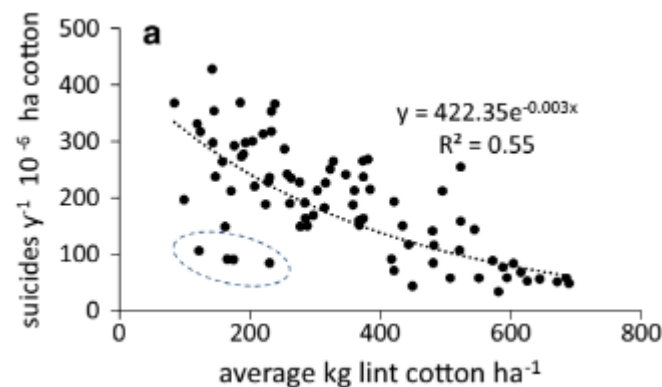
Case study: cotton in India (part 2)

- PBDM analysis indicates that lower planting density caused by higher seed cost leads to:
 - lower yields as the plant prioritises vegetative growth to fill its space
 - An elongated growing season, leading to susceptibility to other pests
- Increased resistance over time
- Farmers locked into a cycle

Average national seed cotton yields (kg/ha) 2020-2021

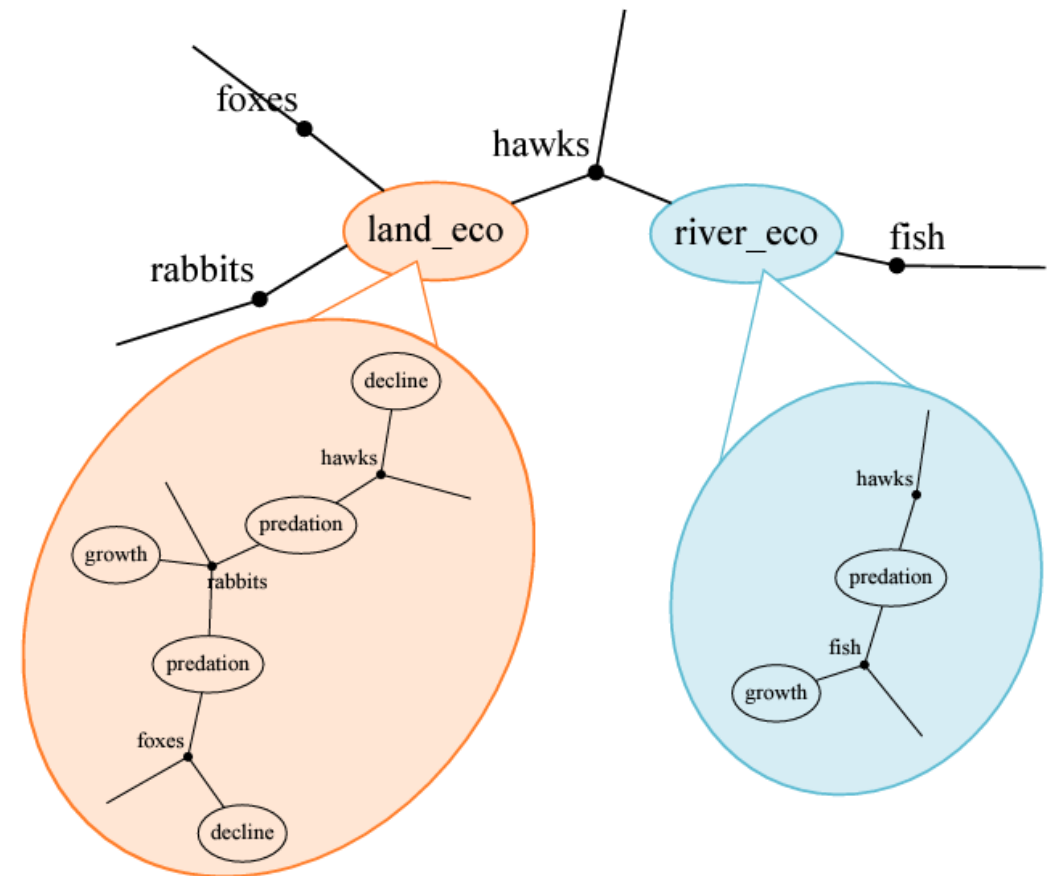


2021 data - International Cotton Advisory Committee, W



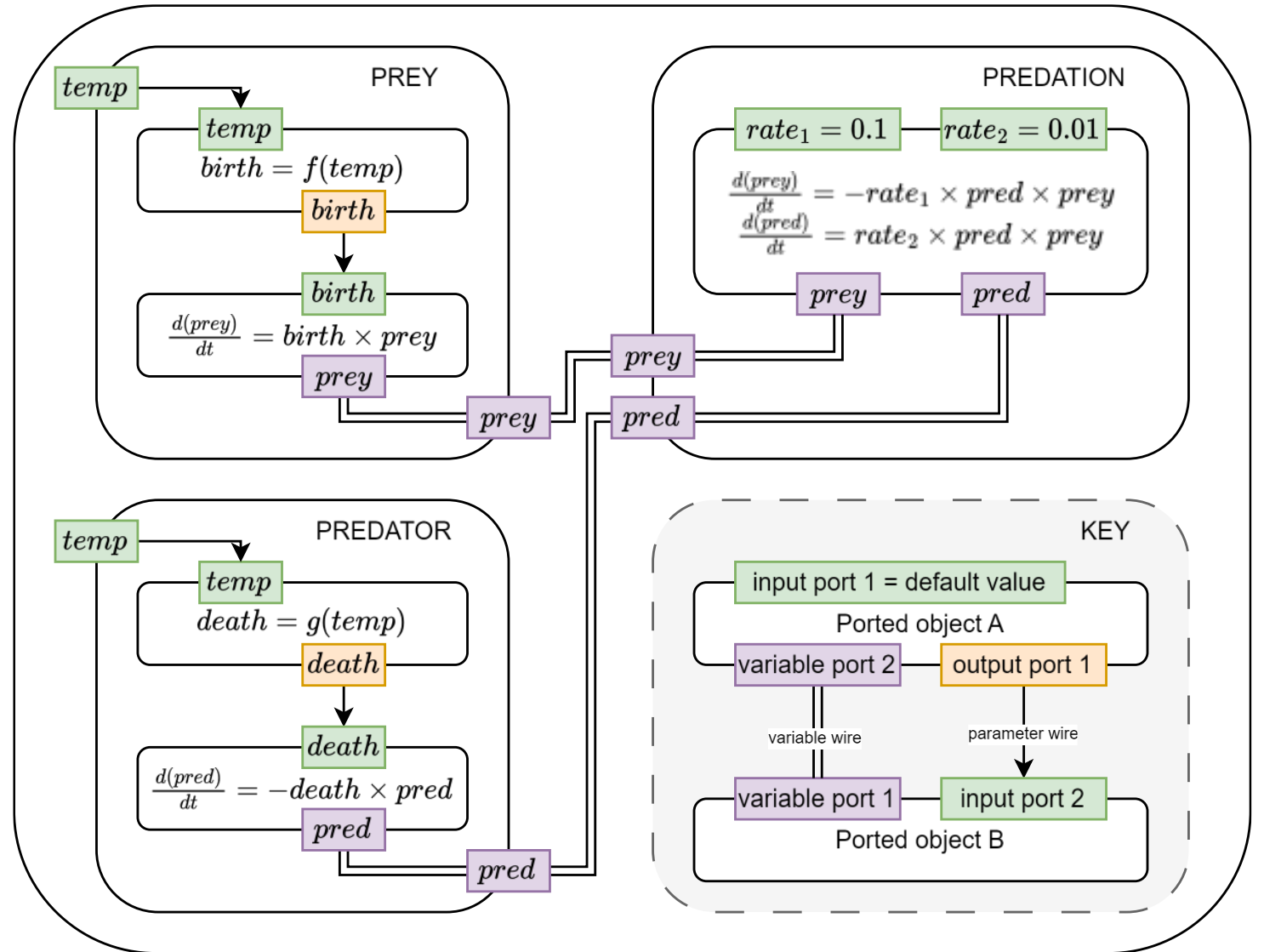
Our implementation

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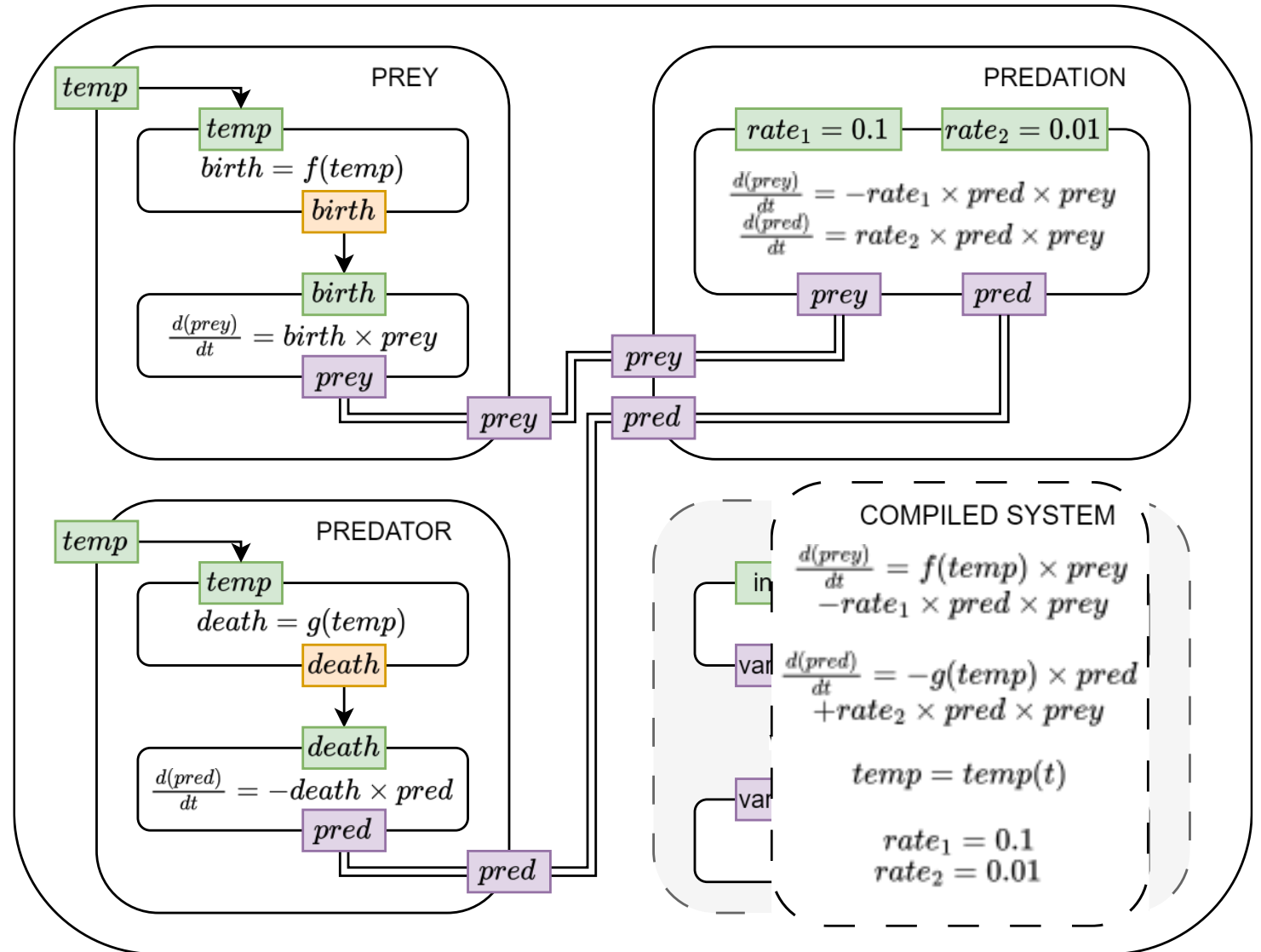
Example: temperature- dependency

- Diagrammatic representation of predator-prey
- In this form, it's easy to add temperature-dependent birth and mortality functions



Example: temperature- dependency

- Compilation collects equations connected by variable wires and aggregates them
- Functions connected by parameter wires undergo partial substitution



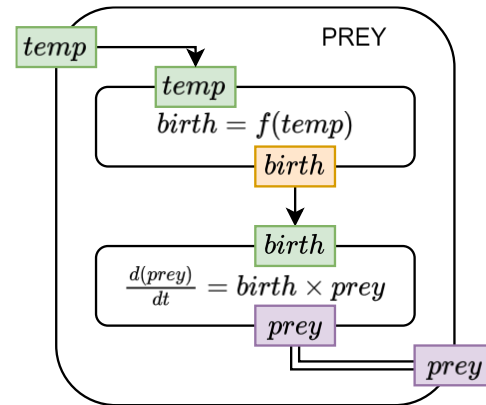
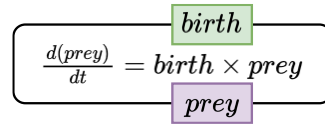
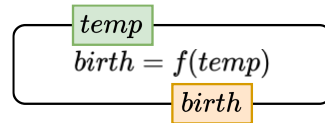
Ported objects as code

This system represents the differential equation

$$\frac{d(\text{prey})}{dt} = f(\text{temp}) * \text{prey}$$

where

$$f(\text{temp}) = 1 - \text{temp}^2$$



```
##### Birth #####
```

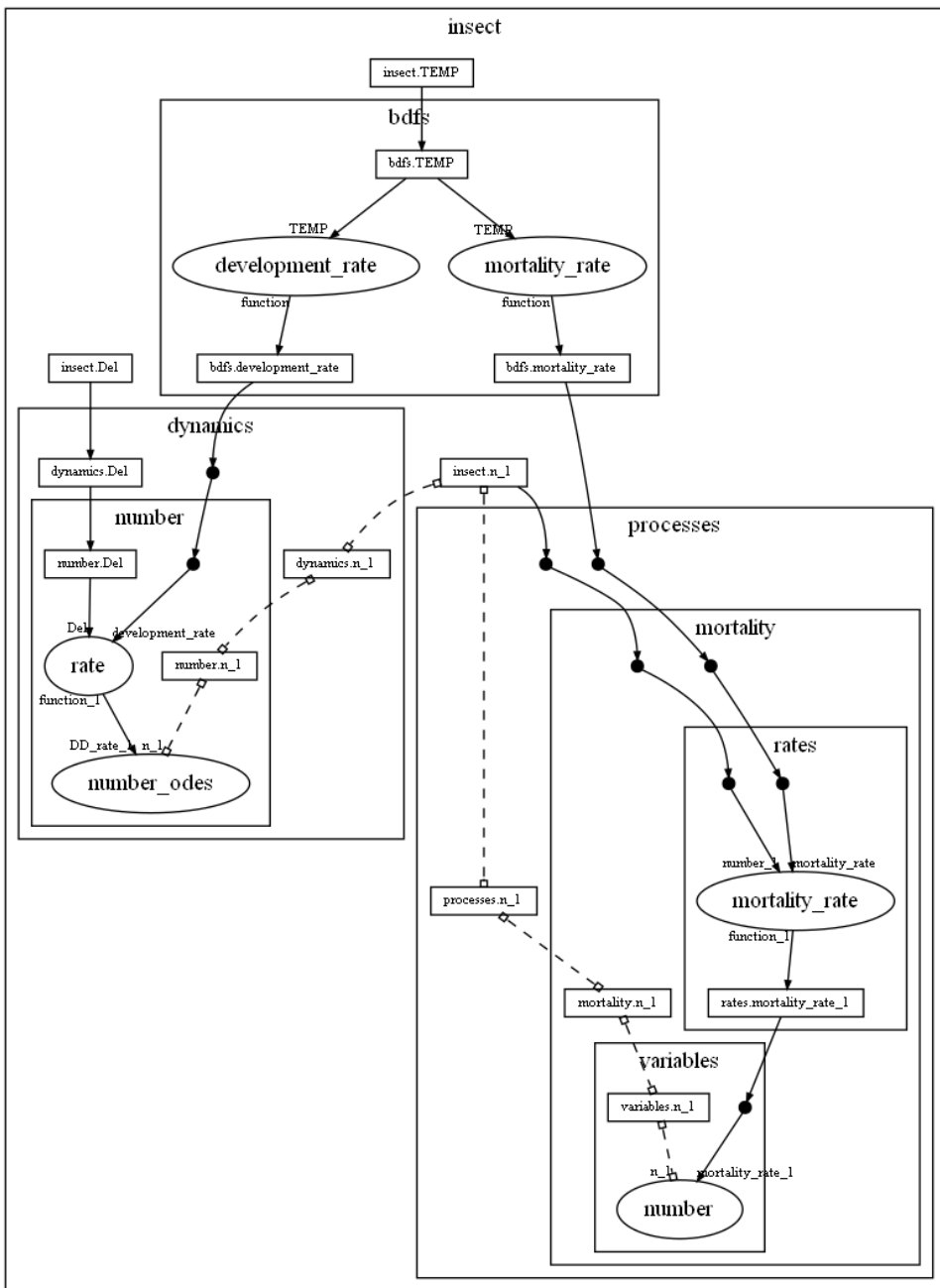
```
birth = FunctionalPortedObject(
    name="birth_rate",
    assignments=("birth", "1 - temp**2")
)
```

```
##### Prey dynamics #####
```

```
prey_dyn = VariablePortedObject(
    name="dyn",
    assignments=[("prey", "birth*prey")],
)
```

```
##### Prey functional population #####
```

```
prey = CompositePortedObject(
    name="prey",
    children=[birth, prey_dyn],
    variable_ports=["prey"],
    input_ports=["temp"],
    directed_wires=[
        ("temp", ["birth_rate.temp"]),
        ("birth_rate.birth", ["dyn.birth"]),
    ],
    variable_wires=[(["dyn.prey"], "prey")],
)
```

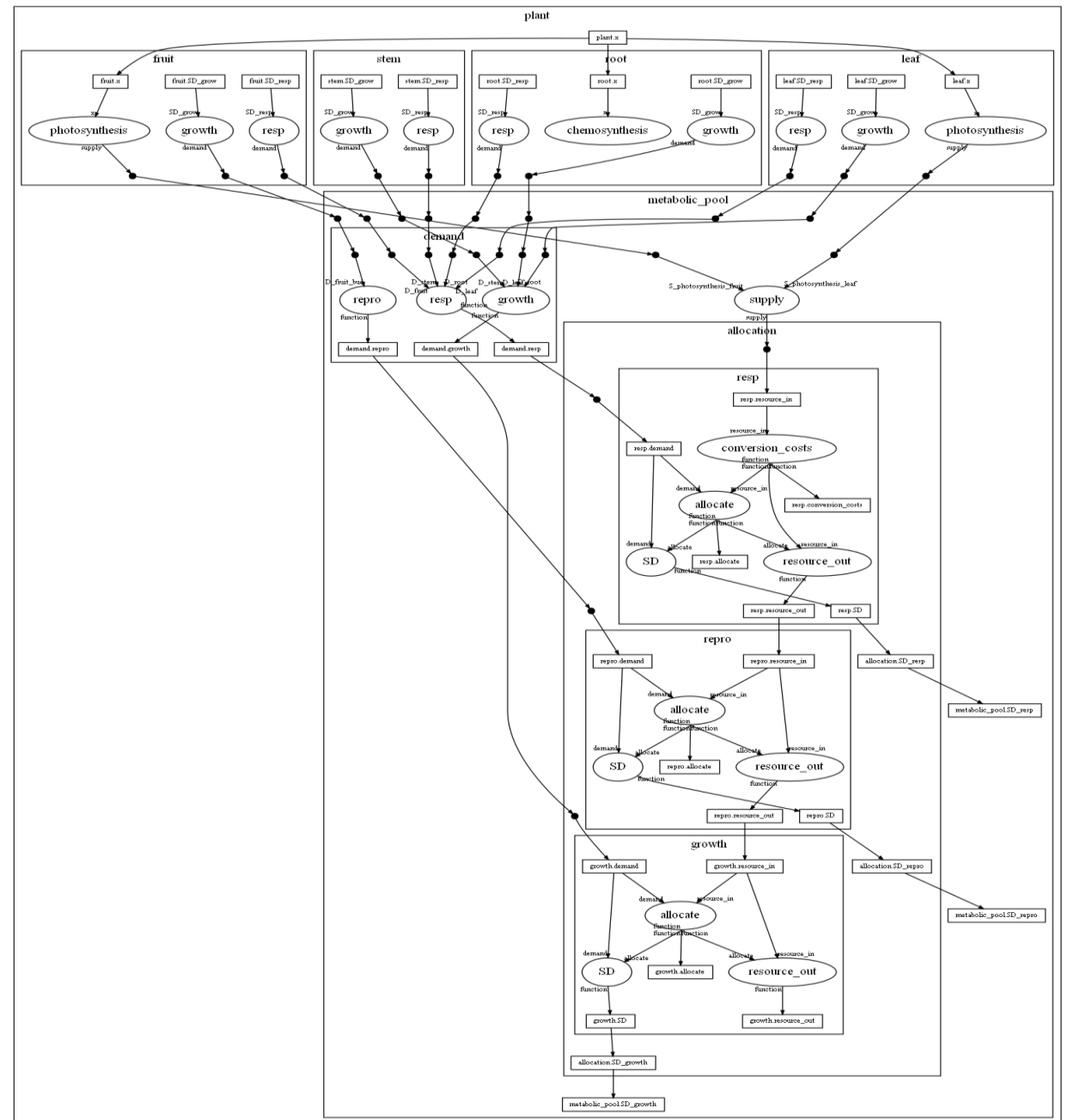


Capturing PBDM

- Every organism or sub-organism of a population is captured as a **functional population** with:
 - Biodemographic functions (rates for growth, development, reproduction, predation, etc.)
 - Population dynamics (age and stage structure models)
 - Processes (variable or resource creation, e.g. mortality, photosynthesis)
 - Metabolic pool (supply-demand resource allocation)

Metabolic pool

This object calculates a set of scalars, there are no variables involved!



```
##### Insect functional population #####
```

```
F = FunctionalPopulation(  
    name="insect",  
    age_structure = {  
        "k": 5,  
    },  
    Del = 220,  
    variable = "n",  
    bdfs = {  
        "development_rate": {  
            "function": "a*(TEMP - T_min)/(1 + b**(TEMP - T_max))",  
            "inputs": {"a": 1, "b": 2.5, "T_min": 9.5, "T_max": 35.5}  
        },  
        "mortality_rate": {  
            "function": "zerone(a*TEMP**2 + b*TEMP + c)",  
            "inputs": {"a": 0.00098, "b": -0.00098, "c": 0.0001}  
        }  
    },  
    dynamics = {  
        "number": {  
            "type": "distributed_delay",  
            "rate": {  
                "function": "development_rate * k/Del",  
                "inputs": {"development_rate": "insect.bdfs.development_rate"}  
            }  
        }  
    },  
    processes = {  
        "mortality": {  
            "rates": {  
                "mortality_rate": {  
                    "type": "age_structured",  
                    "function": "mortality_rate * number",  
                    "inputs": {"mortality_rate": "insect.bdfs.mortality_rate"},  
                    "age_structured_inputs": {"number": "insect.n"}  
                }  
            }  
        },  
        "variables": {  
            "number": {  
                "type": "age_structured",  
                "function": "- mortality_rate",  
                "age_structured_inputs": {"mortality_rate"}  
            }  
        }  
    }  
)
```

Other features

- Code interface for creating components of functional populations (bdfs, dynamics, processes, etc.), with internal automation to create objects and wires
- Automated hierarchical searching for parameters (pull vs. push behaviour), e.g. Del
- Facility to implement system-wide parameters (TEMP) and utility functions (zerone)
- Relative hierarchical address-based system to pull or share information with non-immediate siblings (insect.bdfs.mortality_rate)



Thank you!

- IDEMS: <https://idems.international>
- CASAS: <http://casasglobal.org>
- psymple:
 - Repo: <https://github.com/casasglobal-org/psymple>
 - Docs: <https://casasglobal-org.github.io/psymple>