

PETRI NET BASED MODEL VALIDATION IN SYSTEMS BIOLOGY

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Cottbus**

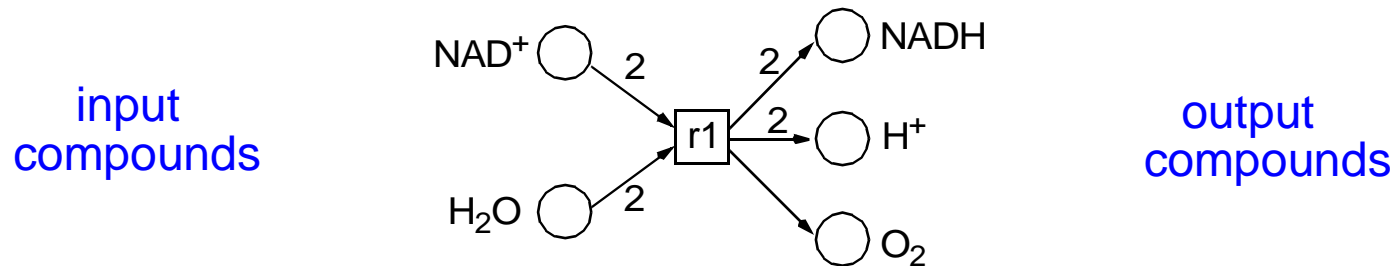
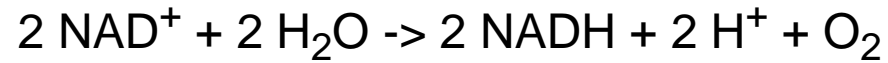
Dep. of CS

Ina Koch

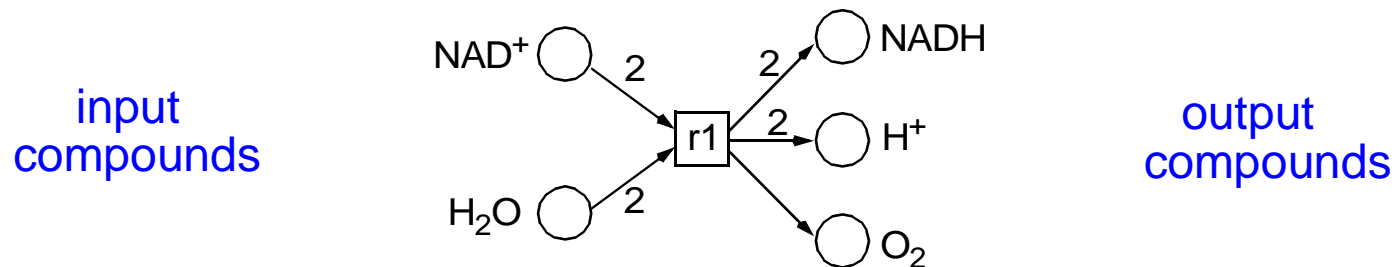
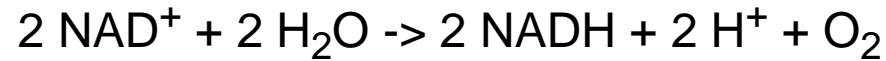
**Technical University of Applied Sciences
Berlin**

Dep. of Bioinformatics

□ chemical reactions → atomic actions → Petri net transitions



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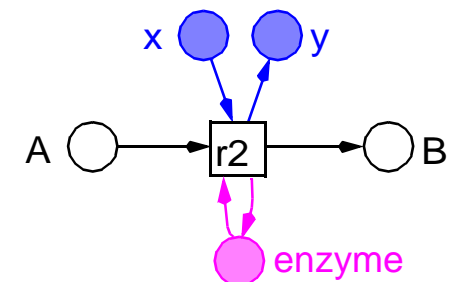


□ chemical compounds

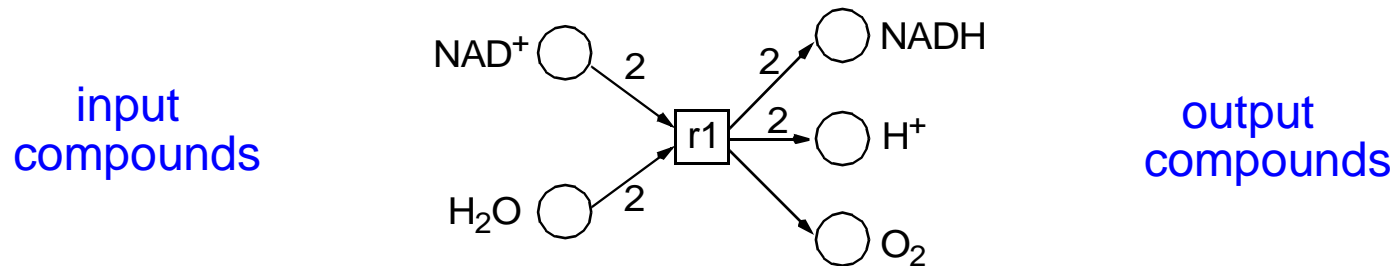
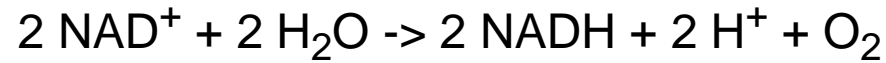
- primary compounds
- auxiliary compounds, ubiquitous → fusion nodes
- catalyzing compounds

→ Petri net places

- metabolites
- e. g. electron carrier
- enzymes

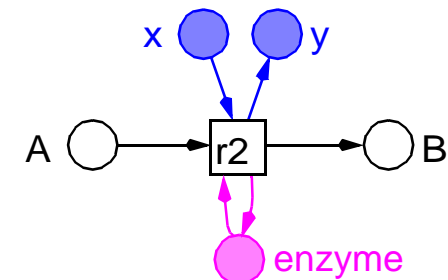


☐ chemical reactions → atomic actions → Petri net transitions



☐ chemical compounds → Petri net places

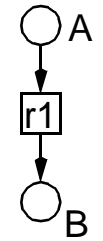
- | | |
|--|--------------------------|
| - primary compounds | - metabolites |
| - auxiliary compounds, ubiquitous → fusion nodes | - e. g. electron carrier |
| - catalyzing compounds | - enzymes |



☐ stoichiometric relations → Petri net arc multiplicities

☐ compounds distribution → marking

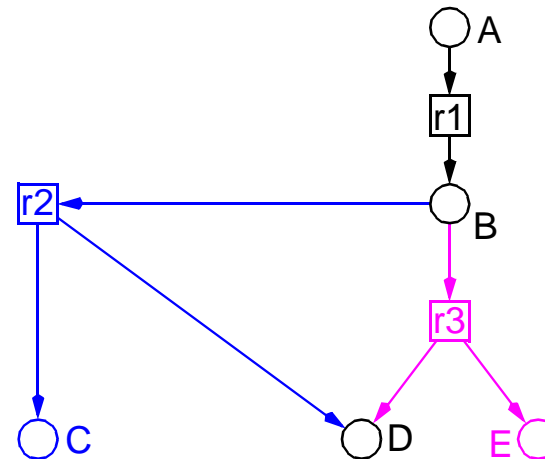
r1: A -> B



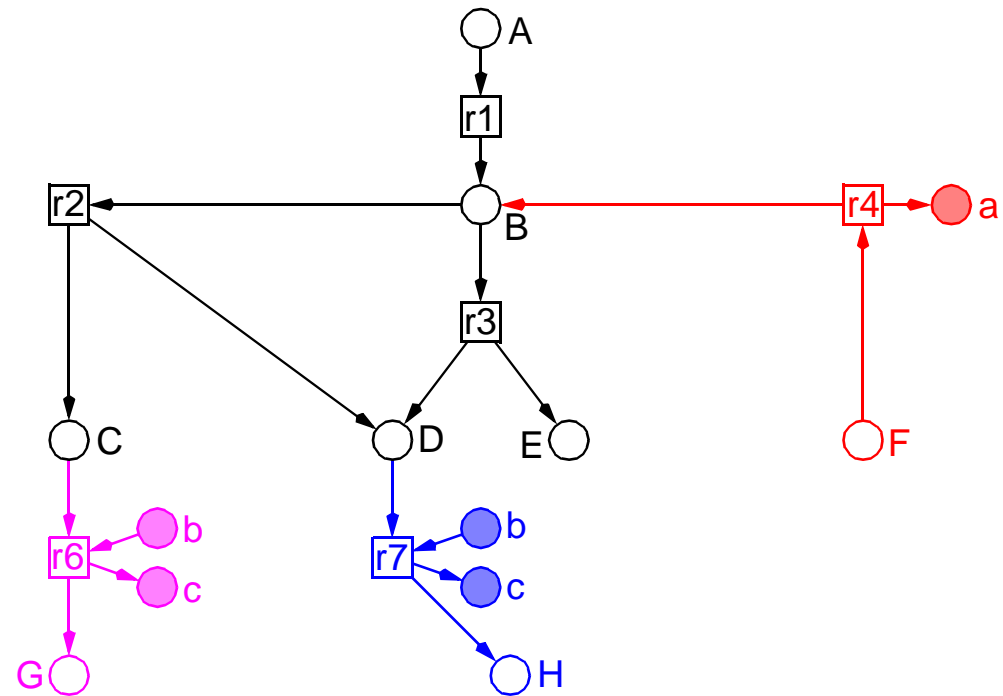
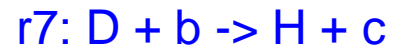
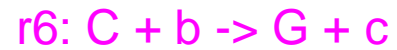
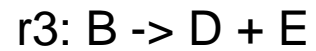
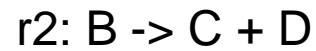
r1: A -> B

r2: B -> C + D

r3: B -> D + E

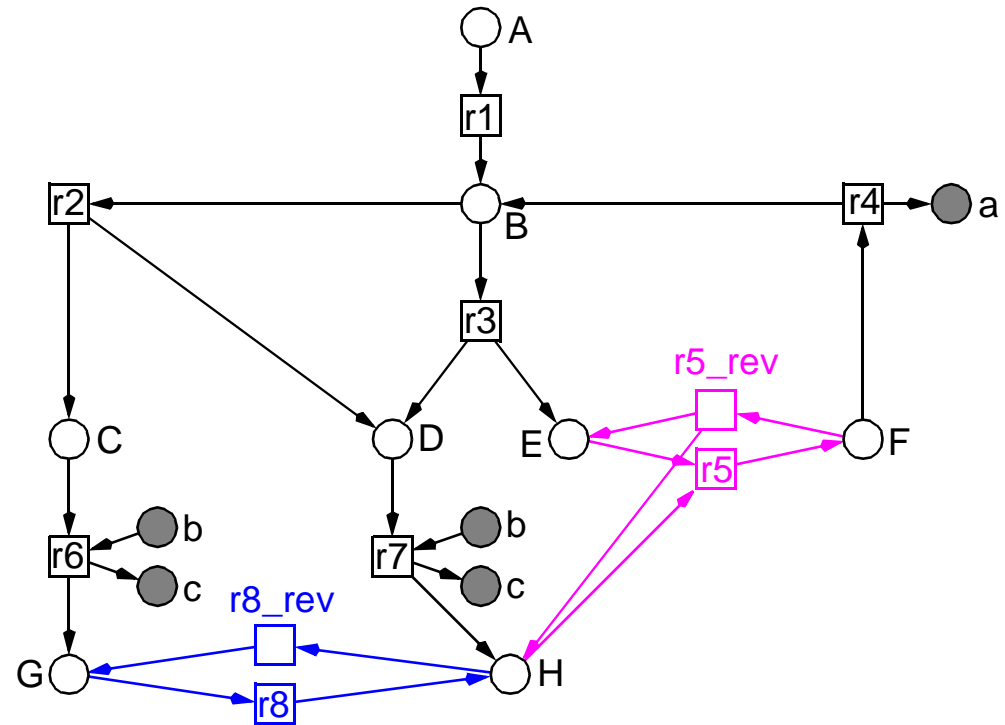


-> alternative reactions



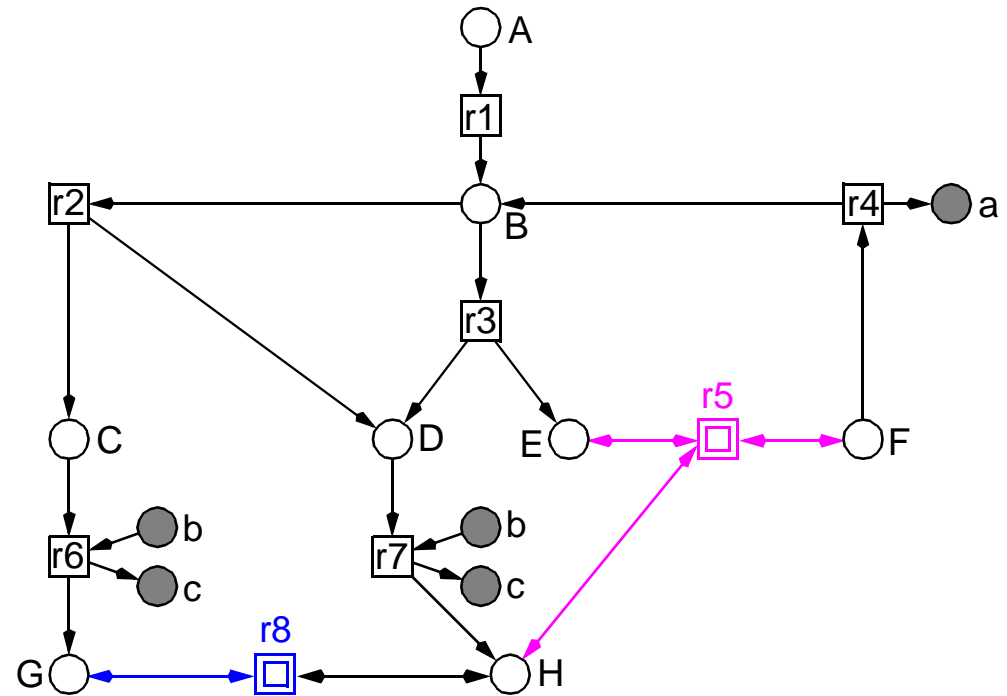
-> concurrent reactions

- r1: $A \rightarrow B$
- r2: $B \rightarrow C + D$
- r3: $B \rightarrow D + E$
- r4: $F \rightarrow B + a$
- r5: $E + H \leftrightarrow F$
- r6: $C + b \rightarrow G + c$
- r7: $D + b \rightarrow H + c$
- r8: $H \leftrightarrow G$



-> reversible reactions

- r1: $A \rightarrow B$
- r2: $B \rightarrow C + D$
- r3: $B \rightarrow D + E$
- r4: $F \rightarrow B + a$
- r5: $E + H \leftrightarrow F$
- r6: $C + b \rightarrow G + c$
- r7: $D + b \rightarrow H + c$
- r8: $H \leftrightarrow G$



-> reversible reactions
- hierarchical nodes

r1: $A \rightarrow B$

r2: $B \rightarrow C + D$

r3: $B \rightarrow D + E$

r4: $F \rightarrow B + a$

r5: $E + H \leftrightarrow F$

r6: $C + b \rightarrow G + c$

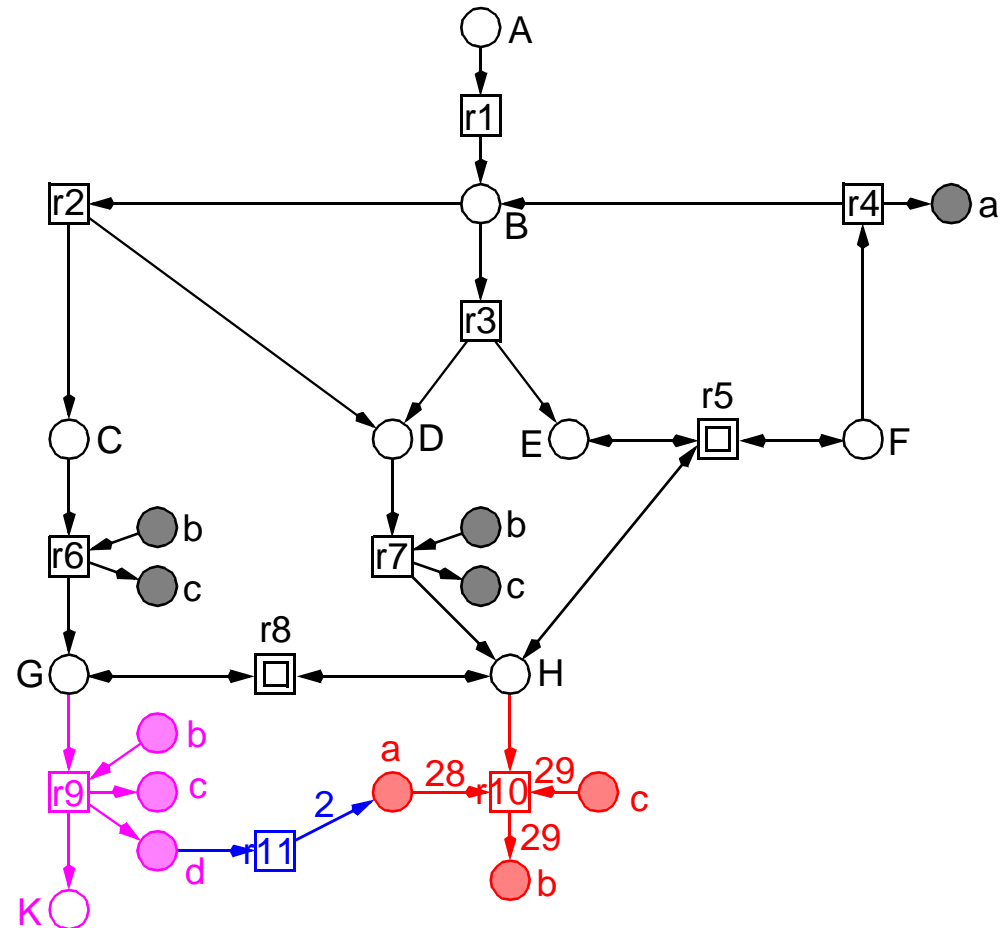
r7: $D + b \rightarrow H + c$

r8: $H \leftrightarrow G$

r9: $G + b \rightarrow K + c + d$

r10: $H + 28a + 29c \rightarrow 29b$

r11: $d \rightarrow 2a$



r1: $A \rightarrow B$

r2: $B \rightarrow C + D$

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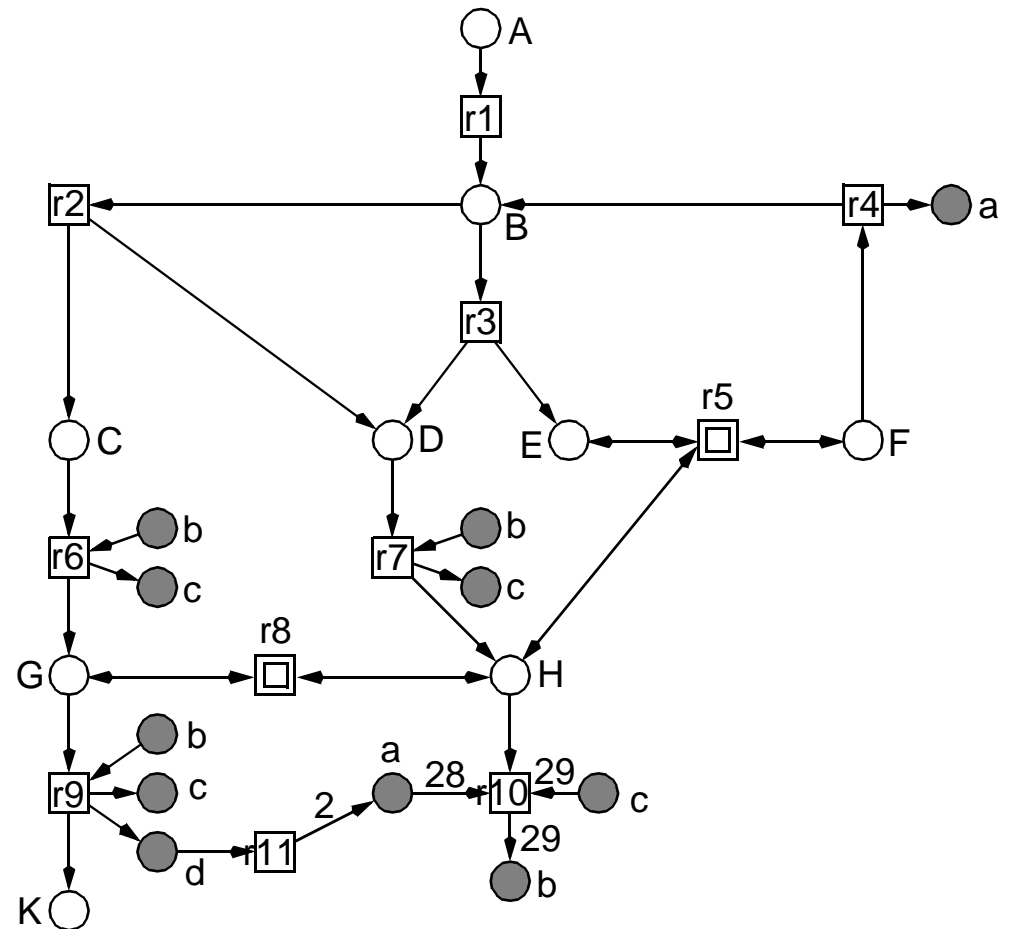
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r8: $H \leftrightarrow G$

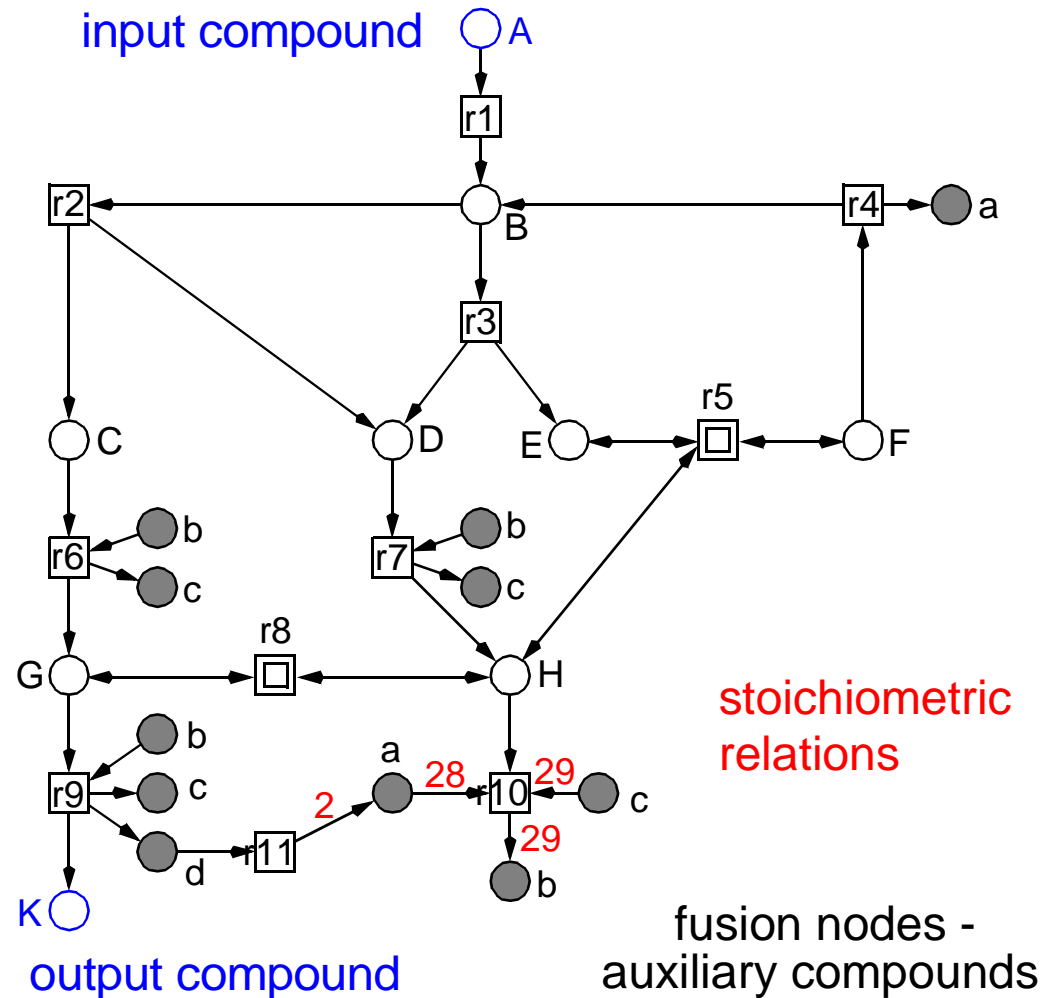
r9: $G + b \rightarrow K + c + d$

r10: $H + 28a + 29c \rightarrow 29b$

r11: $d \rightarrow 2a$



- r1: $A \rightarrow B$
- r2: $B \rightarrow C + D$
- r3: $B \rightarrow D + E$
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- r8: $H \leftrightarrow G$
- r9: $G + b \rightarrow K + c + d$
- r10: $H + 28a + 29c \rightarrow 29b$
- r11: $d \rightarrow 2a$



- ❑ networks of chemical reactions

- ❑ **biologically interpreted Petri net**
 - > *partial order sequences of chemical reactions*
 - *transforming input into output compounds*
 - *respecting the given stoichiometric relations*

❑ networks of chemical reactions

❑ **biologically interpreted Petri net**

-> *partial order sequences of chemical reactions*

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❑ **typical (structural) properties**

INA

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

❑ **observation**

-> *tend to grow fast*

❑ networks of chemical reactions

❑ **biologically interpreted Petri net**

-> *partial order sequences of chemical reactions*

- *transforming input into output compounds*
- *respecting the given stoichiometric relations*

❑ typical (structural) properties

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

❑ observation

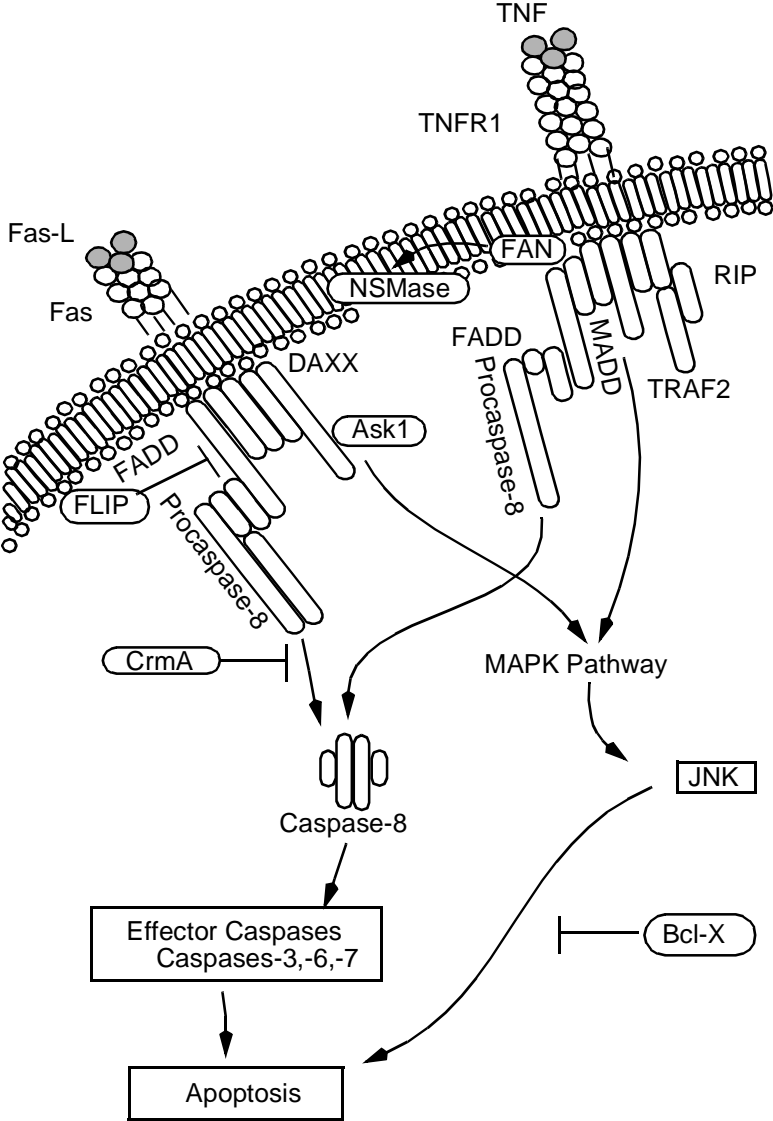
-> *tend to grow fast*

- ❑ **network structure** **-> PROBLEM 1**
 - > *dense, apparently unstructured*
 - > *hard to read*

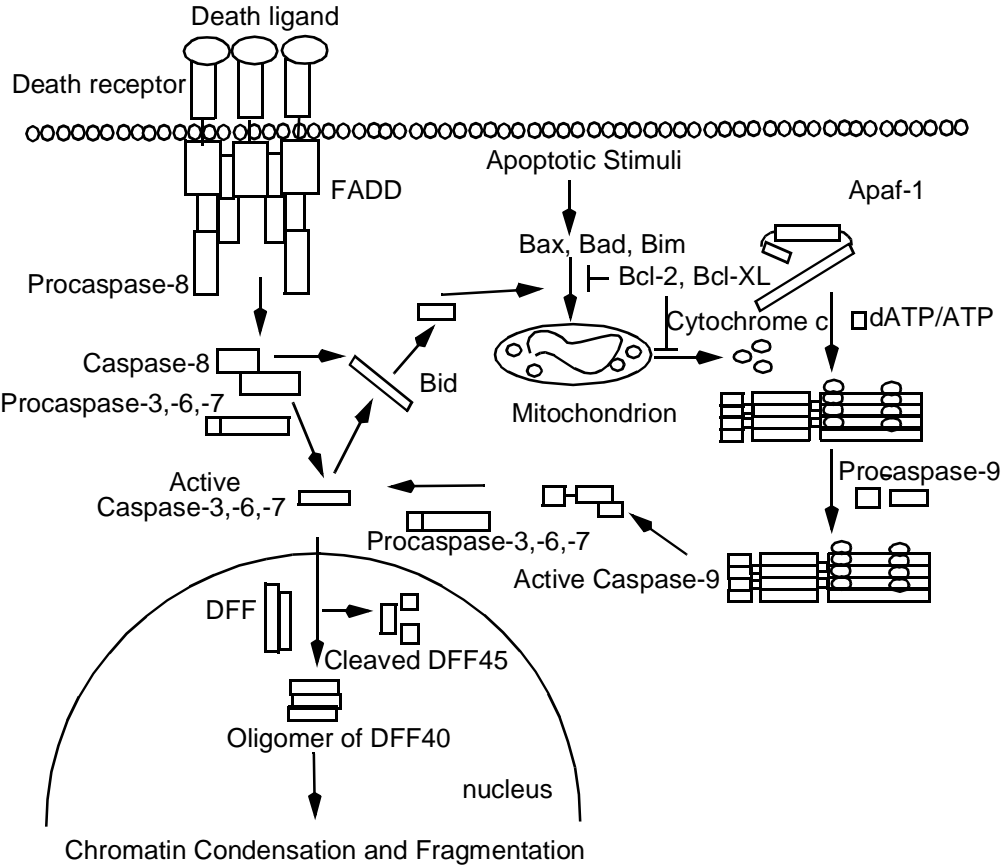
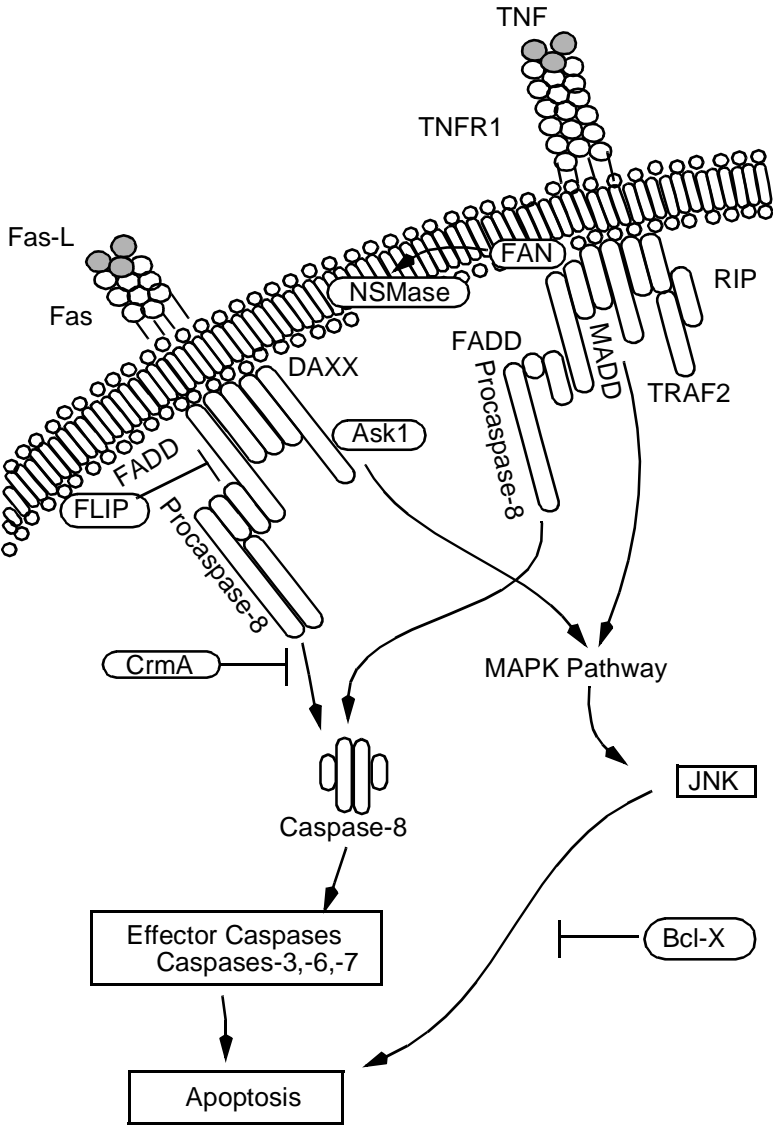
- ❑ **knowledge** **-> PROBLEM 2**
 - > *uncertain*
 - > *growing, changing*
 - > *distributed over independent data bases, papers, journals, . . .*

- ❑ **various, mostly ambiguous representations** **-> PROBLEM 3**
 - > *verbose descriptions*
 - > *diverse graphical representations*
 - > *contradictory and / or fuzzy statements*

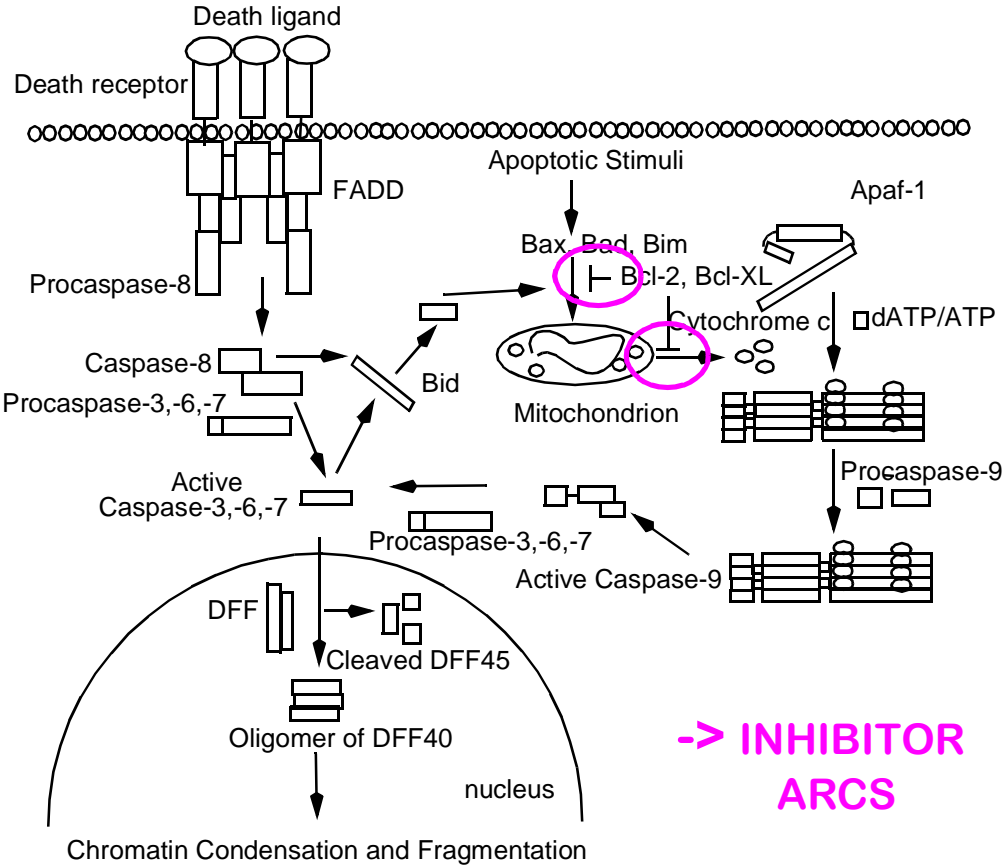
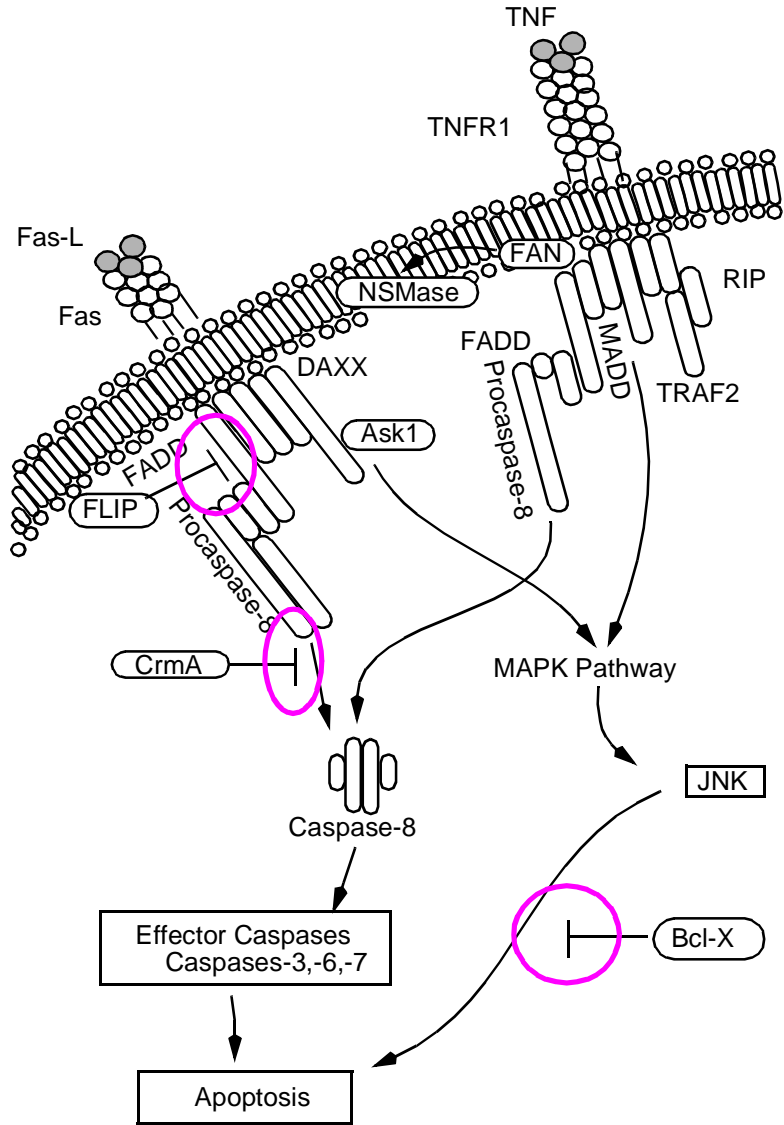
 - > *some examples*



-> CASE STUDY 1



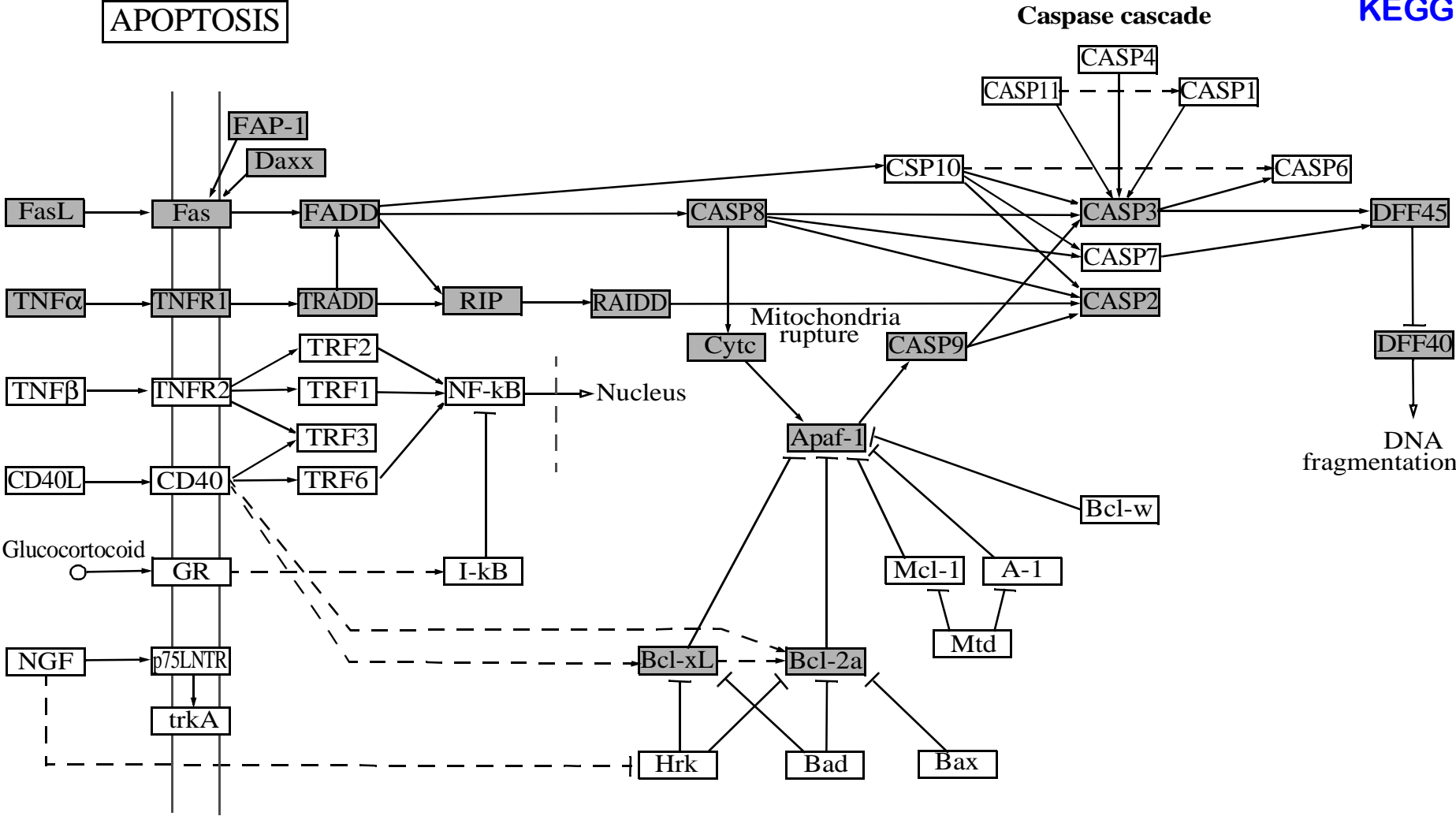
-> CASE STUDY 1



-> INHIBITOR ARCS

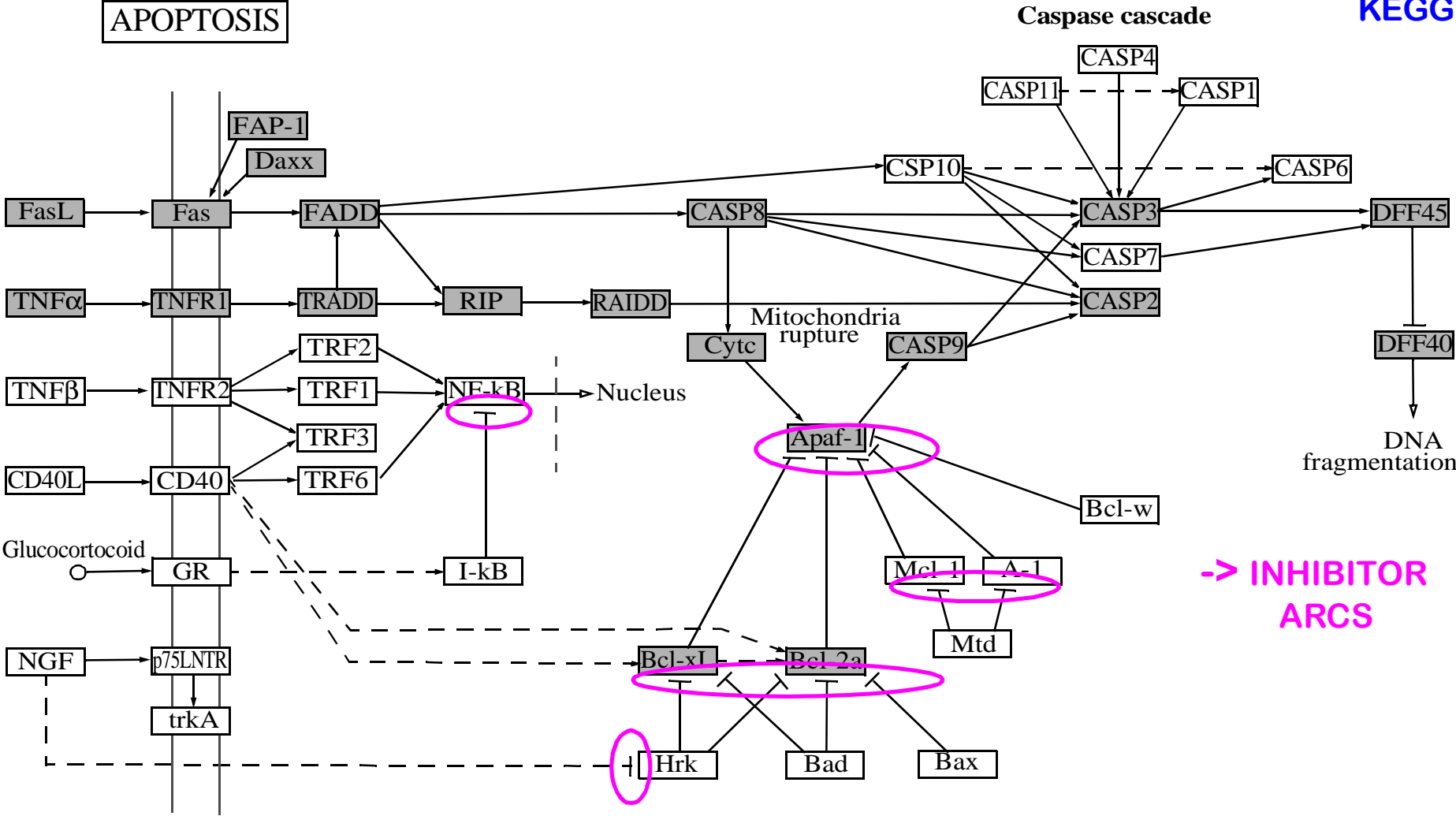
-> CASE STUDY 1

KEGG



-> CASE STUDY 1

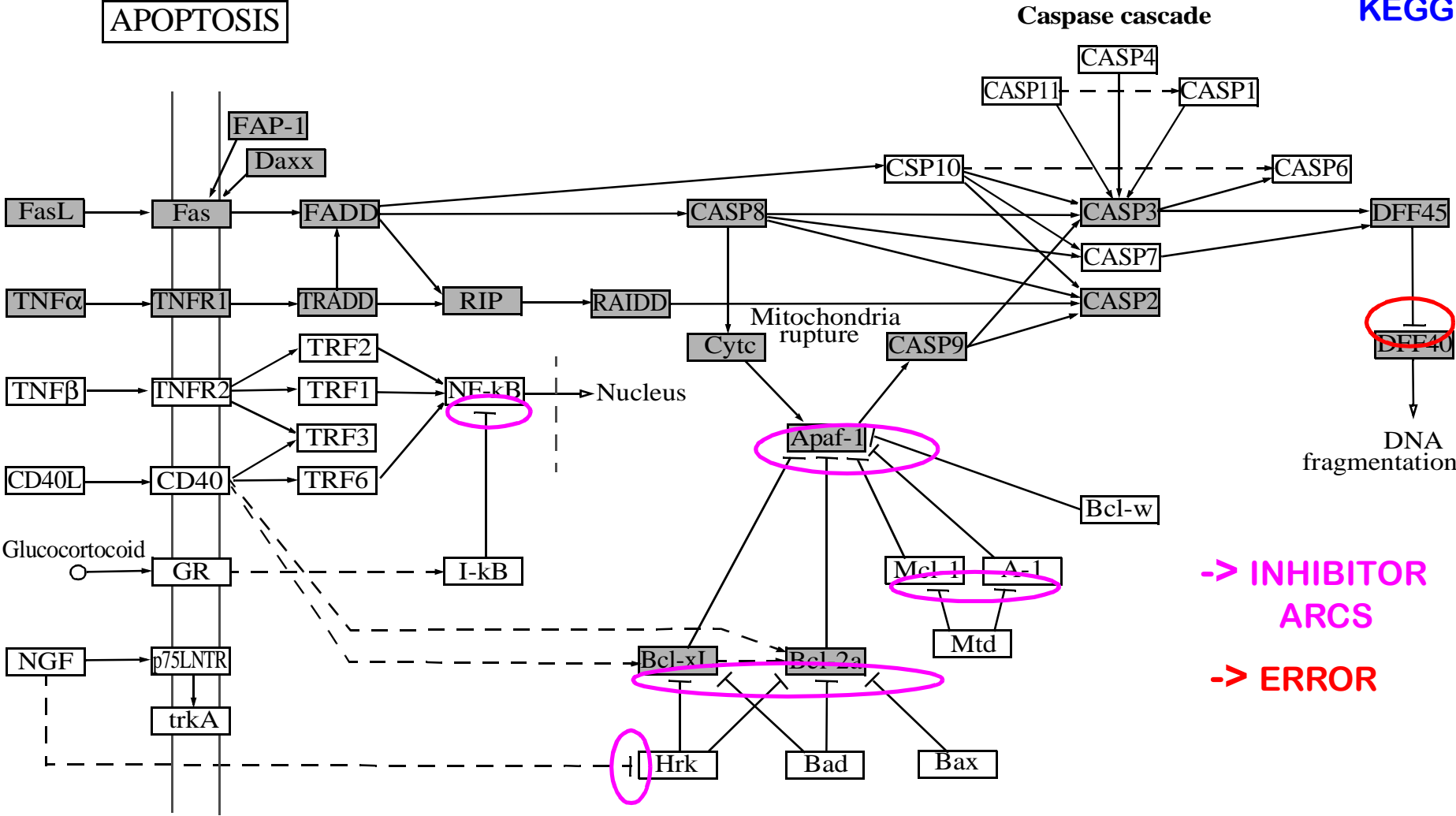
KEGG



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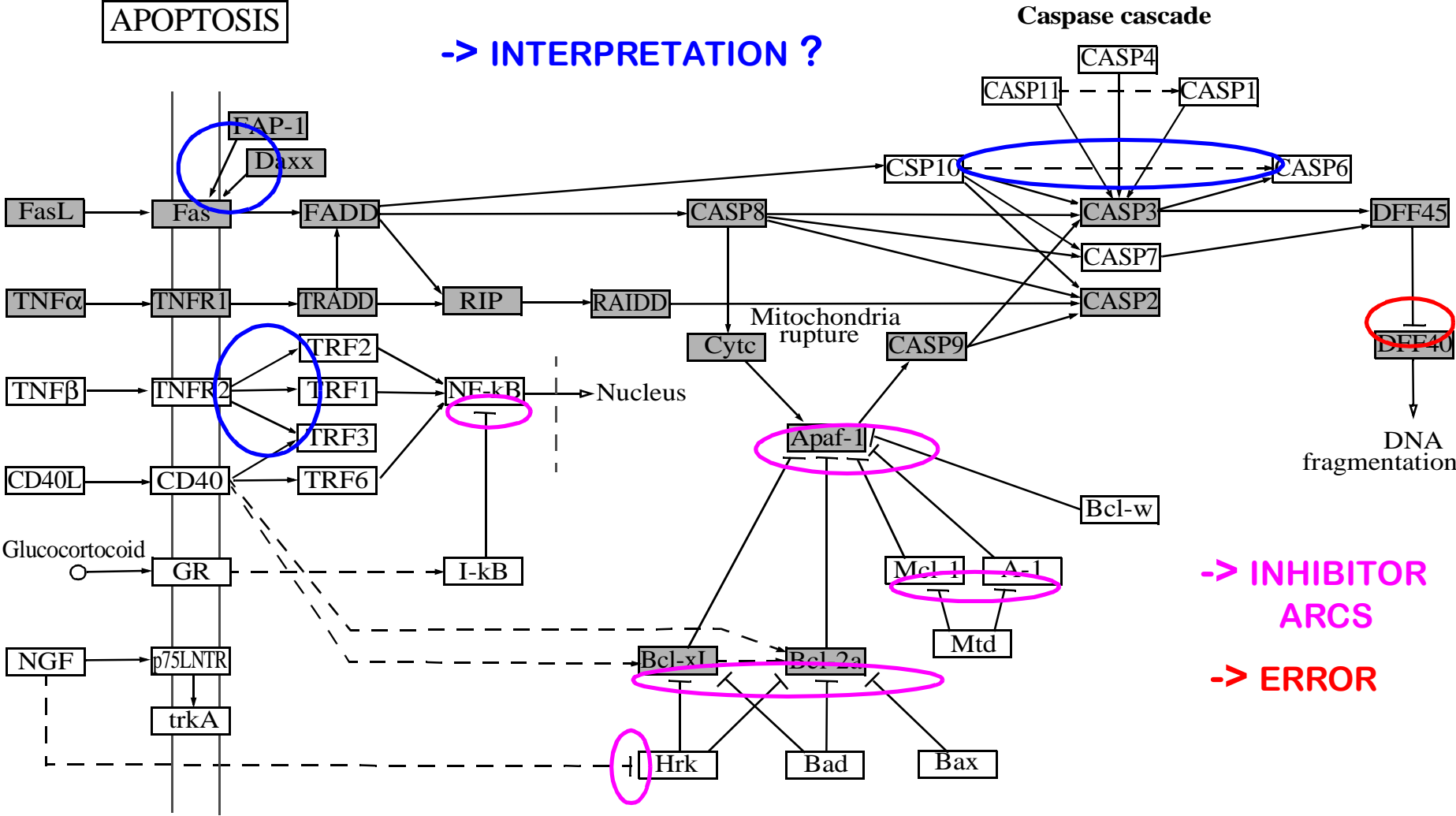
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KEGG



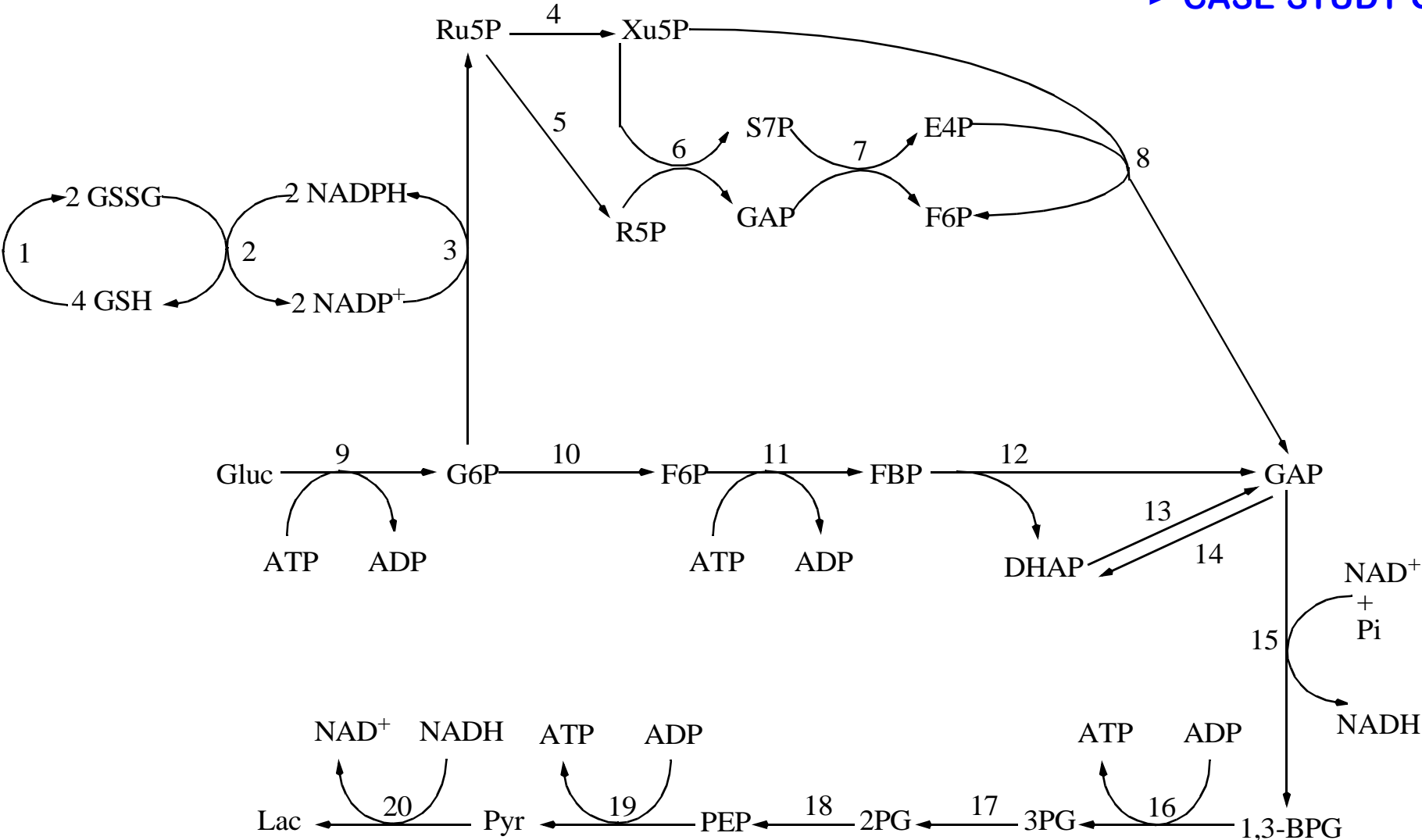
-> INHIBITOR ARCS
-> ERROR

-> CASE STUDY 1

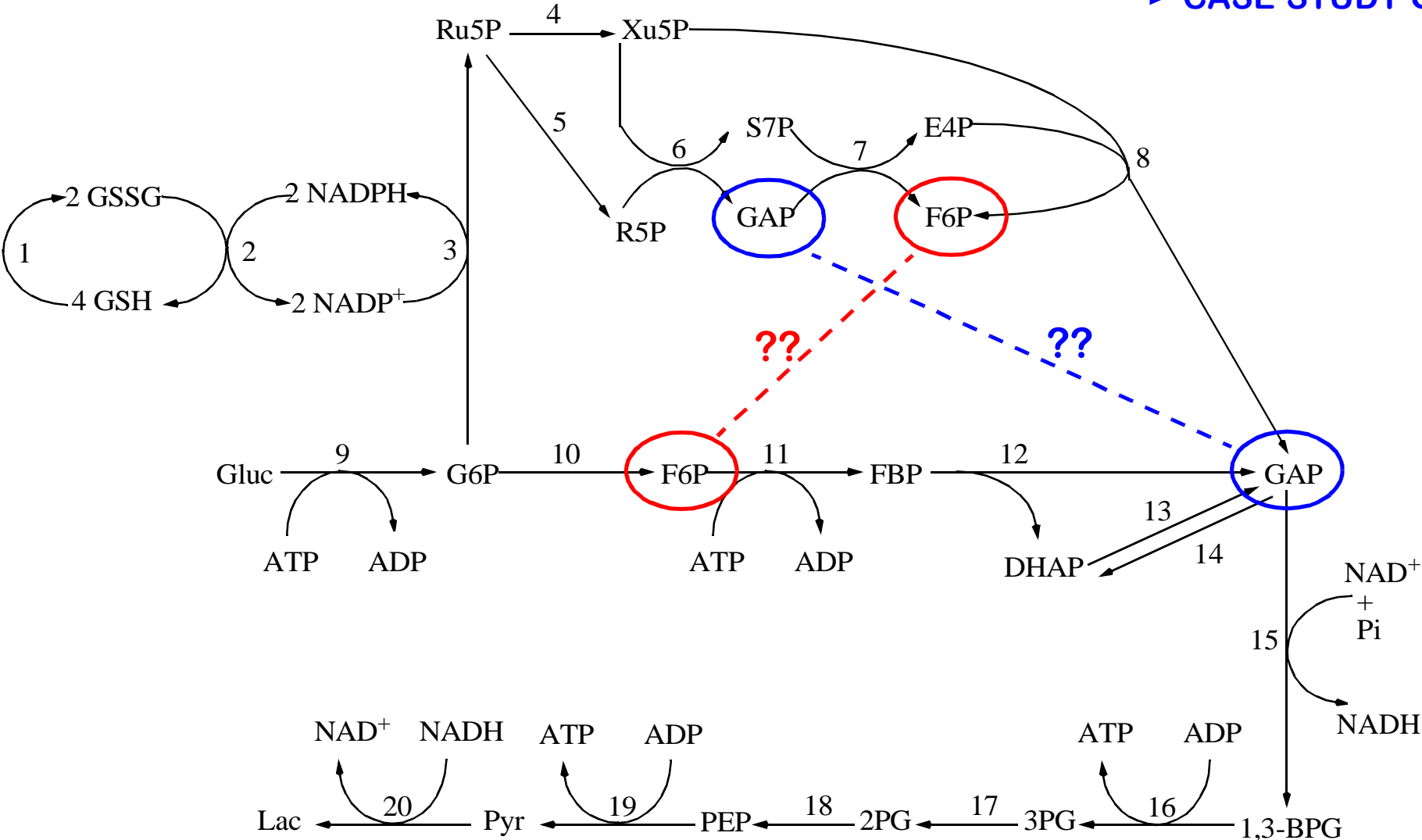


-> CASE STUDY 1

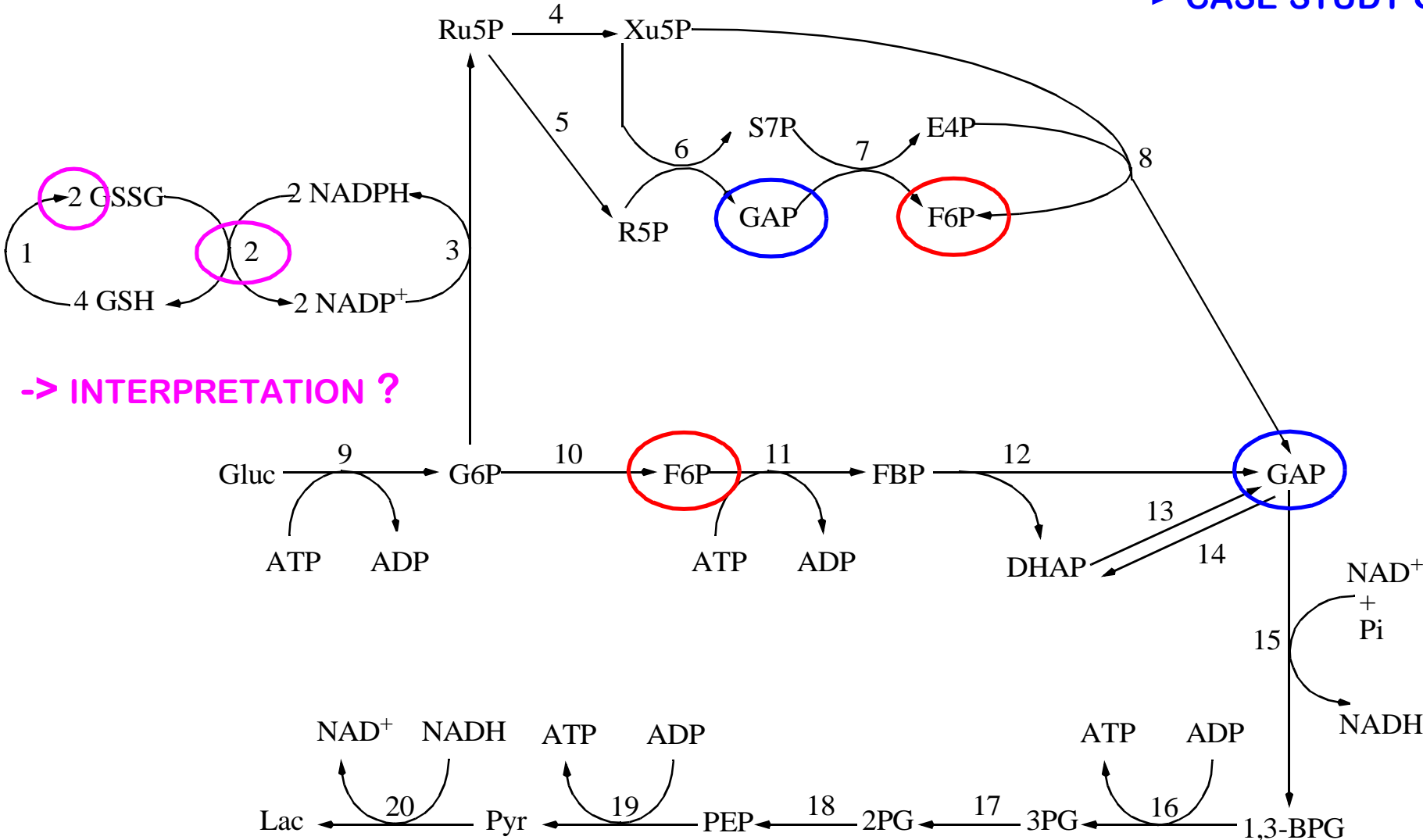
-> CASE STUDY 3



-> CASE STUDY 3



-> CASE STUDY 3



- ❑ patchwork
 - > *likely to be erroneous*

- ❑ long-term purpose
 - > *(quantitative) behaviour prediction*

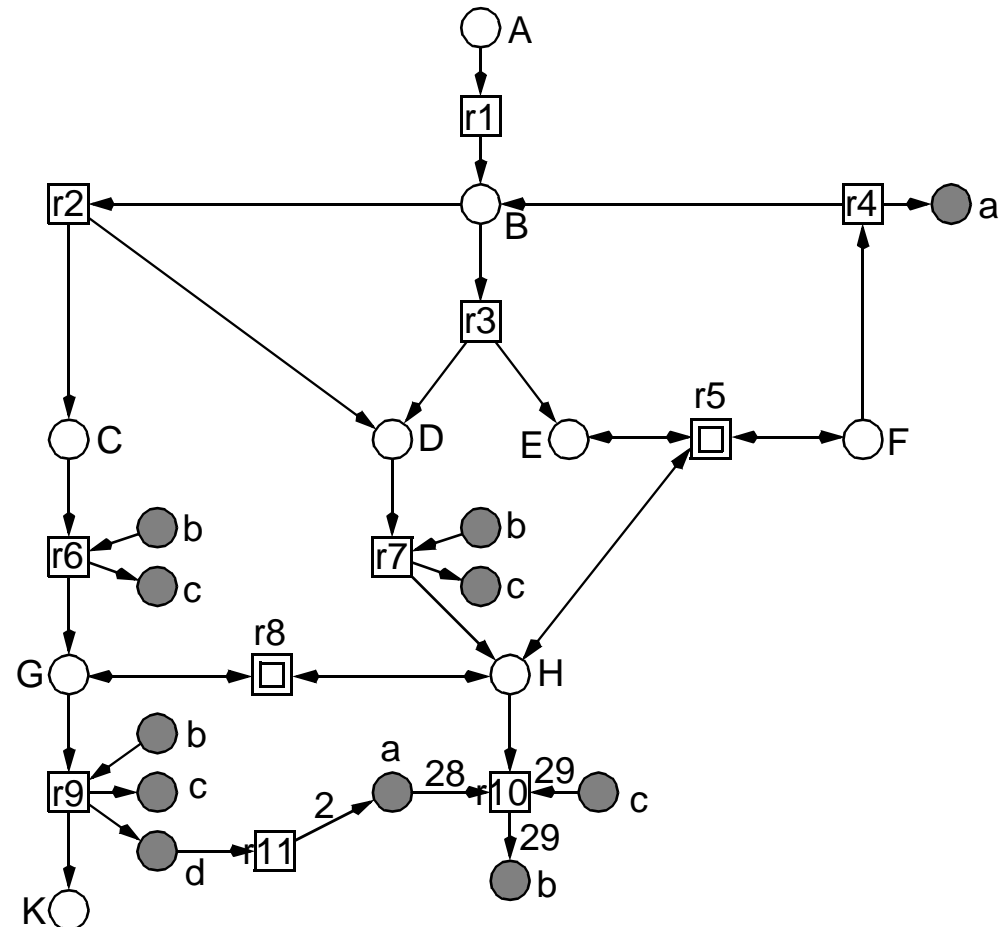
- ❑ necessary intermediate step
 - > *model validation* -> *validation criteria ?*

- ❑ patchwork
 - > *likely to be erroneous*
- ❑ long-term purpose
 - > *(quantitative) behaviour prediction*
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- ❑ **steady state behaviour** -> **pathways**
 - > *all possible flows preserving the given compounds distribution*
 - > *elementary modes = minimal T-invariants*
- ❑ **consistency criteria** -> **pathways analysis**
 - > *CTI*
 - > *no minimal T-invariant without biological interpretation*
 - > *no known biological behaviour without corresponding T-invariant*

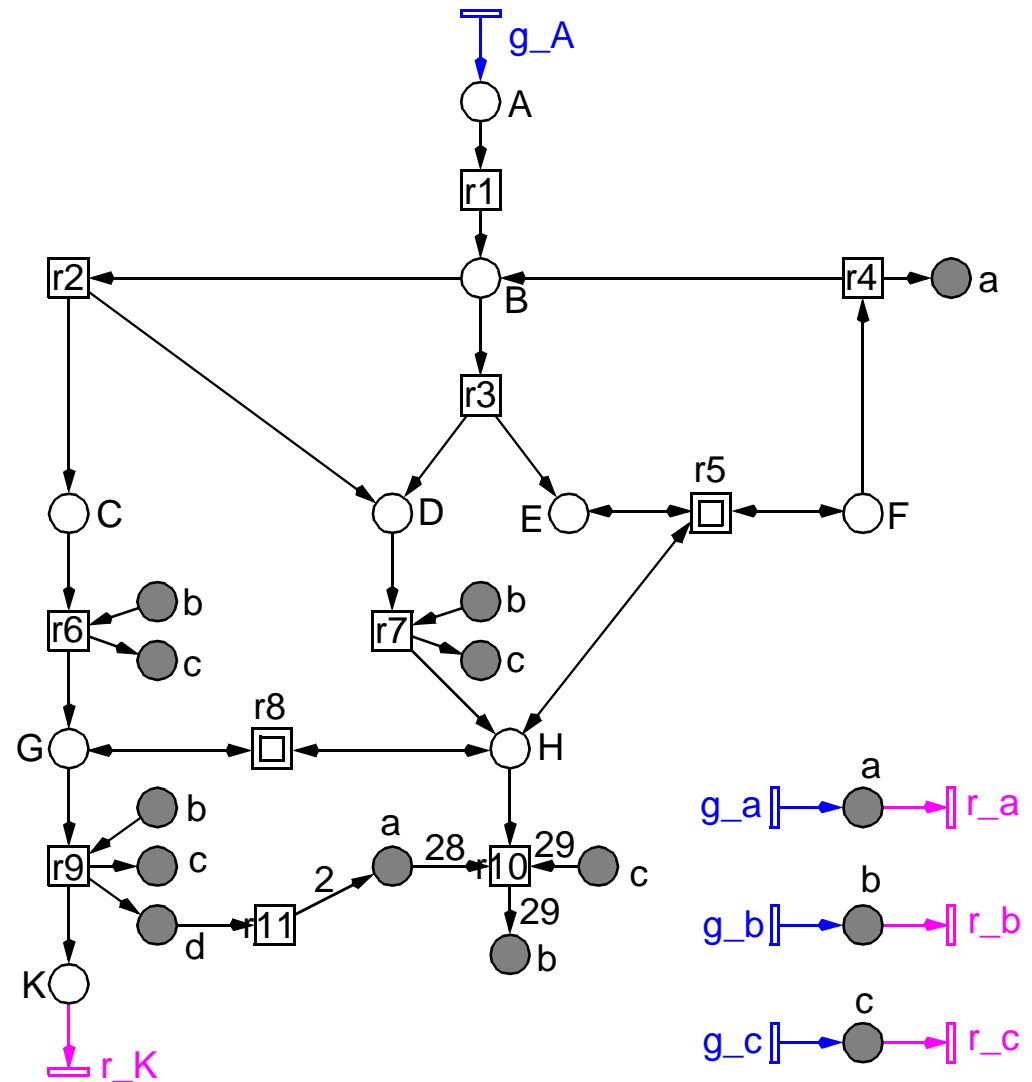
- ❑ patchwork
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 - > *CTI*
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- ❑ **Lautenbach, 1973**
- ❑ **T-invariants** -> *multisets of transitions*
 - > *integer solutions of $Cx = 0, x \neq 0, x \geq 0$*
- ❑ **minimal T-invariants**
 - > *there is no T-invariant with a smaller support* -> *sets of transitions*
 - > *gcd of all entries is 1*
- ❑ **any T-invariant is a non-negative linear combination of minimal ones**
 - > *multiplication with a positive integer*
 - > *addition*
 - > *Division by gcd*
- ❑ **Covered by T-Invariants (CTI)**
 - > *each transition belongs to a T-invariant*

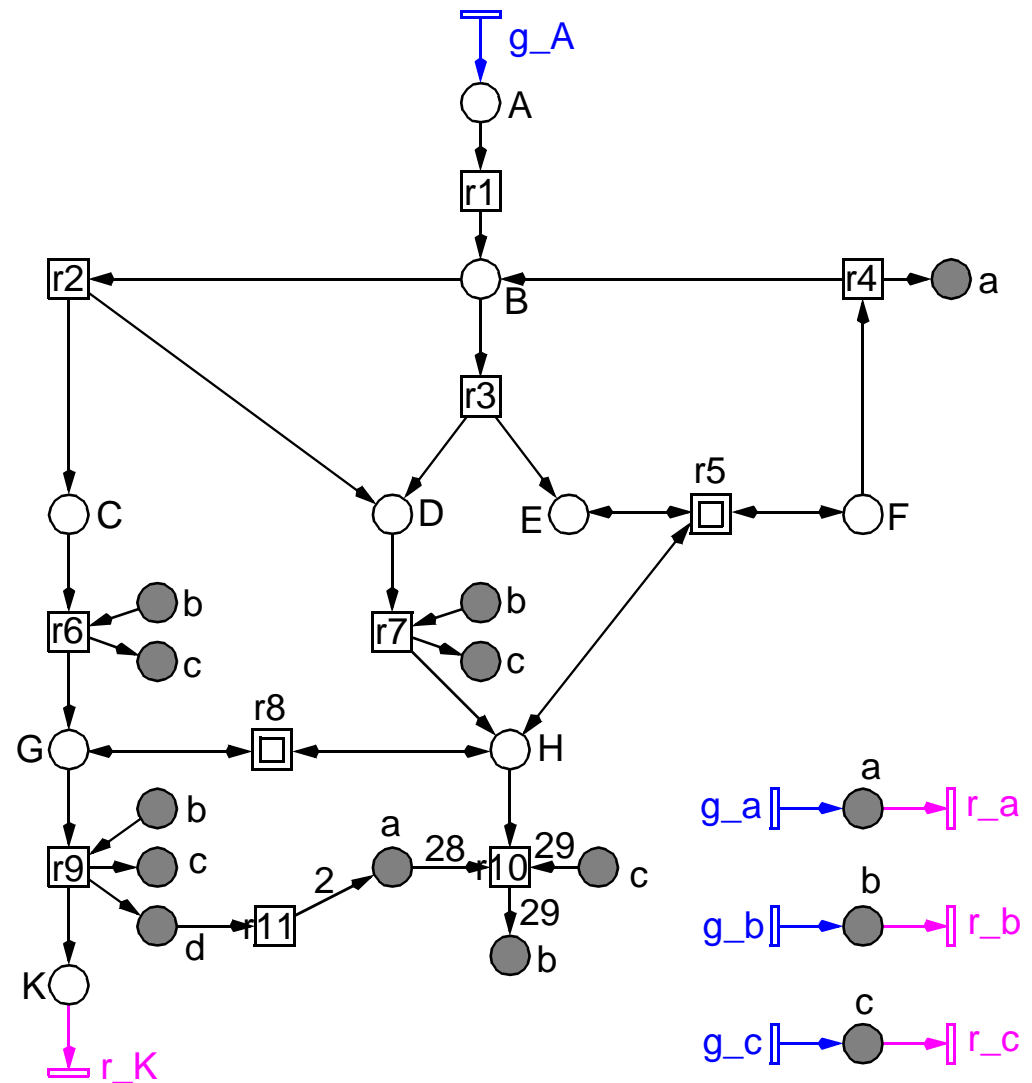
- ❑ to animate the model
 - > infinite substance flow
 - > deeper insights
- ❑ to validate the model
 - > consistency criteria
- ❑ steady flow
 - > input substances
 - > output substances
- ❑ auxiliary substances
 - > as much as necessary
- ❑ **minimal assumptions**



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 - > as much as necessary
- ❑ **minimal assumptions**



- input substances
-> *generating pre-transitions*
- output substances
-> *consuming post-transitions*
- auxiliary substances
-> *both*
- **no boundary places, but boundary transitions**
- transitions without pre-places
-> *live*
-> *all post-places are unbounded*
- **steady state behaviour**
-> *empty marking reproduction*



trivial min. T-invariants (5)

- boundary transitions of auxiliary compounds

-> (g_a, r_a) , (g_b, r_b) ,
 (g_c, r_c)

- reversible reactions

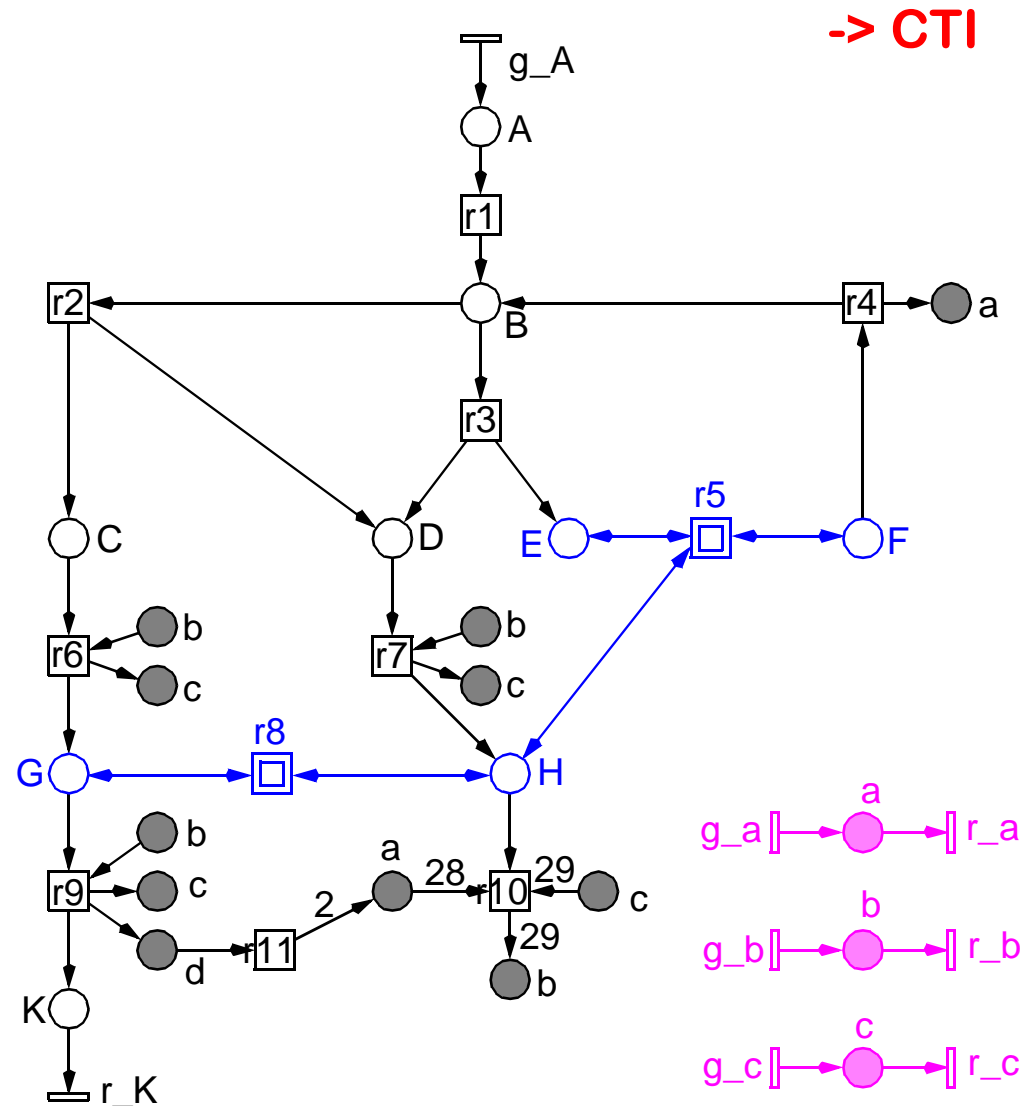
-> $(r5, r5_{rev})$, $(r8, r8_{rev})$

non-trivial min. T-invariants (7)

- covering boundary transitions of input / output compounds

-> *i/o-T-invariants*

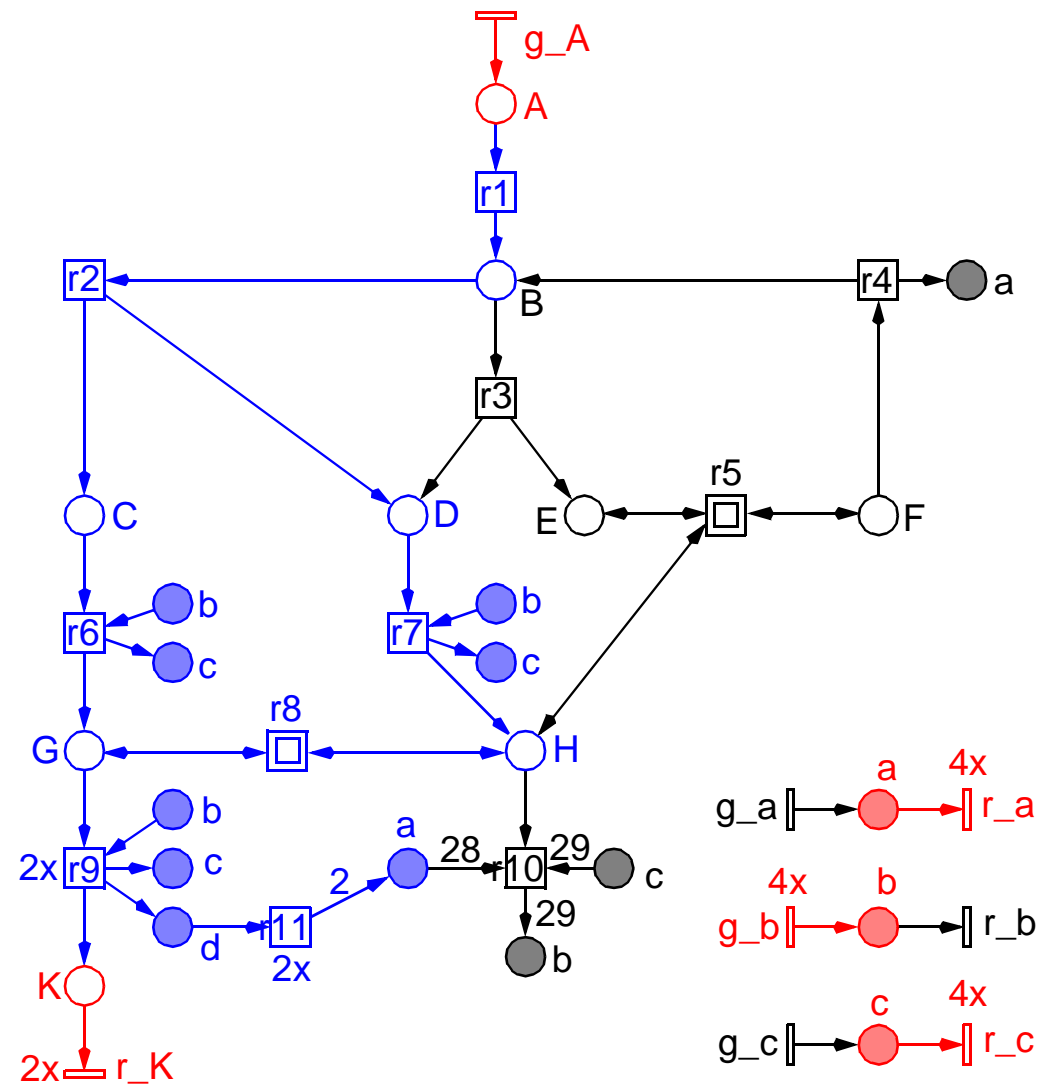
- inner cycles



□ i/o-T-invariant, example

12		0.r1	:	1
		1.r2	:	1,
		3.r8_rev	:	1,
		4.r6	:	1,
		5.r7	:	1,
		9.r9	:	2,
		12.r11	:	2,
		13.g_A	:	1,
		14.r_K	:	2,
		15.g_b	:	4,
		18.r_c	:	4,
		20.r_a	:	4

□ sum equation



□ **STYLE 1A**

- > *weak assumptions*
- > *infinite flow into/out the network*

□ **STYLE 1B**

- > *firm assumptions*
- > *finite, but sufficient reservoir of auxiliary compounds*

□ **STYLE 2**

- > *strong assumptions*
- > *finite, but sufficient reservoir of auxiliary compounds*
- > *quantitative relations of input/output compounds*



**INCREASING
STRENGTH**

❑ **weak assumptions**

❑ **input compounds**

-> *generating pre-transitions*

❑ **output compounds**

-> *consuming post-transitions*

no assumptions about quantitative relations of input/output compounds

❑ **auxiliary compounds**

-> *generating pre-transitions & consuming post-transitions*

-> *infinite reservoir*

❑ **typical properties**

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

❑ **weak assumptions**

❑ **input compounds**
 -> *generating pre-transitions*

❑ **output compounds**
 -> *consuming post-transitions*

} *no assumptions about quantitative relations of input/output compounds*

❑ **auxiliary compounds**
 -> *generating pre-transitions & consuming post-transitions*
 -> *infinite reservoir*

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?	N	Y	N	N	?	N	?	N	n	Y	Y	N				

- ❑ **firm assumptions**
 - ❑ **input compounds**
 - > *generating pre-transitions*
 - ❑ **output compounds**
 - > *consuming post-transitions*
 - ❑ **auxiliary compounds**
 - > *neither generating pre-transitions nor consuming post-transitions*
 - > *finite reservoir* -> *P-invariants (= traps = co-traps)*
 - > *Which (minimal) initial token distribution makes the net live ?*
 - ❑ **typically expected properties**
 - > *see style 1*
- no assumptions about quantitative relations of input/output compounds*

❑ strong assumptions

- > quantitative relations of input/output compounds
- > finite reservoir of auxiliary compounds

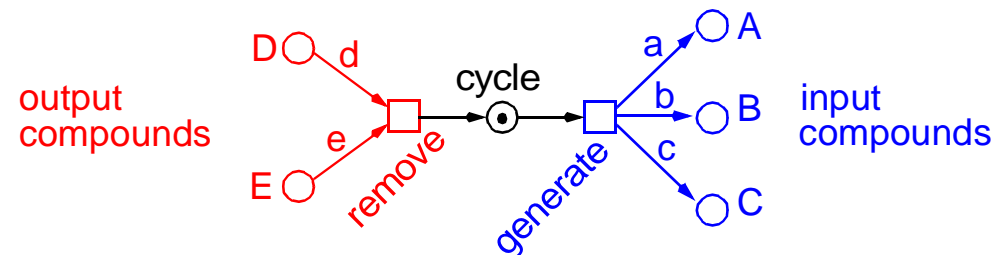
❑ typically expected properties

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

❑ additional model component

-> network sum equation



❑ How to compute ? For alternative paths ?

❑ **strong assumptions**

- > *quantitative relations of input/output compounds*
- > *finite reservoir of auxiliary compounds*

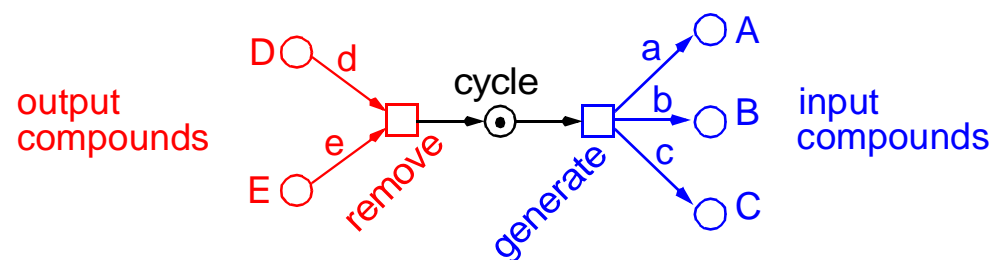
❑ **typically expected properties**

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

❑ **additional model component**

-> *network sum equation*



❑ **How to compute ? For alternative paths ?**

❑ case study 1

- > *signal-transduction network - apoptosis*
- > *no stoichiometric relations - ordinary place/transition net*
- > *many read arcs, resolved for analysis*
- > *environment behaviour, style 1A*

❑ case study 2

- > *metabolic network - carbon metabolism in potato tuber*
- > *stiochiometric relations known - non-ordinary place/transition net*
- > *many reversible reactions*
- > *environment behaviour, style 1B*

❑ case study 3

- > *metabolic network - glycolysis and pentose phosphate metabolism*
- > *coloured nets (Design-CPN)*
- > *environment behaviour, style 2, computed by prototype tool **SY / Genrich***

- ❑ **case study 1** **-> 37 P / 45 T -> 10 t-inv's**
 - > *signal-transduction network - apoptosis*
 - > *no stoichiometric relations - ordinary place/transition net*
 - > *many read arcs, resolved for analysis*
 - > *environment behaviour, style 1A*

- ❑ **case study 2** **-> 17 P / 25 T -> 19 t-inv's / 3 p-inv's**
 - > *metabolic network - carbon metabolism in potato tuber*
 - > *stiochiometric relations known - non-ordinary place/transition net*
 - > *many reversible reactions*
 - > *environment behaviour, style 1B*

- ❑ **case study 3** **-> 32 P / 22 T -> 1 t-inv / 39 p-inv's**
 - > *metabolic network - glycolysis and pentose phosphate metabolism*
 - > *coloured nets (Design-CPN)*
 - > *environment behaviour, style 2, computed by prototype tool SY / Genrich*

- ❑ **extensions**
 - > *read arcs*
 - > *inhibitor arcs !?*

- ❑ **efficient computation of minimal invariants**
 - > *exponential complexity*
 - > *compositional approach ?*

- ❑ **analysis of bounded, but not safe non-ordinary nets with inhibitor arcs**
 - > *huge state spaces, beyond exponential growth (?)*
 - > *smaller, bounded version of case study 2 $\geq 10^{10}$ states (IDD-based mc tool)*

- ❑ **analysis of unbounded nets**
 - > *besides T-invariant analysis ?*

- ❑ **model checking**
 - > *relevant properties ?*

FURTHER CASE STUDIES

- blood clotting
(hemostasis versus fibrinolysis)
- the whole *E. coli* pathway
- the whole potato tuber pathway
- detailed glycolysis in humans
- G1/S - phase in mammalian cells
- lipoprotein metabolism (liver)

FURTHER CASE STUDIES

- ❑ blood clotting (hemostasis versus fibrinolysis) -> Gerry Neumann / BTU
- ❑ the whole E. coli pathway -> Nina Kramer / TFH
- ❑ the whole potato tuber pathway -> Nina Kramer / TFH
- ❑ detailed glycolysis in humans -> Thomas Runge / BTU
- ❑ G1/S - phase in mammalian cells -> Thomas Kaunath / TFH
- ❑ lipoprotein metabolism (liver) -> Daniel Schrödter / BTU

- ❑ **representation of bionetworks by Petri nets**
 - > *unifying view*
 - > *animation*
 - > *model validation against consistency criteria*
 - > *qualitative/quantitative behaviour prediction*

- ❑ **three styles of environment description**

- ❑ **steady state behaviour**
 - > *pathways* -> *T-invariants*
 - > *elementary modes* -> *minimal T-invariants*

- ❑ **consistency criteria**
 - > *CTI*
 - > *T-invariant <-> biological interpretation*

- ❑ **many challenging questions for analysis techniques**

**GRAZIE
PER LA VOSTRA
ATTENZIONE !**