

# NoPain – Meeting

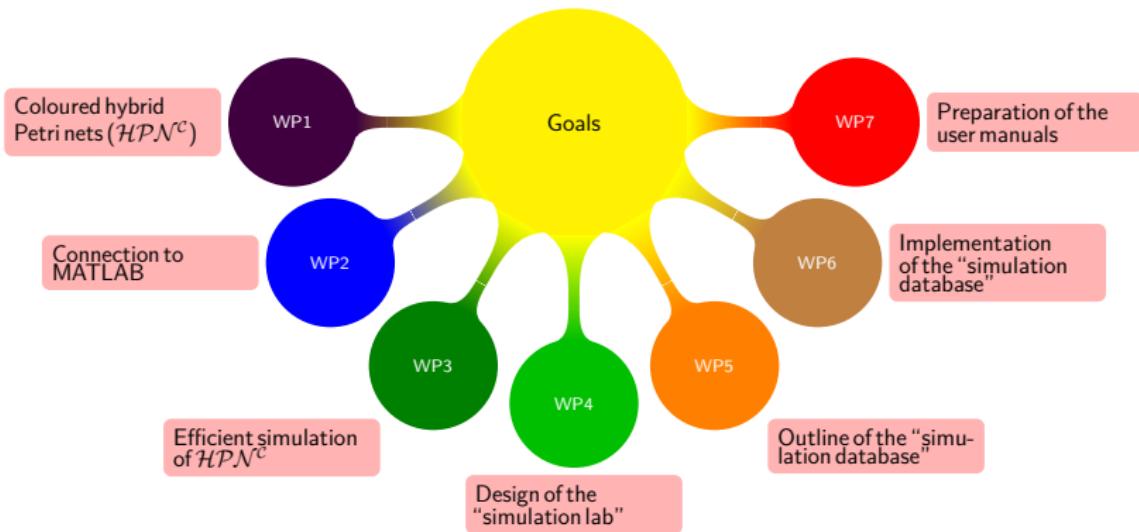
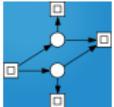
Monika Heiner    Christian Rohr

Department of Computer Science  
Brandenburg University of Technology Cottbus

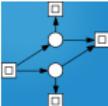
<http://www-dssz.informatik.tu-cottbus.de>

May 14, 2014

# Work Packages



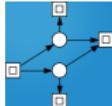
# WP3



## Efficient simulation of $\mathcal{HPN}^c$

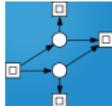
- a. Predecessor WPs: BTU-WP1, OvGUM-WP1
  - b. Successor WPs: BTU-WP4
- 
- Examination of the Petri net models with regard to parallelisation potential
  - Investigation of optimisation possibilities and performance comparisons with alternative tools, i.e. StochKit2, Cain...

# Tool comparison



- Starting point: How many stochastic simulation tools are available?
- SBML Software Summary: > 100 tools related to simulation.
- Selection criteria needed!

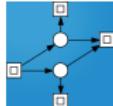
# Tool comparison



## Selection criteria

- 1 *Stochastic simulation tool.* There are different approaches to simulate biochemical reaction networks, such as deterministic or hybrid simulation, but we are only interested in stochastic simulation tools.
- 2 *Algorithms used by the Simulator.* There are a couple of algorithms for stochastic simulation, such as *direct method* [Gillespie 1977], first reaction method [Gillespie 1976], next reaction method [Gibson et al. 2000] and  $\tau$ -leaping [Gillespie 2001]. The stochastic simulation tool must support at least the Gillespie's direct method.
- 3 *License type.* The use of the simulation tool must be free of charge.
- 4 *SBML support.* The tool must support SBML (Level 2), either directly, or indirectly by connection to a tool supporting SBML.

# Tool comparison

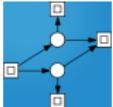


## Candidates

- 1 Cain
- 2 Copasi
- 3 Dizzy
- 4 Marcie
- 5 Snoopy
- 6 StochKit2
- 7 StochPy

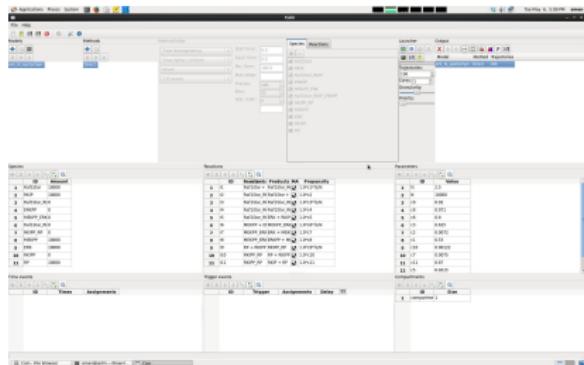
→ may be extended

# Candidates



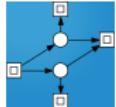
## Cain

- Cain performs stochastic and deterministic simulations of chemical reactions.
- Caltech Center for Advanced Computing Research, Pasadena, California, US.
- Modelling paradigms: stochastic, deterministic.
- Simulation algorithm: direct method, next reaction method,  $\tau$ -leaping.
- Interface: graphical user interface tool.
- File formats: SBML.



<http://cain.sourceforge.net/>

# Candidates



## Copasi

- COPASI is a software application for simulation and analysis of biochemical networks and their dynamics.
- Virginia Bioinformatics Institute, University of Heidelberg, University of Manchester.
- Modelling paradigms: stochastic, deterministic.
- Simulation algorithm: direct method, next reaction method,  $\tau$ -leaping.
- Interface: GUI & CL tool.
- File formats: SBML L2.

The screenshot shows the COPASI software interface. On the left is a menu bar with 'File', 'Edit', 'View', 'Model', 'Analysis', 'Task', 'Help'. Below the menu is a tree view of the model structure: 'Model' (Biochemical, Compartments, Compartment Symbols, Metabolites, Masses, Reactions), 'Mathematical' (Compartment Symbols, Parameter Symbols, Constant Symbols, Fixed Metabolic Symbols, Metabolite Symbols, Differential Equations), 'Tasks' (Steady-State, Stationarity, Steady-State Modes, Mass Conservation), 'Time Course', 'Results', 'Model Tasks' (Optimization, Scan, Fitting), 'Demos' (Pathway, Pys, Reports, Functions, Preferences). The main area displays a table of reactions:

Name	Equation	Kinetics	Dimes	Flux
1 HXT	GLCo = GLC1	HXT kinetics	0	
2 HK	GLC1 + ATP = G6P + ADP	HK kinetics	0	
3 PG	G6P = FBP	PGI kinetics	0	
4 PRK	FBP + ATP -> F16BP + ADP; AMP F26BP	PRK kinetics	0	
5 ALD	F16BP = DHAP + GAP	ALD kinetics	0	
6 TPI	DHAP = GAP	TPI kinetics	0	
7 GAPDH	CAT + NAD = PGC + NADH	GAPDH kinetics	0	
8 PKC	PGC + ADP = PGK + ATP	PKC kinetics	0	
9 PCM	PGK + P2C	PCM kinetics	0	
10 ENO	P2G = PEP	ENO kinetics	0	
11 PYK	PEP + ADP = PYR + ATP	PYK kinetics	0	
12 PDC	PYR -> AcAld + CO2	PDC kinetics	0	
13 ADH	AcAld + NADH -> AcCoA + NADH	ADH kinetics	0	
14 ATPase	ATP -> ADP	ATPase	0	
15 ALD	2 * ADP -> ATP + AMP	Mass action (reversible)	0	
16 G3PDH	DHAP + NADH -> Glycerol + NAD	G3PDH kinetics	0	
17 Glycogen Branch	GDP + ATP -> ADP + Glycogen	Glycogen synthesis kinetics	0	
18 Trehalose Branch	2 * GDP + ATP -> ADP + Trehalose	Trehalose synthesis kinetics	0	
19 Succinate Branch	2 * AcAld + 3 * NAD -> Succinate + 3 * NADH	Succinate kinetics	0	
20				

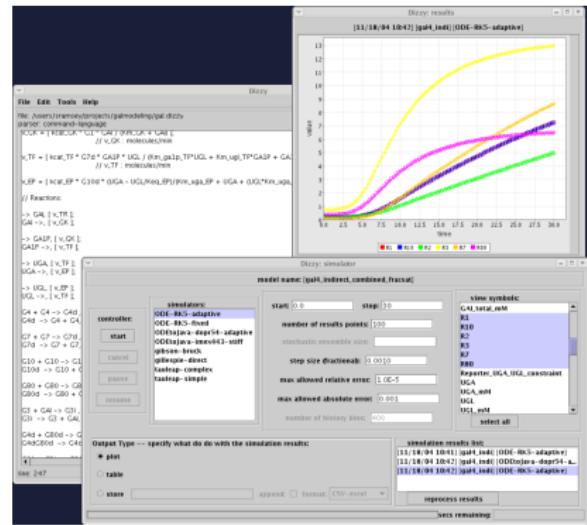
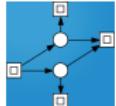
<http://www.copasi.org>

## Dizzy

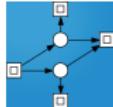
- Dizzy is a chemical kinetics stochastic simulation software package written in Java.
- Institute for System Biology, Seattle, Washington, US.
- Modelling paradigms: stochastic, deterministic.
- Simulation algorithm: direct method, next reaction method,  $\tau$ -leaping.
- Interface: graphical user interface tool.
- File formats: SBML L1V2.

<http://magnet.systemsbiology.net/software/Dizzy/>

## Candidates



## Candidates



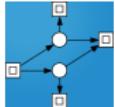
### Marcie

- Marcie is a tool for qualitative and quantitative analysis of Generalized Stochastic Petri nets with extended arcs.
- BTU Cottbus, Germany.
- Modelling paradigms: stochastic.
- Simulation algorithm: direct method, next reaction method,  $\tau$ -leaping.
- Interface: command line tool.
- File formats: ANDL, PNML.



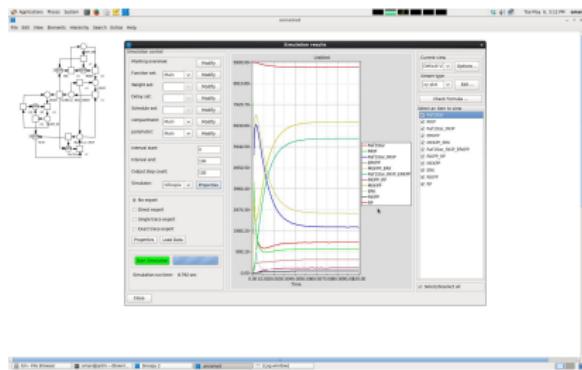
<http://www-dssz.informatik.tu-cottbus.de/DSSZ/Software/Marcie>

# Candidates



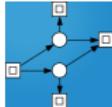
## Snoopy

- Snoopy is a software tool to design, animate and simulate hierarchical graphs, among others Petri nets.
- BTU Cottbus, Germany.
- Modelling paradigms: stochastic, deterministic and hybrid.
- Simulation algorithm: direct method.
- Interface: graphical user interface tool.
- File formats: SBML L2, ANDL.



<http://www-dssz.informatik.tu-cottbus.de/DSSZ/Software/Snoopy>

## Candidates



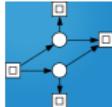
### StochKit2

- StochKit is an extensible stochastic simulation framework developed in C++.
- University of California, Santa Barbara, US.
- Modelling paradigms: stochastic.
- Simulation algorithm: direct method, next reaction method,  $\tau$ -leaping.
- Interface: command line tool.
- File formats: SBML L2.



<http://engineering.ucsbg.edu/~cse/StochKit>

# Candidates



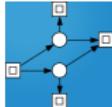
## StochPy

- StochPy is a versatile modeling package for stochastic simulation.
- VU University Amsterdam, NL.
- Modelling paradigms: stochastic.
- Simulation algorithm: direct method, next reaction method,  $\tau$ -leaping.
- Interface: command line tool.
- File formats: SBML L2.



<http://stochpy.sourceforge.net/>

# Test suite



- (colored) stochastic Petri net
- standard arcs, no read, inhibitor, modifier arcs
- mass-action kinetics
- scalable

## stochastic Petri nets

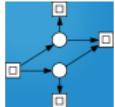
- RKIP inhibited ERK Pathway
- Mitogen-activated Protein Kinase
- Angiogenesis

## colored stochastic Petri nets

- Prey Predator
- Gradient
- Repressilator

→ may be extended

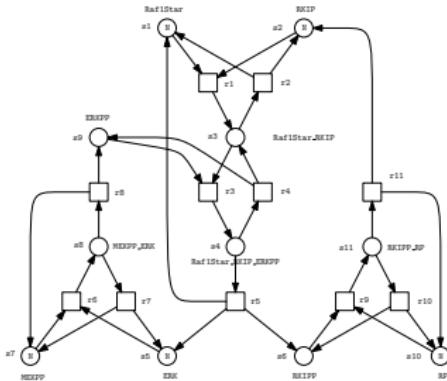
# Test suite



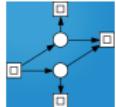
## RKIP inhibited ERK Pathway [Gilbert et al. 2006]

- # places: 11
- # transitions: 11
- # arcs: 34
- scalable in N – the initial number of tokens on the places ERK, MEKPP, Raf1Star, RKIP and RP

RKIP/MEK-ERK signalling pathway [volkenhauser 2003], [Calder 2006]

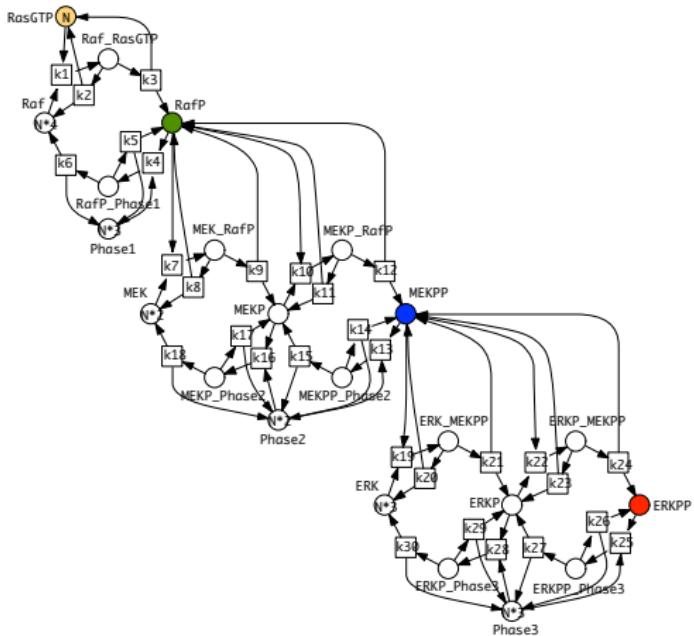


# Test suite

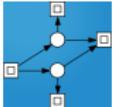


## Mitogen-activated Protein Kinase [Levchenko et al. 2000], [Heiner et al. 2008]

- # places: 22
- # transitions: 30
- # arcs: 90
- scalable in N – the multiplier of initial number of tokens on the places Raf, RasGTP, RafP\_Phase1, MEKP\_Phase2, ERk, ERKP\_Phase3

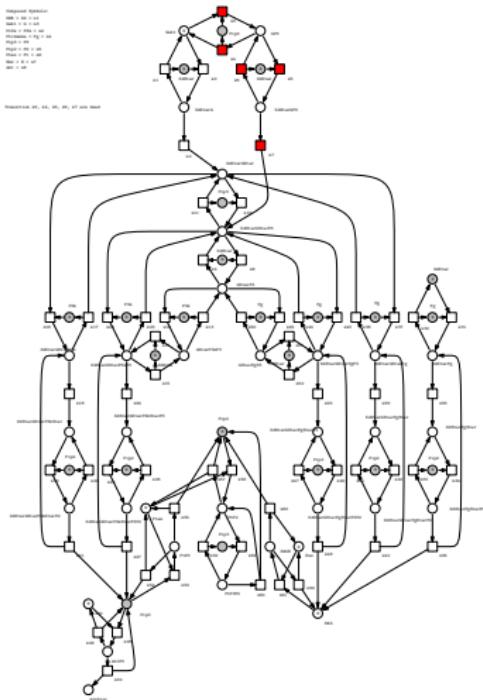


## Test suite

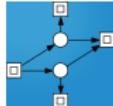


### Angiogenesis [Napione et al. 2009]

- # places: 39
- # transitions: 64
- # arcs: 185
- scalable in N – the initial number of tokens on the places Gab1, KdStar, P3k, Pg, Pip2, DAG, Enz and Akt
- *dead states*

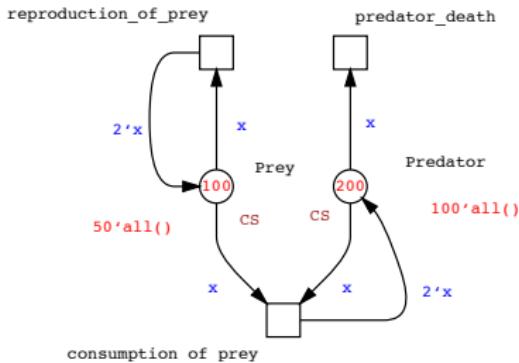


# Test suite

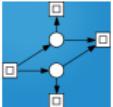


## Prey Predator

- # places:  $2 * N$
- # transitions:  $3 * N$
- # arcs:  $6 * N$
- scalable by # of places, transitions and arcs
- *unbounded*

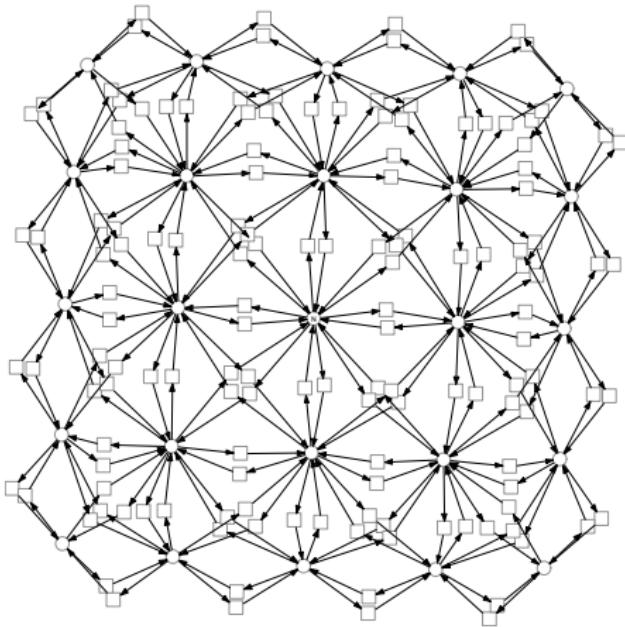


## Test suite

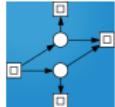


### Gradient [Gilbert et al. 2013]

- # places:  $N^2$
- # transitions:  
 $8 * N^2 - 12 * N + 4$
- # arcs:  $2 * |T|$
- scalable by # of places, transitions and arcs

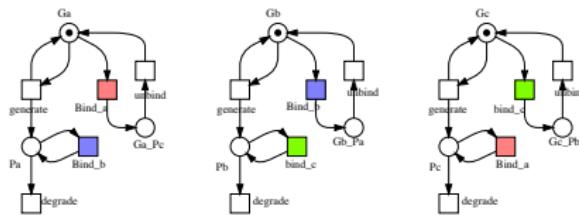


## Test suite

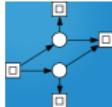


## Repressilator [Liu 2012]

- # places:  $3 * N$
- # transitions:  $4 * N$
- # arcs:  $10 * N$
- scalable by # of places, transitions and arcs



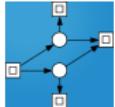
# Simulation parameters



The assumptions and constraints while performing simulation are:

- *Simulation algorithm*: direct method.
- *Simulation results*: mean token value of the places (species).
- *Simulation time*: from 0 time units to  $t$  time units (model specific).
- *Simulation runs*: 1; 100; 10 000; 1 000 000
- *Threshold*: max. 1h run time
- *Threads*: 1 and 4 threads
- *Model parameter*: 4 different values of  $N$
- *Experiment*: a particular value of  $N$ , number of runs and threads
  - each experiment performed 10 times
  - 320 experiments per model and tool
  - worst case 320h, usually 12h

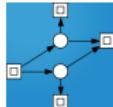
# Comparison criteria



## Performance measures

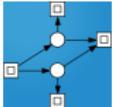
- average run time per experiment
- peak memory consumption per experiment
- simulation results
- multi-threading coefficient

# Setup



- Dell Precision T7400
- CPU: Intel® Xeon® CPU E5440 @ 2.83GHz
- RAM: 4x1024MB DDR2 FB-DIMM @ 667MHz
- OS: CentOS release 6.5 (64bit)

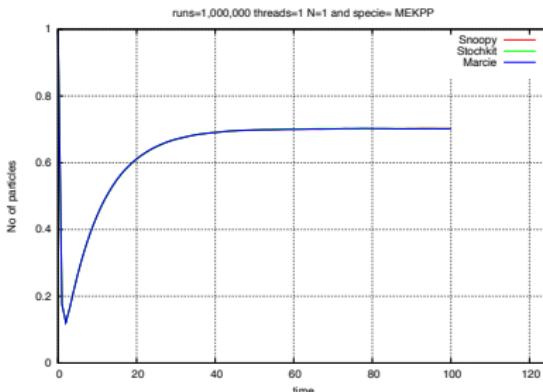
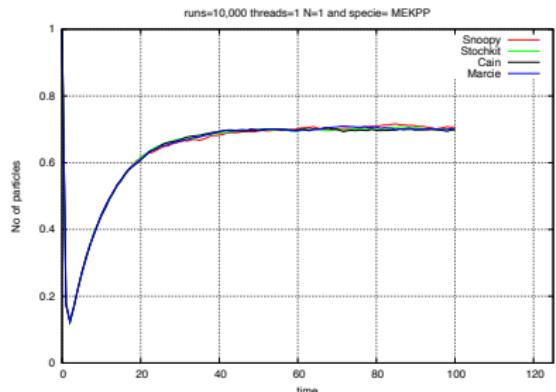
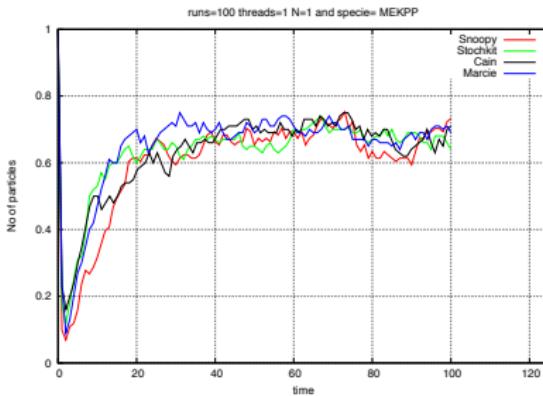
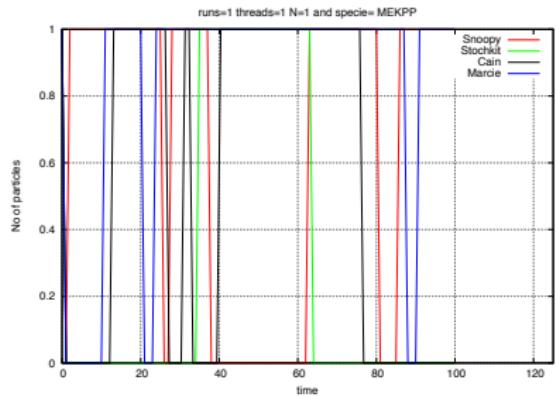
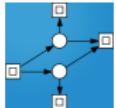
# Results



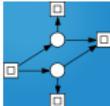
## RKIP inhibited ERK Pathway

- *Model parameter:*  $N \in \{1, 100, 10000, 1000000\}$
- *Tools:* Cain, Marcie, Snoopy, StochKit2

# Results – ERK



# Results

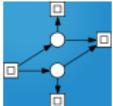


## Snoopy, average runtime (in sec) for ERK.

N	threads	runs			
		1	100	10,000	1,000,000
1	1	0.0002	0.0018	0.1658	16.8030
	4	1.0003	1.0014	1.0079	4.9084
100	1	0.0009	0.0989	8.9830	884.4062
	4	1.0005	1.0084	3.0072	233.9180
10,000	1	0.0898	8.8005	875.7929	†
	4	1.0004	3.0085	231.8182	†
1,000,000	1	9.0178	889.899	†	†
	4	9.4008	243.3228	†	†

† runtime > 1h

# Results

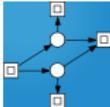


## Snoopy, peak memory consumption (in KB) for ERK.

N	threads	runs			
		1	100	10,000	1,000,000
1	1	37,576	37,752	37,904	37,988
	4	37,512	37,767	37,824	39,604
100	1	37,580	39,748	39,507	39,968
	4	40,196	40,160	39,900	39,932
10,000	1	39,980	39,752	41,928	†
	4	40,032	40,112	39,568	†
1,000,000	1	39,600	39,460	†	†
	4	39,796	39,004	†	†

† runtime > 1h

# Results

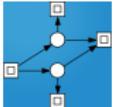


Marcie, average runtime (in sec) for ERK.

N	threads	runs			
		1	100	10,000	1,000,000
1	1	0.0	0.0	0.0	13.0
	4	0.0	0.0	0.0	3.0
100	1	0.0	0.0	6.0	617.6
	4	0.0	0.0	1.0	162.5
10,000	1	0.0	6.0	620.3	†
	4	0.0	1.0	161.8	†
1,000,000	1	6.0	621.2	†	†
	4	6.0	163.5	†	†

† runtime > 1h

# Results

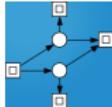


## Marcie, peak memory consumption (in KB) for ERK.

N	threads	runs			
		1	100	10,000	1,000,000
1	1	0,000	0,000	5,172	3,128
	4	3,126	0,000	5,324	5,324
100	1	0,000	5,172	3,132	3,156
	4	0,000	5,324	5,328	5,360
10,000	1	3,124	3,152	3,156	†
	4	3,128	5,328	5,356	†
1,000,000	1	3,148	3,160	†	†
	4	3,128	5,364	†	†

† runtime > 1h

# Results



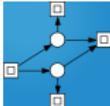
## CAIN, average runtime (in sec) for ERK.

N	threads	runs			
		1	100	10,000	1,000,000
1	1	0.0222	0.1160	8.1655	*
	4	0.0231	0.0943	4.2285	*
100	1	0.0231	0.1426	10.9276	*
	4	0.0239	0.1048	5.1622	*
10,000	1	0.0315	1.8656	183.8095	*
	4	0.0338	0.6837	60.1041	*
1,000,000	1	1.7569	173.7179	†	*
	4	1.7658	56.9456	†	*

† runtime > 1h

\* tool crash while performing simulation

# Results



## CAIN, peak memory consumption (in KB) for ERK.

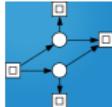
Table: CAIN peak memory consumption (in KB) for ERK.

N	threads	runs			
		1	100	10,000	1,000,000
1	1	110,048	113,544	201,795	*
	4	110,520	117,912	109,125	*
100	1	112,196	112,960	199,904	*
	4	110,944	117,316	203,208	*
10,000	1	110,080	114,324	199,728	*
	4	110,468	118,568	202,600	*
1,000,000	1	111,200	115,408	†	*
	4	111,792	118,192	†	*

† runtime > 1h

\* tool crash while performing simulation

# Results

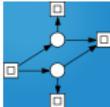


## StochKit2, average runtime (in sec) for ERK.

N	threads	runs			
		1	100	10,000	1,000,000
1	1	0.0080	0.0134	0.4421	42.7381
	4	0.0080	0.0172	0.1284	11.5534
100	1	0.0080	0.0425	3.3970	338.0346
	4	0.0083	0.0276	0.9099	88.4614
10,000	1	0.0380	2.9934	294.4733	†
	4	0.0381	0.8301	77.7298	†
1,000,000	1	2.9665	296.6058	†	†
	4	2.9649	80.5857	†	†

† runtime > 1h

# Results

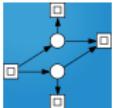


## StochKit2, peak memory consumption (in KB) for ERK.

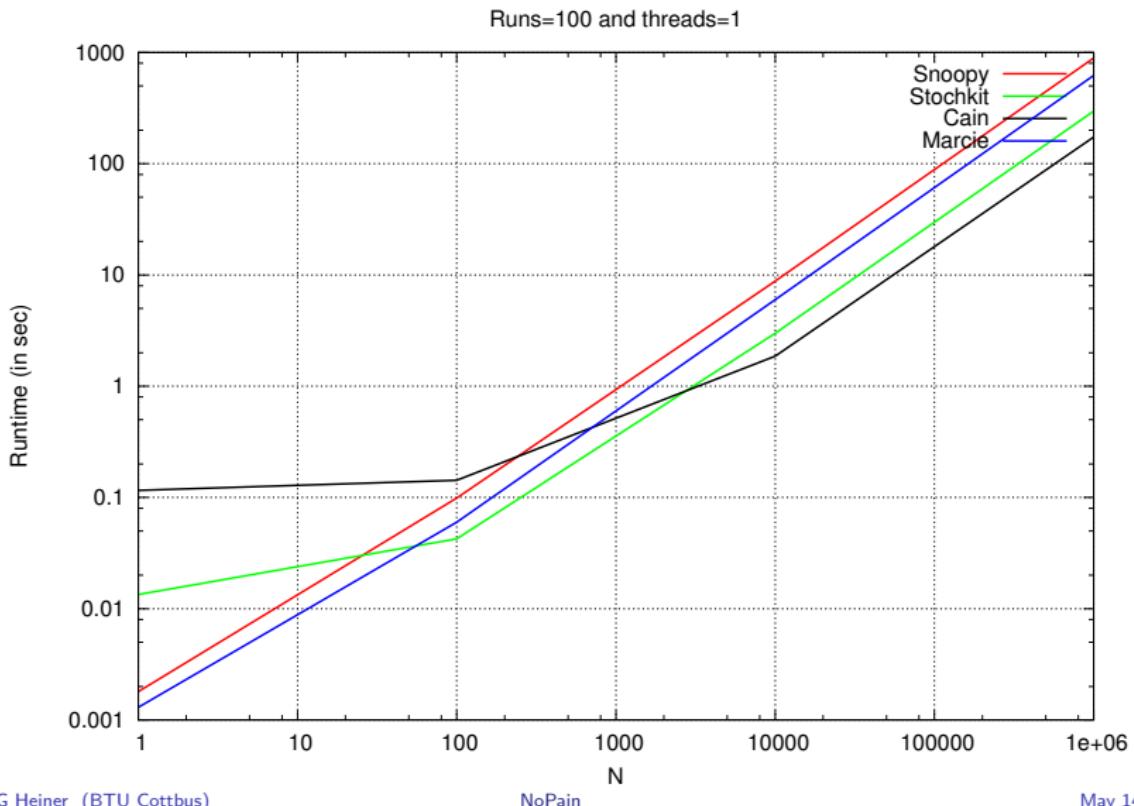
N	threads	runs			
		1	100	10,000	1,000,000
1	1	2,748	2,752	9,904	9,924
	4	2,748	2,748	20,560	24,800
100	1	2,748	2,748	9,982	9,924
	4	2,748	2,748	24,786	26,832
10,000	1	2,748	9,904	9,932	†
	4	2,748	24,800	24,876	†
1,000,000	1	9,964	9,968	†	†
	4	9,916	24,920	†	†

† runtime > 1h

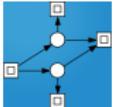
# Result



## Comparison: average run time

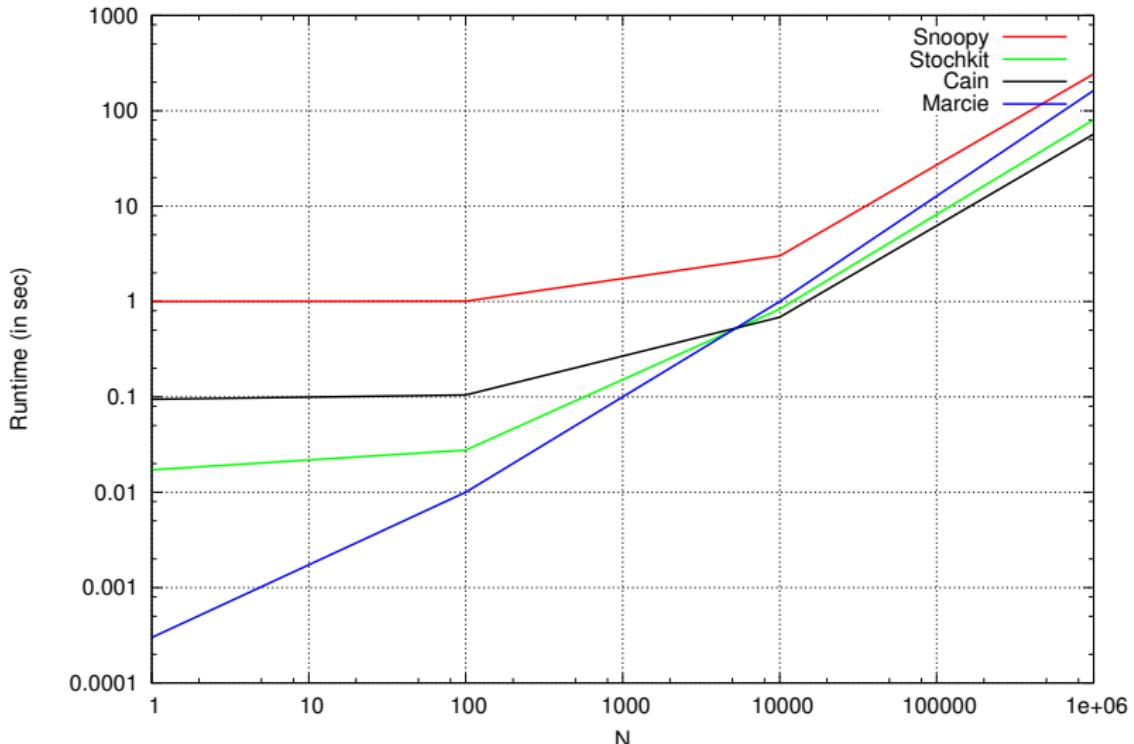


# Result

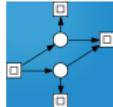


## Comparison: average run time

Runs=100 and threads=4



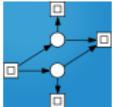
# Results



## Multithreading Coefficient

Tool	Threading Coefficient	Variation
CAIN	3.0544	0.01
MARCIE	3.8112	0.02
SNOOPY	3.7387	0.07
STOCHKIT	3.7474	0.07

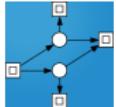
# Conclusions



## So far

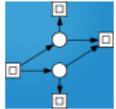
- 1 *CAIN* fastest, highest memory consumption (leak?)
- 2 *StochKit2* very fast
- 3 *Marcie* fast, lowest memory consumption
- 4 *Snoopy*

# Milestones

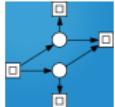


	2013				2014				2015			
	Q1	Q2	Q3	Q4	Q1	Q2	Q3	Q4	Q1	Q2	Q3	Q4
WP1	M1											
WP2		M2										
WP3			M3									
WP4					M4							
WP5						M4						
WP6							M5					
WP7									M6			

Next steps...



- finish tool comparison
- go on with WP 4 & 5



Thank you for your attention!