

# Bayesian parameter synthesis of Markov population models.

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## Motivation

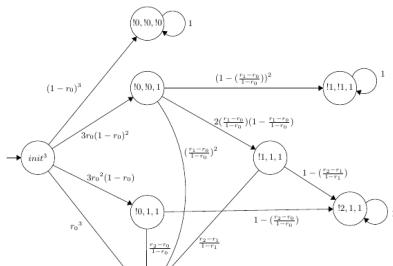
In this thesis, we study *population processes*. Kingman [1] defines *population processes* as stochastic models of discrete state spaces, in which:

- ▶ Each state in the state space represent the number of individuals in a category or a colony.
- ▶ Changing from a state to another state represents an increase or decrease of the number of individuals.

## Example

Examples of population process:

- ▶ A bee colony of initially  $n$  individuals. Assume that one bee can sting randomly with a probability  $p$ , we can construct a parametric Discrete Time Markov Chain to represents the population process.
- ▶ Number of computation nodes which are alive in a server cluster, with an assumption that an arbitrary node dies with probability  $p$ .



## Question

As we study a Markov population process, the following questions are raised:

- ▶ *Parametric model*: How can we encompass unknown features into the population model?
- ▶ *Parameter synthesis*: Given a parametric population model and observed data of the population, how can we infer the model parameters?
- ▶ *Model composition*: How can we generalize aggregate a multi-agents population model from single-agent behaviour model?

In the scope of this thesis, we limit our study to discrete-time model.

## Approach

- ▶ Model individual behaviour after a parametric Markov Decision Process.
- ▶ Model collective behaviour by compositing individual models to a parametric Discrete Time Markov Chain.
- ▶ Use data-informed Bayesian inference to synthesize the parametric Discrete Time Markov Chain parameters.

## Data

As we use Bayesian inference, we need data.

- ▶ In the thesis, we use synthetic data, obtained by simulating the parametric model using a concrete assignment of parameters.
- ▶ Using *synthetic data* has an advantage over using real data. As the concrete parameters are known, it is possible to measure the distance between the synthesized parameters and true parameters.

## Single agent model.

We model the behaviour of a single bee as a Markov Decision Process. Let  $\mathcal{S}$  be the individual model, we have

$$\mathcal{S} = (S, A, P_a, R_a)$$

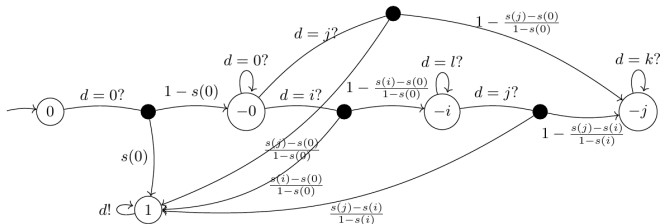
in which

- ▶  $S$  is the set of states.
- ▶  $A$  is the set of actions.
- ▶  $P_a(s, s')$  is the probability of transitioning from state  $s$  to state  $s'$  given action  $a$ .
- ▶  $R_a(s, s')$  is the *reward* received after transitioning from state  $s$  to state  $s'$  given action  $a$ .



## Single agent model.

### Example of a single bee model



**Figure:** Generic single bee model (developed by Matej Hajnal and Tatjana Petrov)

## Multi-agent model

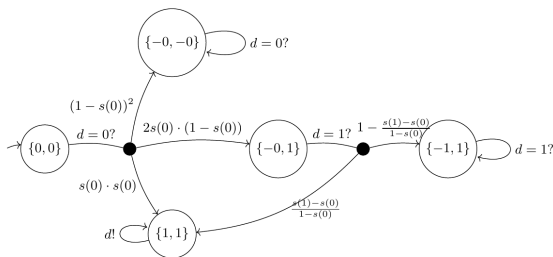
To model collective behavior of multiple agents, we construct product of individual models. Let  $\mathcal{M}$  be the multiple agents pDTMC model, we constr

$$\mathcal{M} = (\mathcal{S}_1 || \mathcal{S}_2 || \dots || \mathcal{S}_k)$$

Composition of MDP are mentioned in [4]. Asynchronous and synchronous semantics for constructing pDTMC from multiple pMDP are currently developed by Tatjana Petrov.

## Multi-agent model

Example of a multi-agent model.



**Figure:** Example of 2 bees model (developed by Matej Hajnal and Tatjana Petrov)

## Properties

**Question:** How can different parameters of single agent affect the population?

**Answer:** Given a model  $\mathcal{M}_\Theta$ , to find the probability of having a certain number of individuals at the steady state, we

- ▶ represents population at steady state by a BSCC  $s_i$ , with  $i$  is the population size.
- ▶ checking the model of against  $PCTL P_?(FGs_i)$

We can survey further constraints on model and properties:

- ▶ Surviving percentage: lumping BSCCs.
- ▶ Reduce parameter space: apply a linear/sigmoidal constraints over parameter space  $\Theta$ .

## Related work

Gareth Molyneux et al. [3] presented *ABCSeq* framework for Bayesian Verification of CTMC.

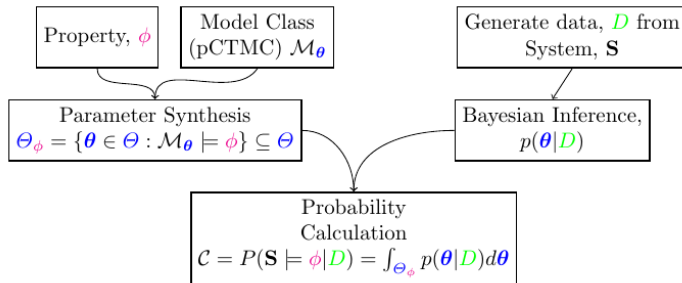
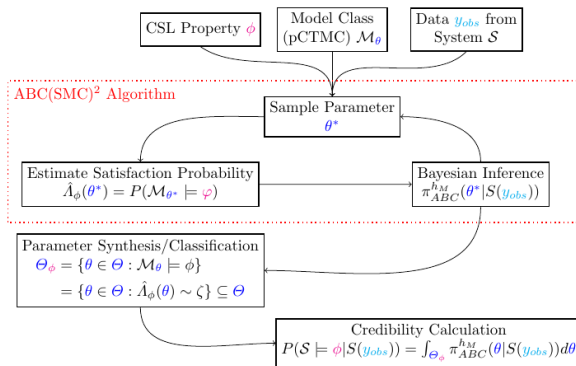


Figure: ABCSeq Bayesian verification framework.

## Related work

In [2], the authors present  $ABC(SMC)2$  to improve  $ABCSeq$  framework for better performance.



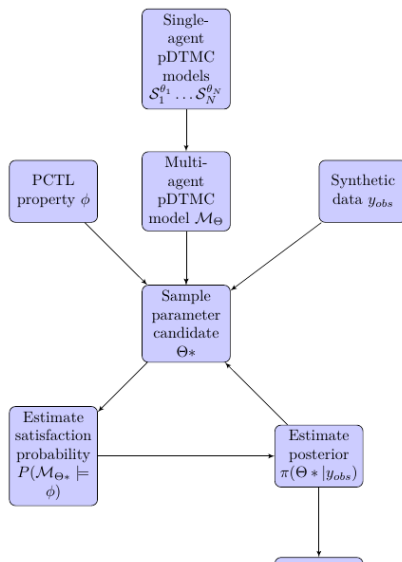
**Fig. 1.** Bayesian Verification via  $ABC(SMC)^2$ .

## Proposed Framework

We develop a similar framework for parameter synthesis of pDTMC based on [2] and [3]. Compare to the work by Gareth Molyneux et al., our framework should

- ▶ Works with discrete time model.
- ▶ Verify PCTL property.
- ▶ Since the model is of discrete-time, the closed form solution (symbolic) for a PCTL property is in some cases obtainable. In such cases, we can compute the exact likelihood without simulation.

# Proposed Framework





## Tools

For probabilistic model checking and parameter synthesis, we use STORM probabilistic model checker

- ▶ **Extensible:** High quality C++ APIs - this is important.
- ▶ **Scalable:** Faster compare to PRISM.
- ▶ **Capable:** STORM factorizes symbolic results on-the-fly.

## Case study

We study the defensive behaviour of a bee colony.

- ▶ Bees response to stimulations from the environment by *stinging*.
- ▶ After *stinging*, an individual bee releases *pheromone* and dies.

Our questions concerns the relation between the concentration of pheromone in the environment and the aggressiveness of each individual in the colony.

## Case study

As we study the biological system, we have the following research questions:

1. Given a population of bee, how many individuals left in the steady state.
2. How does an individual's behaviour change the collective behaviour? Does each individual become more aggressive given the

## Timeline

### Thesis milestones

1. **07.12.2020**: Model and properties lists.
2. **21.12.2020**: Framework implementation and results.
3. **10.01.2021**: Model improvement.
4. **30.01.2021**: Thesis submission.

Progress is reported weekly.

## References

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2  
: Simultaneous Inference and Model Checking of Chemical Reaction Networks”. In: *International Conference on Computational Methods in Systems Biology*. Springer. 2020, pp. 255–279.
- [3] Gareth W Molyneux, Viraj B Wijesuriya, and Alessandro Abate. “Bayesian verification of chemical reaction networks”. In: *International Symposium on Formal Methods*. Springer. 2019, pp. 461–479.
- [4] Ana Sokolova and Erik P De Vink. “Probabilistic automata: