

Possibilities of Petri Net Theory to validate metabolic pathways

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Outline

- Introduction
- Petri net basics
- Analysis possibilities
- Sucrose-to-starch breakdown in the potato tuber
- Simulation of the net
- Conclusions

Introduction

Metabolic Control Analysis - MCA

Metabolic system: connected unit, steady state

MCA is based on solution of systems of differential equations

- MCA Kacser & Burns, *Symp.Soc.Exp.Bio.* (1973)
Heinrich & Rapoport, *Eur.J.Biochem.* (1974)
- Biochemical systems theory
Savageau, *J.Theor.Biol.* (1969)
- Flux oriented theory
Crabtree & Newsholme, *Biochem.J.* (1987)

GEPASI Mendes, *Comp.Appl.Biosci.* (1993)

Introduction

Graph-Theory

- Hybrid graphs Kohn & Letzkus, *J.Theor.Biol.* (1983)
- Bond graphs Lefèvre & Barreto, *J.Franklin Inst.* (1985)
- Net-thermodynamics Mikulecky, *Am.J.Physiol.* (1993)
- Weighted linear graphs Goldstein & Shevelev, *J.Theor.Biol.* (1985)
Goldstein & Selivanov, *Biomed.Biochim.Acta* (1990)
- Meta-nets (with gene expression systems)
Kohn & Lemieux, *J.Theor.Biol.* (1991)
- Bipartite graphs Zeigarnik & Temkin, *Kin.Catalysis* (1994)
- KING (KI Netic Graphs) Zeigarnik, *Kin.Catalysis* (1994)

Introduction

- Why is a model validation (check model consistency) useful?
 - Before starting a quantitative analysis it should be sure that the model is valid.
 - If the systems become larger with many interactions and regulations it could not be done manually any more.

- How model validation could be performed?
By qualitative analysis

Basic dynamic properties: liveness, reversibility, boundedness,
dead states, deadlocks, traps,

Basic structure properties: invariants, robustness, alternative pathways,



Petri net theory provides algorithms and tools to answer these questions.

etri net basics

Petri nets (PhD thesis of Carl Adam Petri 1962)

abstract models of information and control data flows, which allow to describe systems and processes at different abstraction levels and in a unique language
- developed for systems with causal concurrent processes

Applications: business processes, computer communication, automata theory,
operating systems, software dependability

Biological networks: metabolic networks, signal transduction pathways,
gene regulatory networks

Reddy, Mavrovouniotis, Liebman, *Proc. ISMB* (1993), *Comp.Mol.Med.* (1996)

Hofestädt, *J.Syst.Anal., Modell., Sim.* (1994), Hofestädt & Thelen, *In silico Biol* (1998)

Matsuno et al., *Proc.PSB* (2000), *In silico Biol.* (2003), *Proc.IACATPN* (2003) ,

Voss, Heiner, Koch, *BioSystems* (2004), Heiner, Koch, Will, *Proc.Comp.Methods Syst.Biol.*

(2003)

Heiner, Voss, Koch, *In Silico Biology* (2003)

Metabolic Petri Net - MPN

etri net basics

Petri nets: directed, labelled, bipartite graphs

Nodes:
(vertiecs)

places

transitions

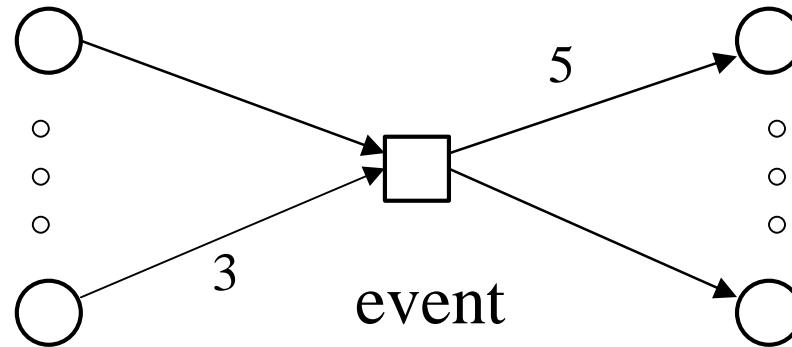


passive elements
conditions
states
chemical compounds
metabolites

active elements
events
actions
chemical reactions
conversions of metabolites
catalysed by enzymes

etri net basics

Arcs: pre-conditions post-conditions
(edges)



etri net basics

Tokens: movable objects in discrete units,
e.g. units of substances (mole)

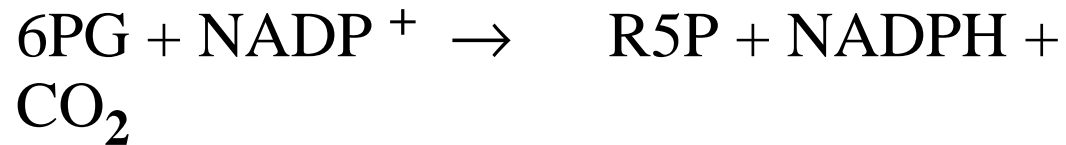
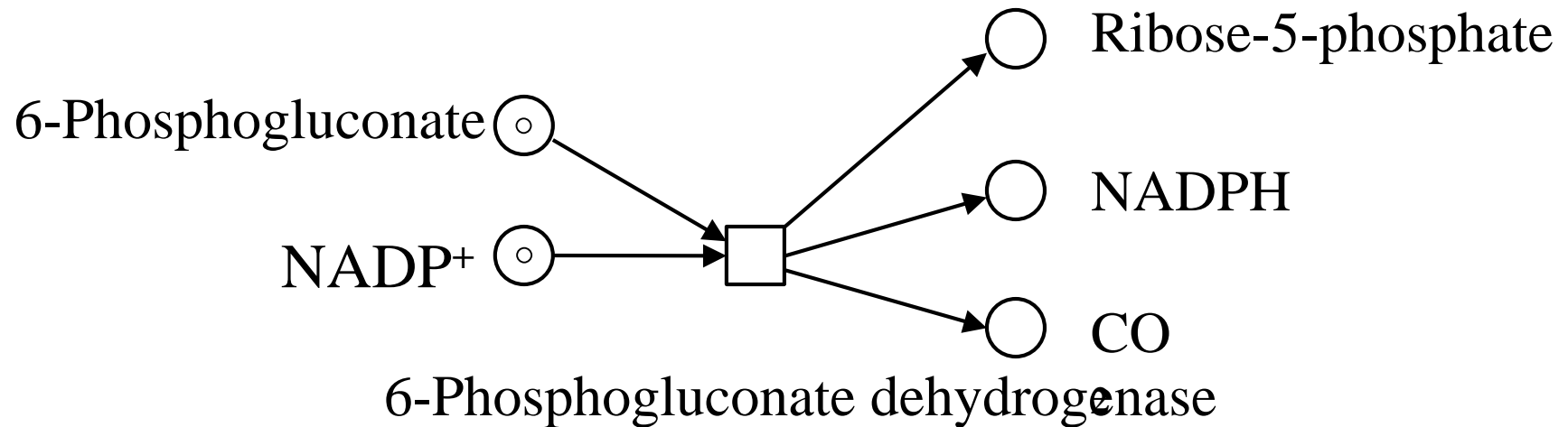
- condition is not fulfilled
- condition is (one time) fulfilled
- Ⓝ condition is n times fulfilled

Marking: system state, token distribution, initial marking

Token flow: occurring of an event (firing of a transition)

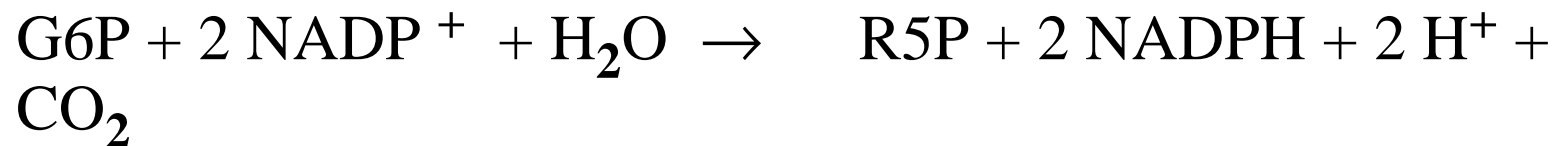
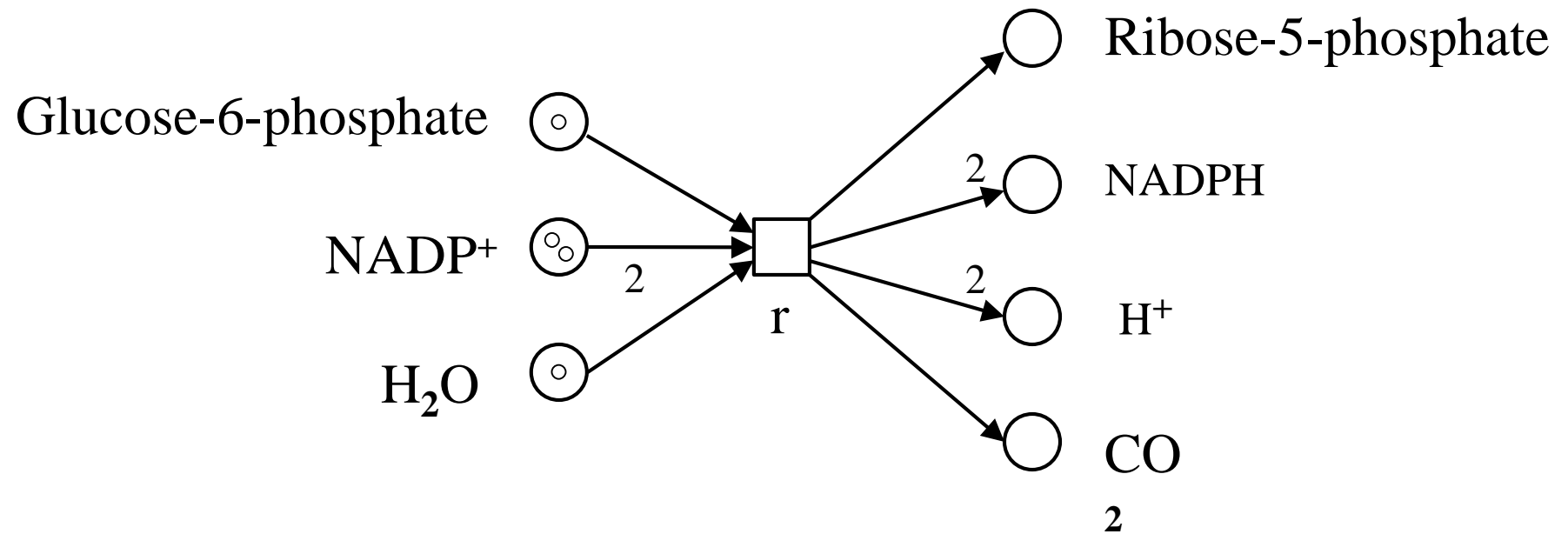
etri net basics

Example: Pentose Phosphate Pathway - one reaction



etri net basics

Example: Pentose Phosphate Pathway - sum reaction



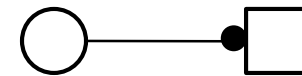
etri net basics

Special places:

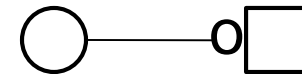
input: substrates (source, e.g. sucrose)

output: products (sink, e.g. starch)

Special arcs: reading arcs



inhibitor arcs



Additional places & transitions:

logical



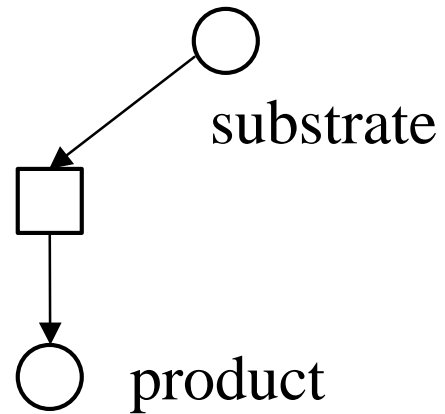
hierarchical



etri net basics

Transitions in MPNs:

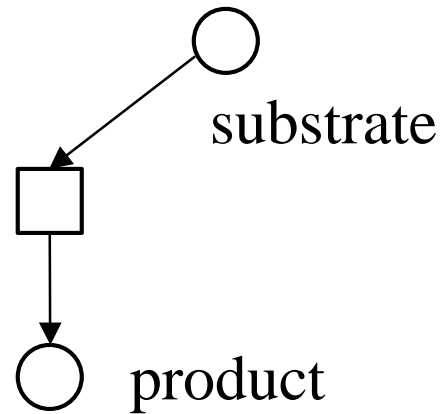
Reaction:



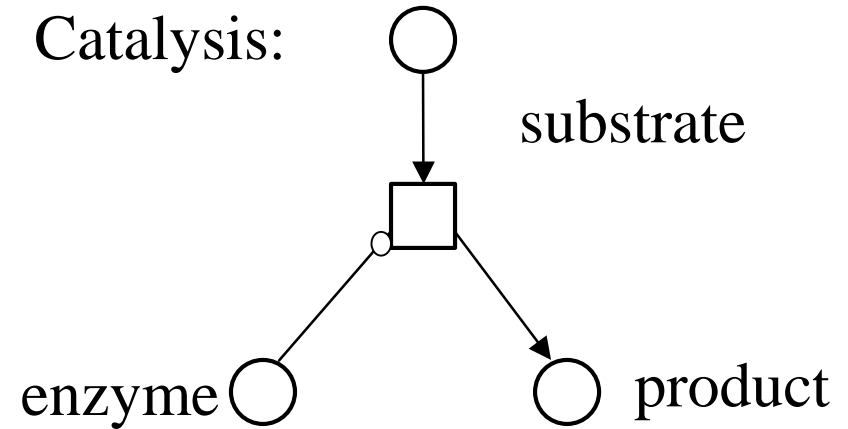
etri net basics

Transitions in MPNs:

Reaction:



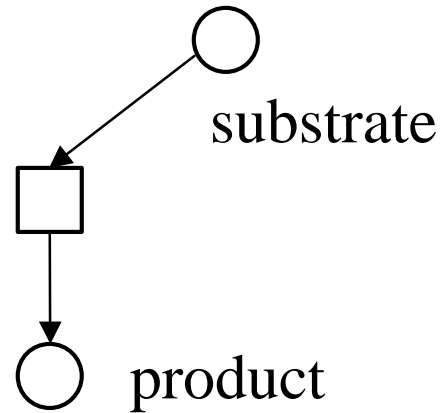
Catalysis:



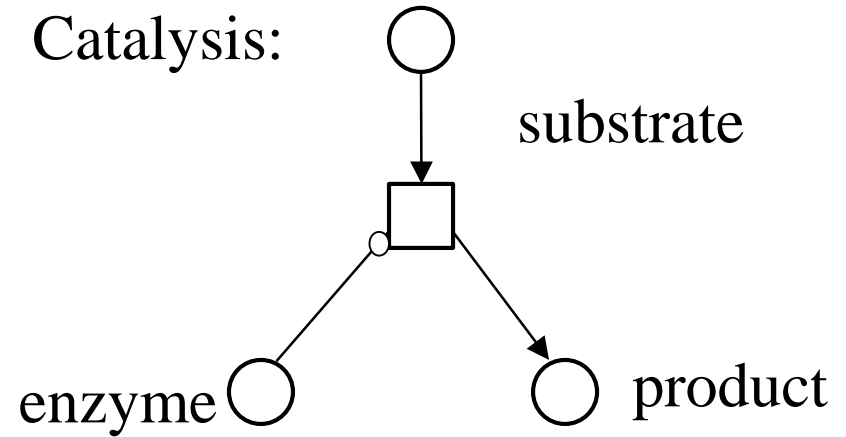
etri net basics

Transitions in MPNs:

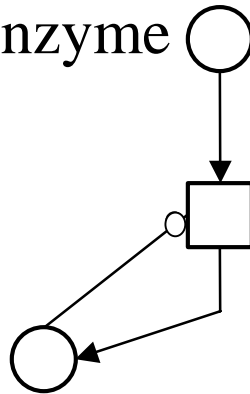
Reaction:



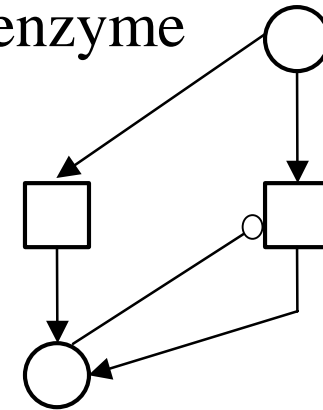
Catalysis:



Auto-catalysis: pro-enzyme



product = enzyme



pro-enzyme

odel validation

- (1) Dynamical (behavioural) properties
- (2) Reachability analysis
- (3) Structural analysis
- (4) Invariant analysis

ynamic (behavioural) properties

liveness and reversibility

- a net is live, if all its transitions are live in the initial marking
- a net is reversible, if the initial marking can be reached from each possible state
- How often can a transition fire? (0-times, n-times, ∞ times)
- infinite systems behaviour, search for dead transitions
- prediction of system deadlocks

ynamic (behavioural) properties

boundedness

- a net is bounded, if there exists a positive integer number k , which represents a maximal number of tokens on each place in all states
- What is the maximal token number for a place?
(0, 1, k , ∞) boundedness (k-bounded)
- for bounded nets special algorithms exist

eachability analysis

How many and which system states could be reached ? (0, 1, k, ∞)

- the reachability graph represents all possible states
- computational problem for large and dense biological networks
- for unbounded networks: computation of the coverability graph
- Is a certain system state again and again reachable?
progressiveness
- Is a certain system state never reachable? safety

structural analysis

- aims at discovering net structures to derive conclusions on dynamic properties

Elementary properties:

ordinary: the multiplicity of every arc is equal one

homogeneous: for any place all outgoing edges have the same multiplicity

pure: there is no transition, for which a pre-place is also a post-place (loop-free)

conservative: for each place the sum of input arc weights is equal to the sum of output arc weights – a conservative net is bounded

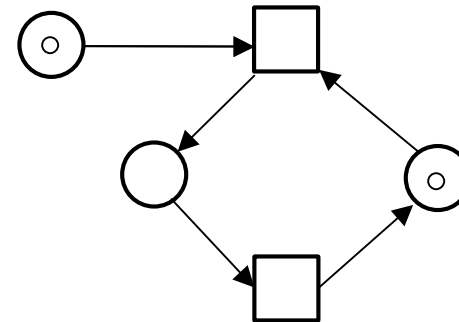
static conflict-free: there are no transitions with a common pre-place

connected, strongly connected: in graph-theoretical sense

structural analysis

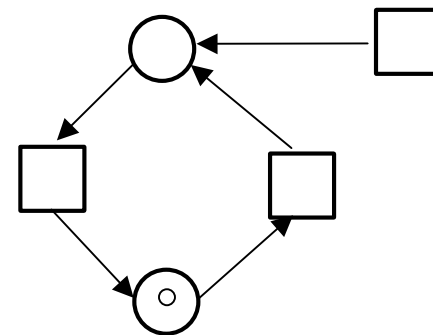
structural deadlock:

a set of places that delivers its tokens until a state is reached, where the place set is empty and there is no possibility to get a new token



trap:

the opposite situation that tokens cannot be removed from a place set



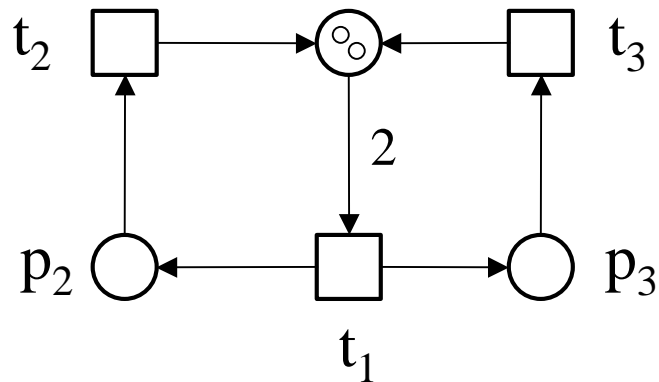
invariant analysis

- properties, which are conserved during the working of the system
- independent of the initial marking
- only the net structure is relevant for their calculation

Are there invariant structures, which are independent from firing of the system?

Place-invariants (P-invariants)
Transition-invariants (T-invariants)

invariant analysis



place (P-) invariant:

$$x C = 0$$

$$-2x_1 + x_2 + x_3 = 0$$

$$x_1 - x_2 = 0$$

$$x_1 - x_3 = 0$$

incidence matrix $C = P \times T$

$$C = \begin{matrix} & \begin{matrix} t_1 & t_2 & t_3 \end{matrix} \\ \begin{matrix} p_1 \\ p_2 \\ p_3 \end{matrix} & \begin{pmatrix} -2 & 1 & 1 \\ 1 & -1 & 0 \\ 1 & 0 & -1 \end{pmatrix} \end{matrix}$$

transition (T-) invariant:

$$C y = 0$$

$$-2y_1 + y_2 + y_3 = 0$$

$$y_1 - y_2 = 0$$

$$y_1 - y_3 = 0$$

T-invariant analysis

Minimal semi-positive solutions are of interest with

- all components of the solution vector are ≥ 0
- basis of the semi-positive solution space such that none solution is contained in another solution, Lautenbach (1973)

The calculation

- of all integer solutions is in P
- of all semi-positive solutions is in P
- of all semi-positive integer solutions is NP-complete, Schrijver (1999)

Extreme Pathways, Schilling et al. (2000)

- minimal basis of semi-positive integer solutions (Hilbert-base)
- subset of T-invariants – biological interpretation?

P-invariant analysis

Interpretation

P-invariants

- set of places, whose weighted sum of tokens is constant
- covered by P-invariants: sufficient condition for boundedness
liveness
- set of metabolites, whose total net concentrations remain unchanged
ADP, ATP
NADP⁺, NADPH

T-invariants

- set of transitions, whose firing reproduces a given marking
- covered by T-invariants: necessary condition for
- minimal set of enzymes which could operate at steady state
- indicate the presence of cyclic firing sequences
Elementary modes
Schuster, Hilgetag, Schuster (1993)

ucrose-to-starch-pathway in potato tuber



- rich in carbohydrates and energy
- a natural source of folate
- full of vitamin C
- low in calories
- good source of niacin, vitamin B6, iodine, thiamine, and minerals
- no cholesterol
- completely fat free

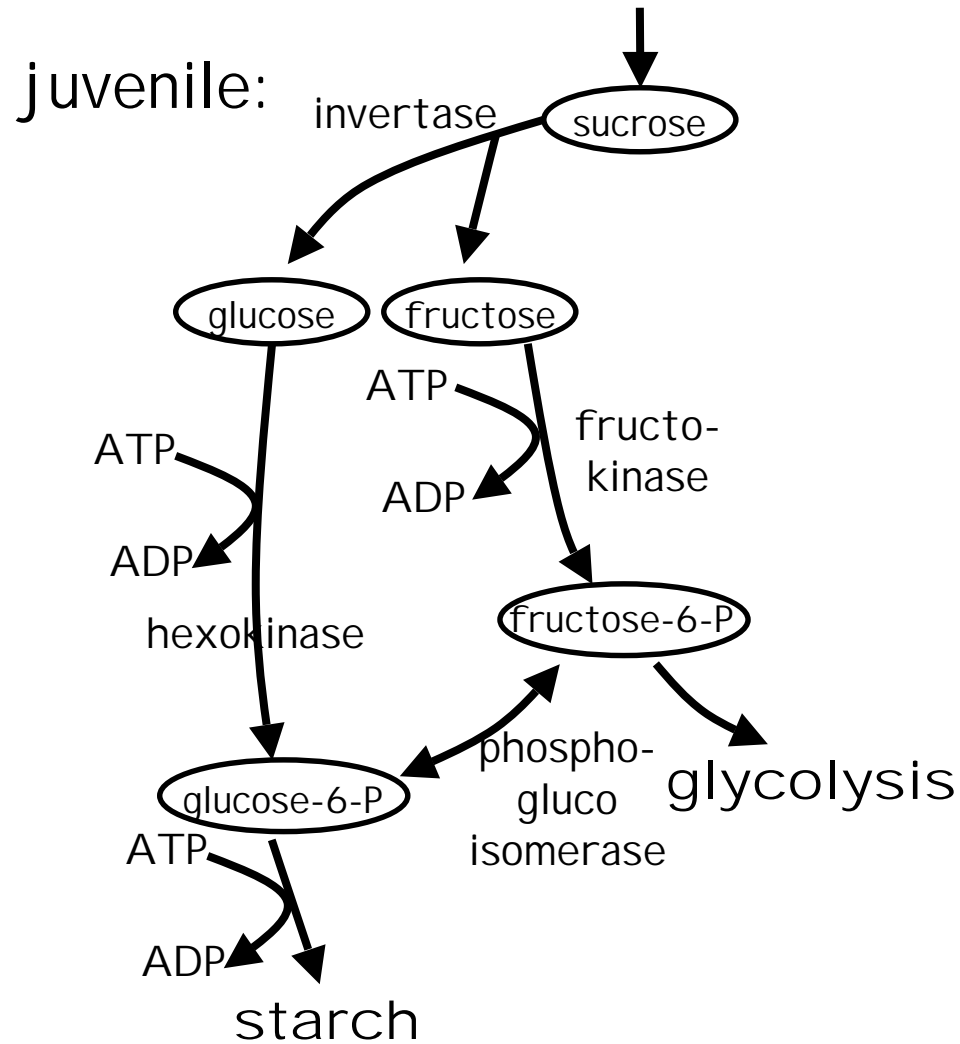
Fernie, Willmitzer, Trethewey (2002)

Research interest: increasing the starch content

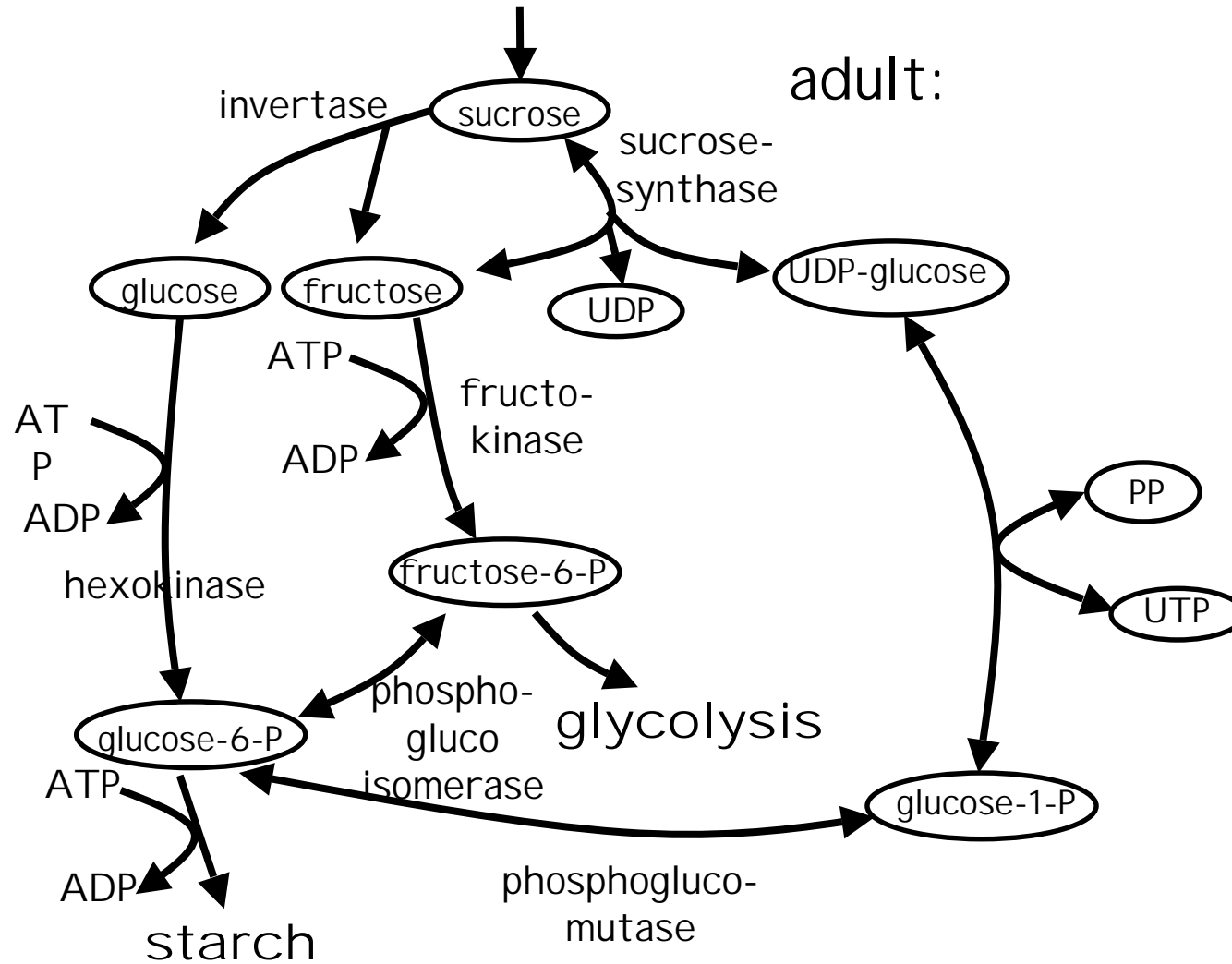
Co-operations: Max Planck Institute for Molecular Plant Physiology, Golm

Brandenburg University of Technology at Cottbus

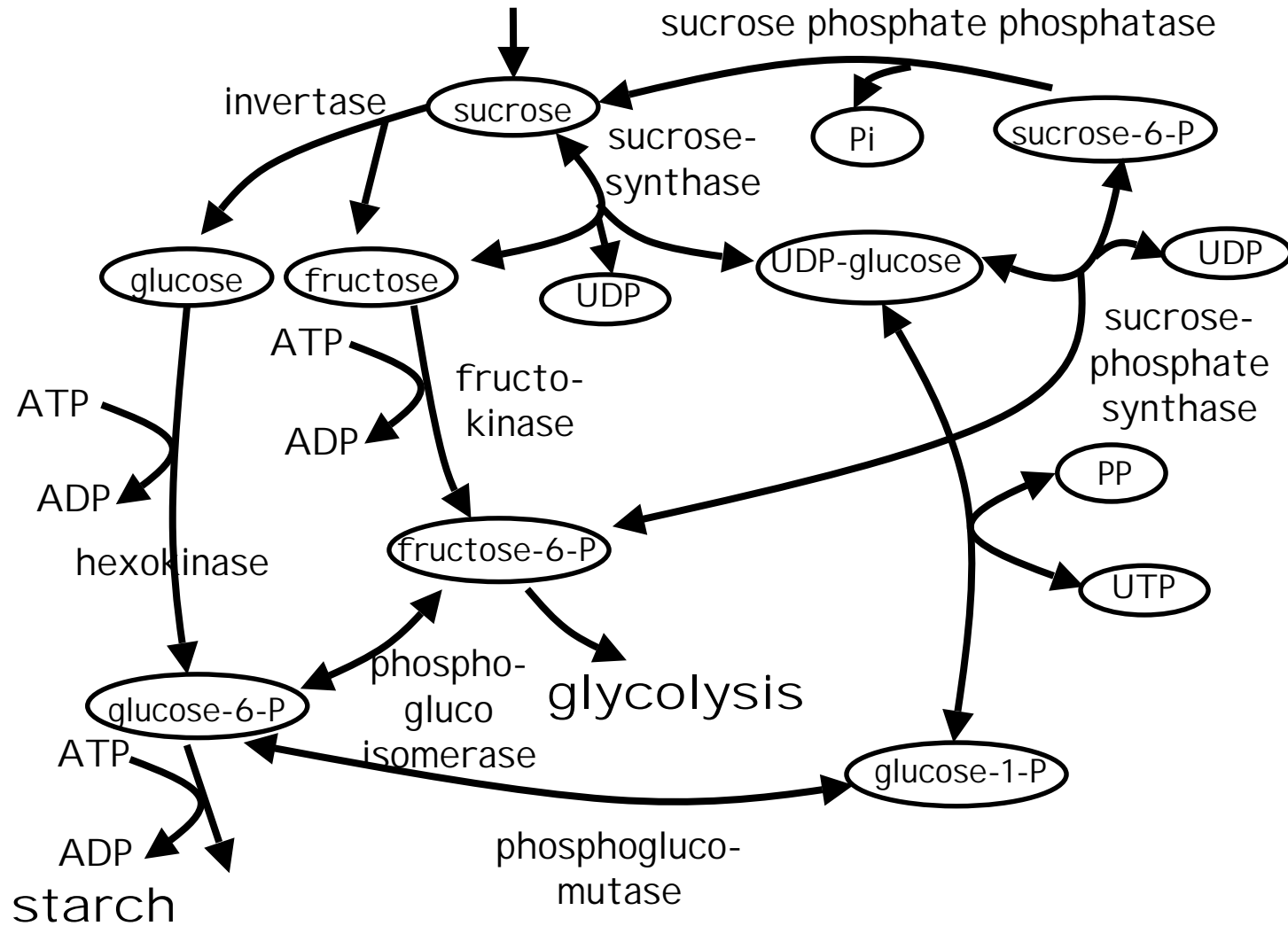
sucrose-to-starch-pathway in potato tuber



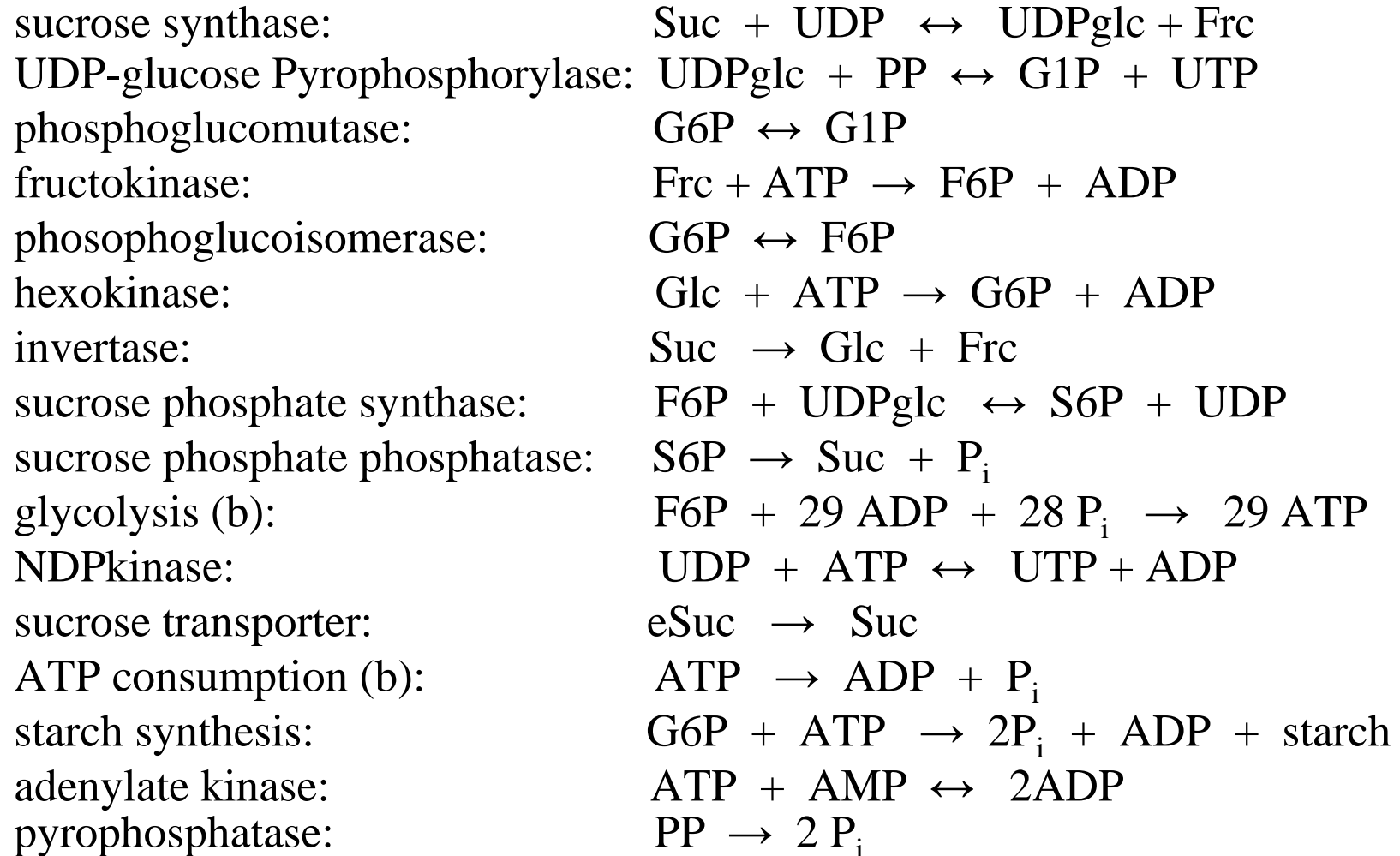
ucrose-to-starch-pathway in potato tuber

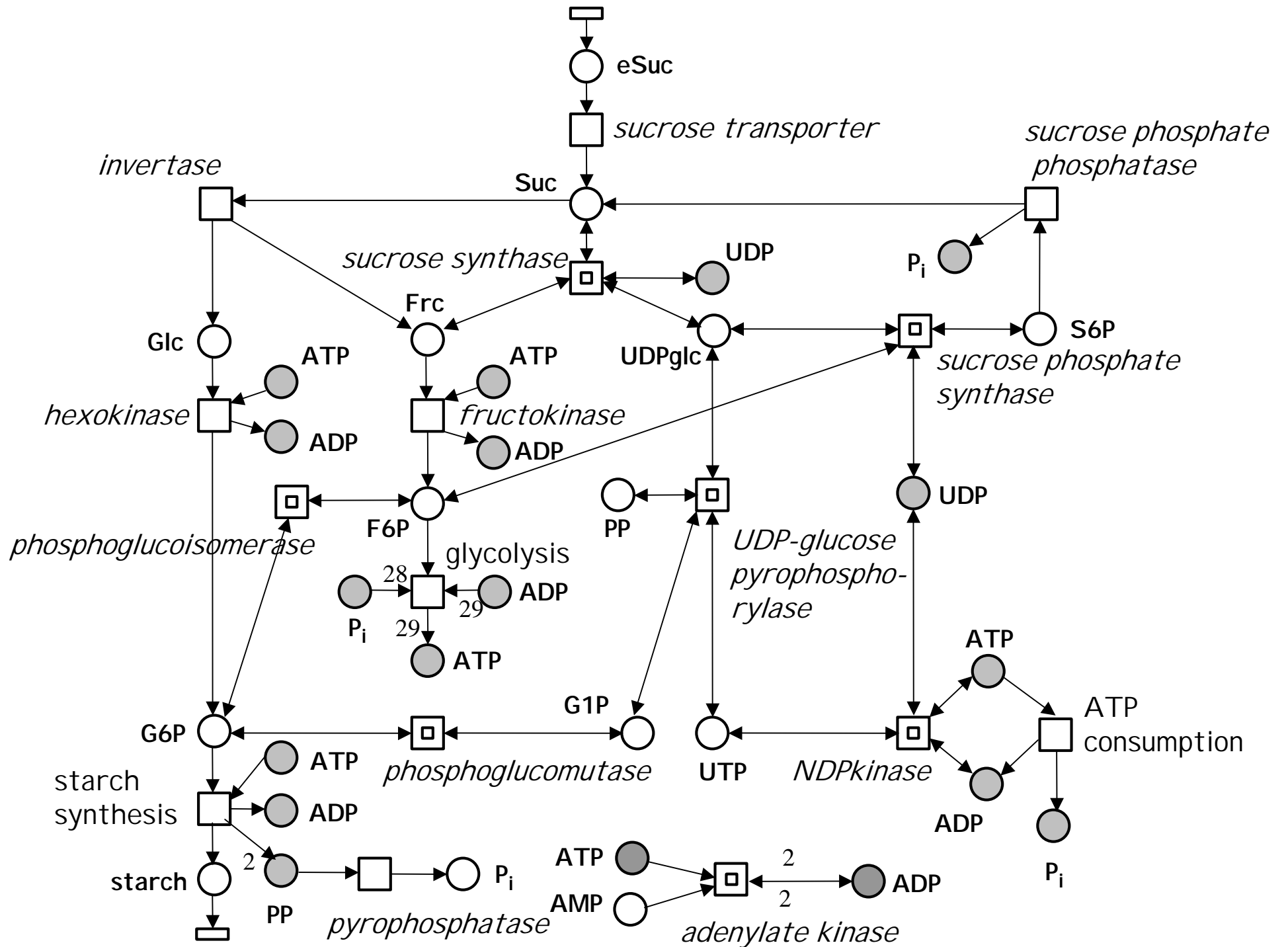


ucrose-to-starch-pathway in potato tuber



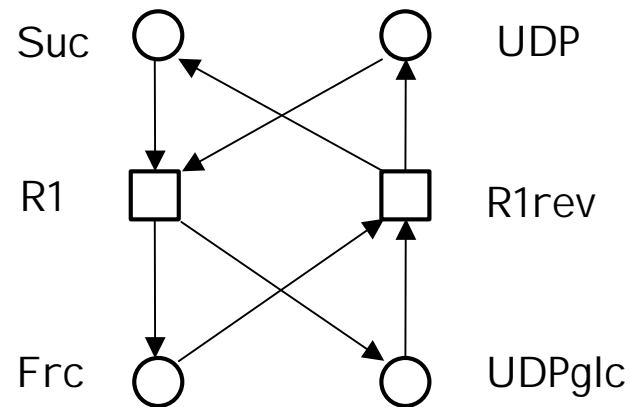
ucrose-to-starch-pathway in potato tuber



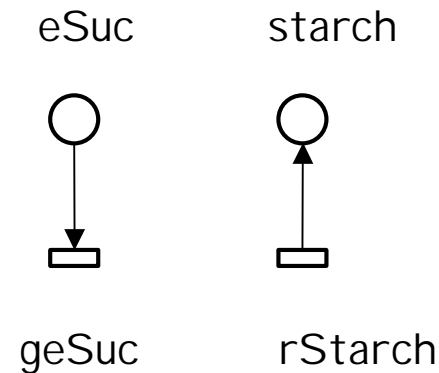


ucrose-to-starch-pathway in potato tuber

A hierarchical node:



Interface to the environment



Tools:

Editing: Ped Heiner BTU Cottbus

Animation: PedVisor <http://www.informatik.tu-cottbus.de/~wwwdssz/>

Qualitative analysis: INA Starke HU Berlin
[http://www.informatik.hu-](http://www.informatik.hu-berlin.de/~starke/ina.html)

[berlin.de/~starke/ina.html](http://www.informatik.hu-berlin.de/~starke/ina.html)

Qualitative analysis using INA

Elementary properties

The net is not statically conflict-free.

The net has transitions without pre-place.

The net is not covered by semipositive P-invariants.

The net is not structurally bounded.

The net is not safe.

The net has transitions without post-place.

The net is not ordinary.

At least the following transitions are live: 0.SucTrans, 1.Inv, 18.geSuc,

At least the following places are simultaneously unbounded: 0.Suc, 1.eSuc, 2.Glc, 3.Frc,

The net is marked.

The net is not homogenous.

The net has no nonempty clean trap.

The net has no places without post-transition.

The net is connected.

The net is pure.

The net is not strongly connected.

The net is not bounded.

The net is not live and safe.

Transition 18.geSuc has no pre-place.

Transition 21.rStarch has no post-place.

The net is not conservative.

The net is not marked with exactly one token

The net has not a non-blocking multiplicity

The net has no places without pre-transition

Maximal in/out-degree: 6

ORD	HOM	NBM	PUR	CSV	SCF	CON	SC	Ft0	tF0	Fp0	pF0	MG	SM	FC	EFC	ES
N	N	N	Y	N	N	Y	N	Y	Y	N	N	N	N	N	N	N

Qualitative analysis using INA

Structural properties

DTP	CPI	CTI	B	SB	REV	DSt	BSt	DTr	DCF	L	LV	L&S
?	N	Y	N	N	?	?	?	?	?	?	?	N

- liveness could not be decided because the net is unbounded and the reachability graph cannot be calculated
- the coverability graph has more than 4 million states

smaller bounded version: more than 10^{10} states of the reachability graph

P-Invariant analysis

The net is not covered by P-invariants.

Following P-invariants were calculated:

1. UDPglc, UTP, UDP
2. ATP, AMP, ADP
3. G6P, F6P, G1P, UTP, ATP(2), ADP, S6P, P_i, PP(2)

T-Invariant analysis

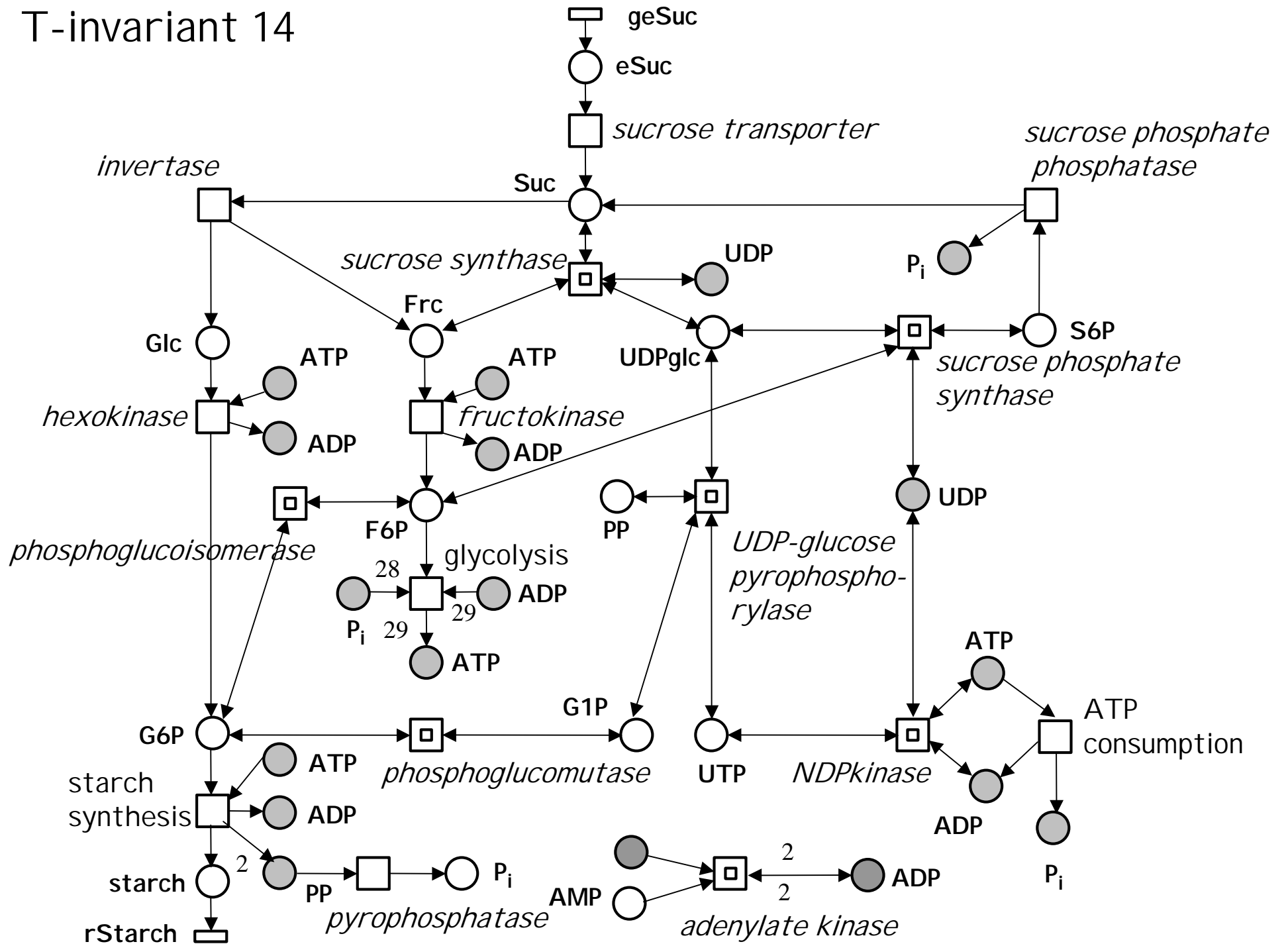
The net is covered by 19 T-invariants

7 trivials: 1. SPS, SPS_rev, 2. UGPase, UGPASE_rev,
3. SuSy_SuSy_rev, 4. PGM, PGM_rev,
5. NDPkin, NDPkin_rev, 6. AdK, AdK_rev,
7. PGI, PGI_rev

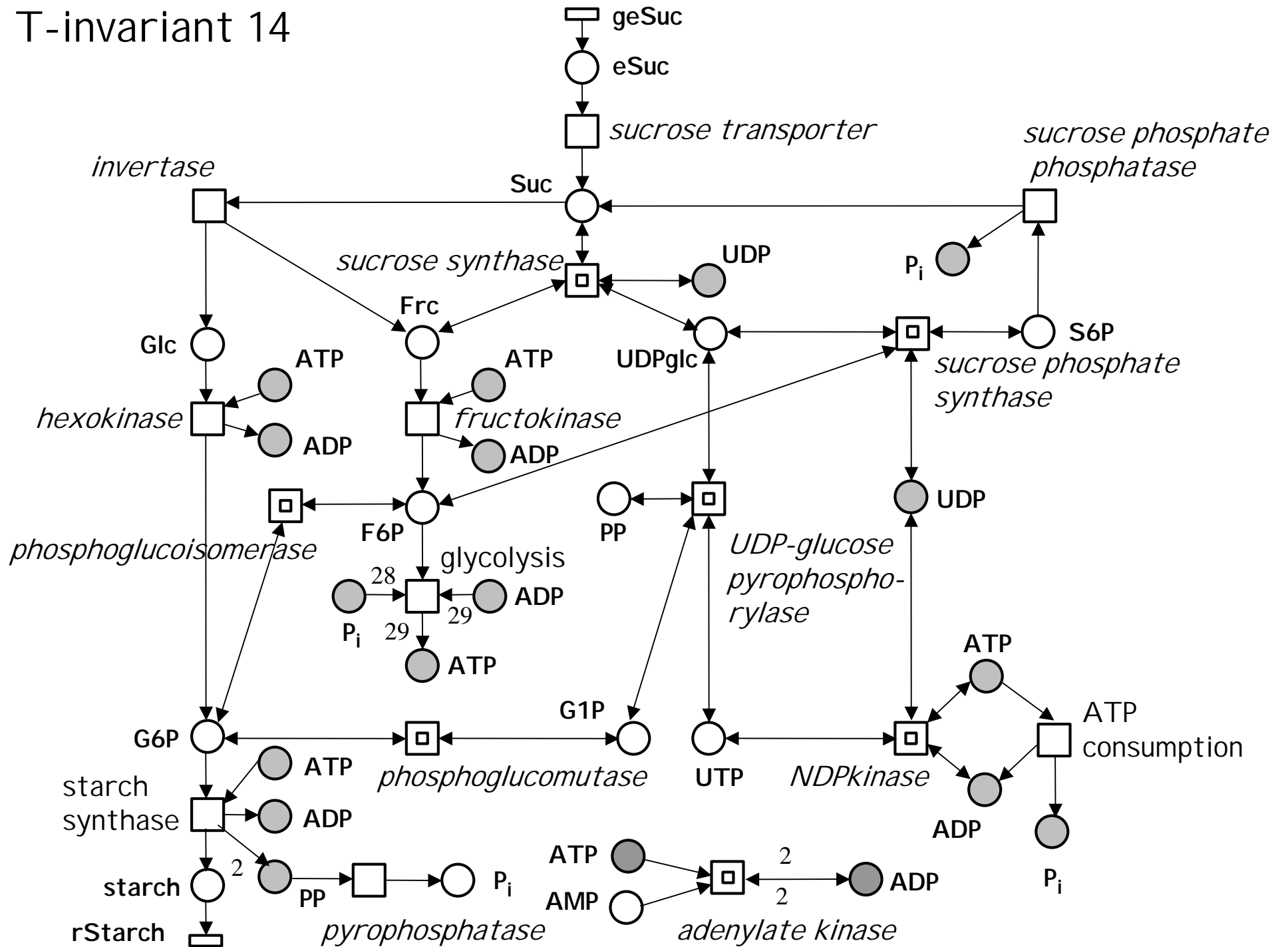
Example:

8		0.sucrose	:	1
		1.invertase	:	1
		4.R5	:	1
		9.hexokinase	:	1
		10.fructokinase	:	1
		18.geSuc	:	1
		19.glycolysis	:	2
		20.ATP	:	56

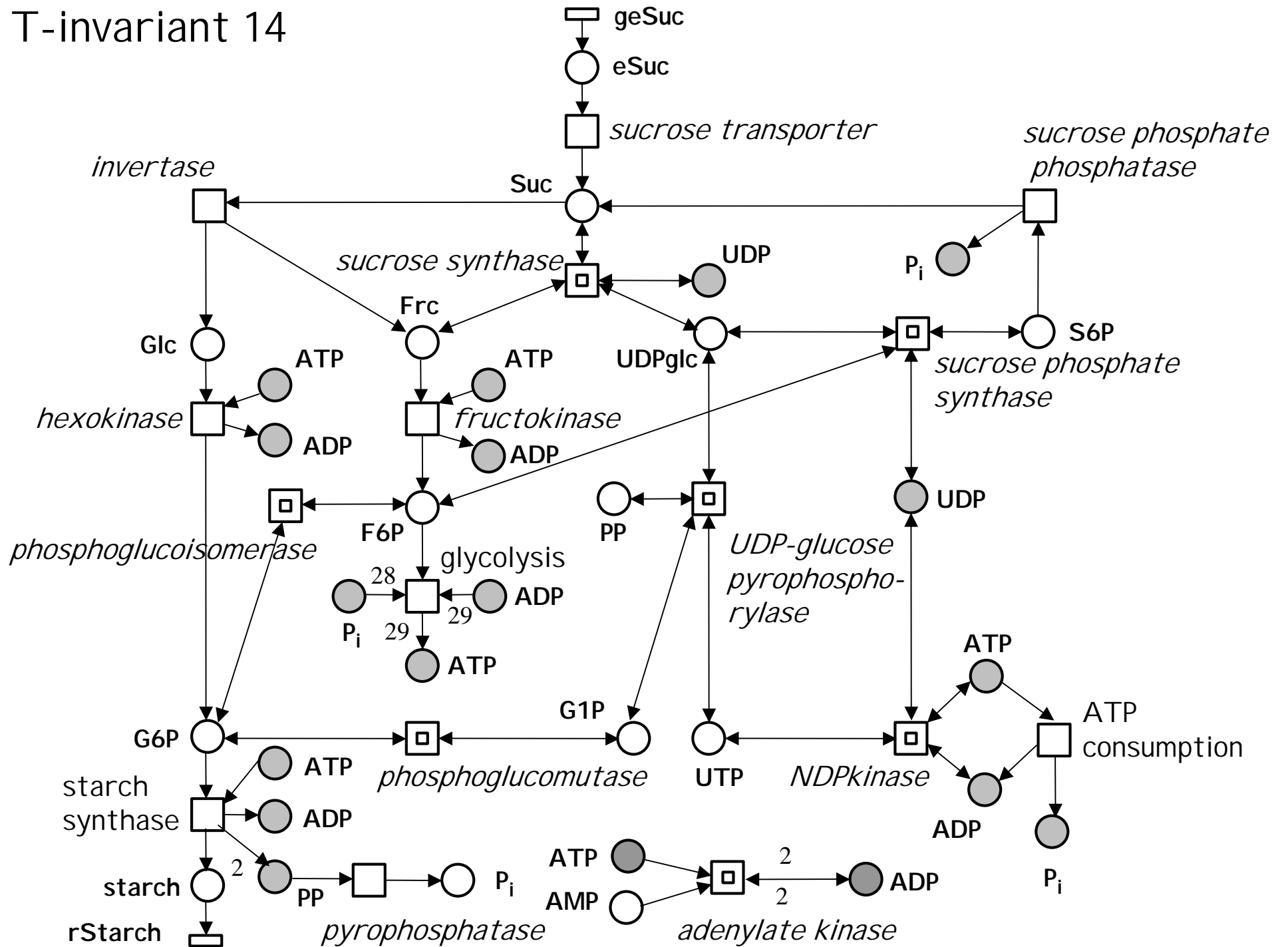
T-invariant 14



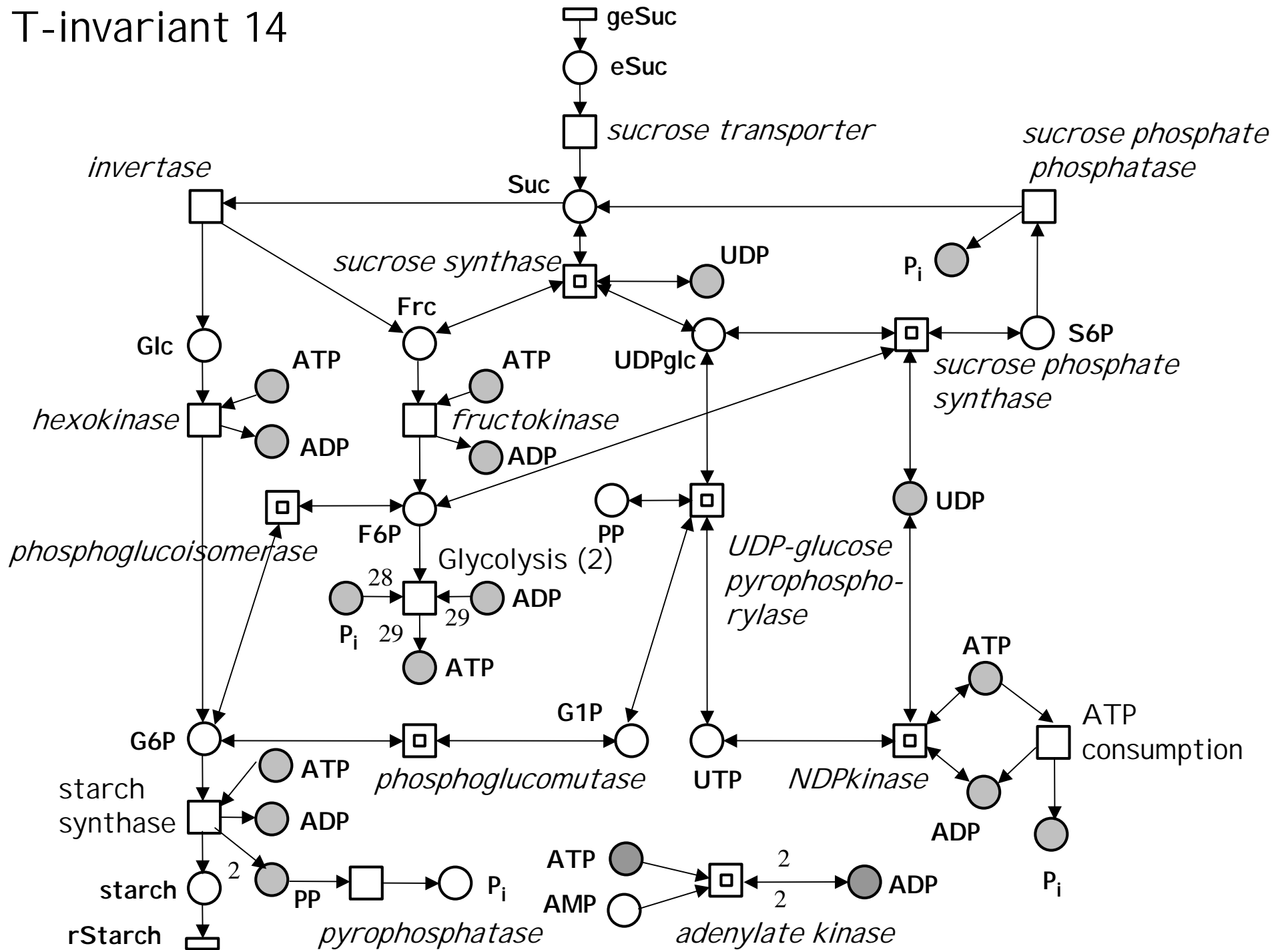
T-invariant 14



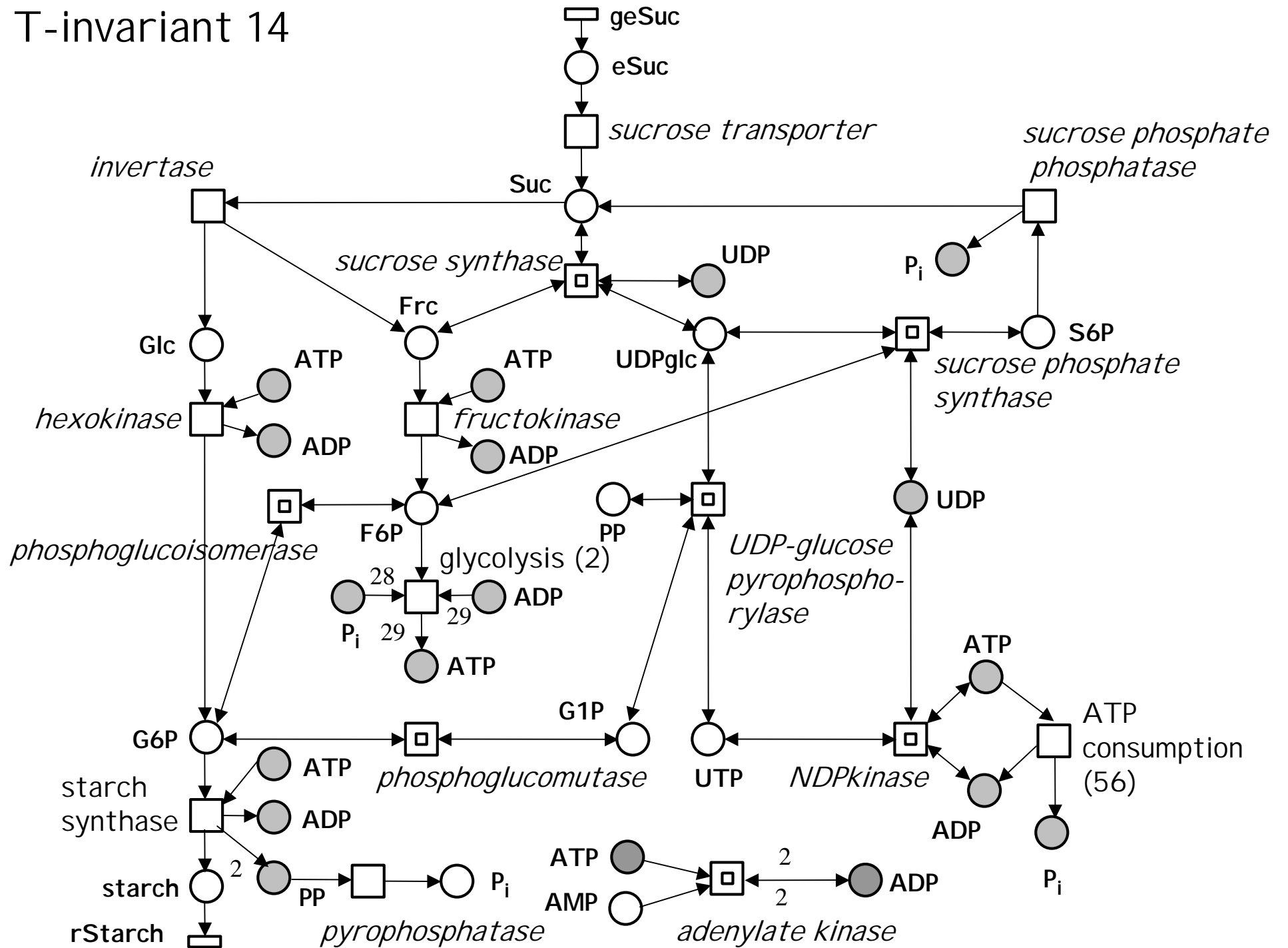
T-invariant 14



T-invariant 14



T-invariant 14



T-Invariant analysis

Invariant number	sucrose cleavage		hexoses go into		ATP cons	ATP used for cycling		
	SuSy	Inv	Glyc	StaSy		Inv SuSy_rev	Inv SPS, SPP	SuSy SPS, SPP
8	x		x	x				x
9	x		x	x	x			
10	x		x	x				
11		x	x	x		x		
12		x	x	x			x	
13		x	x	x				x
14		x	x	x	x			
15		x	x	x				
16		x	x			x		
17		x	x				x	
18		x	x					x
19		x	x		x			

Robustness

Robustness: sensitivity of the system against parameter (fragility) changes (altered enzyme activity, mutations)
(Voit, 2000)

Stelling et al., Nature (2002): linear correlation between robustness and the number of elementary modes (T-invariants)

Our suggestion: - enzyme distribution over T-invariants
- number of alternative paths

Potato net: - fructokinase occurs in all T-invariants
- there is no enzyme that occurs in only one T-invariant

Conclusions & Outlook

Petri nets provide

- (1) a unique description of biological networks
- (2) methods for qualitative analysis to check models by the calculation of system properties.

- (3) The complexity of biological systems make it necessary to extend Petri net methods.
- (4) Automatic interpretation of T-invariants is necessary.

Projects

- Glycolysis-pentose phosphate pathway in erythrocytes
Voss, Heiner, Koch, *BioSystems* in press (2004)
- Apoptosis Heiner, Koch, Will, *Proc.Comp.Methods Syst.Biol.* (2003)
Heiner, Voss, Koch, *In Silico Biology* (2003)

Heiner & Koch, 25th International Conference on Application and Theory of Petri Nets, 21th - 25th June, Bologna, Italy (2004)

Ongoing projects:

1. The whole E.coli pathway Nina Kramer
2. The whole potato tuber pathway Nina Kramer

3. Detailed glycolysis with coloured Petri nets in human
Thomas Runge, BTU Cottbus
4. G1/S - phase in mammalian cells Thomas Kaunath
(tumour cell lines, Duchenne muscle dystrophy)

Thanks!

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Björn Junker (Max Planck Institute for Molecular Plant Physiology Golm)

**Grazie per la vostra
attenzione!**