

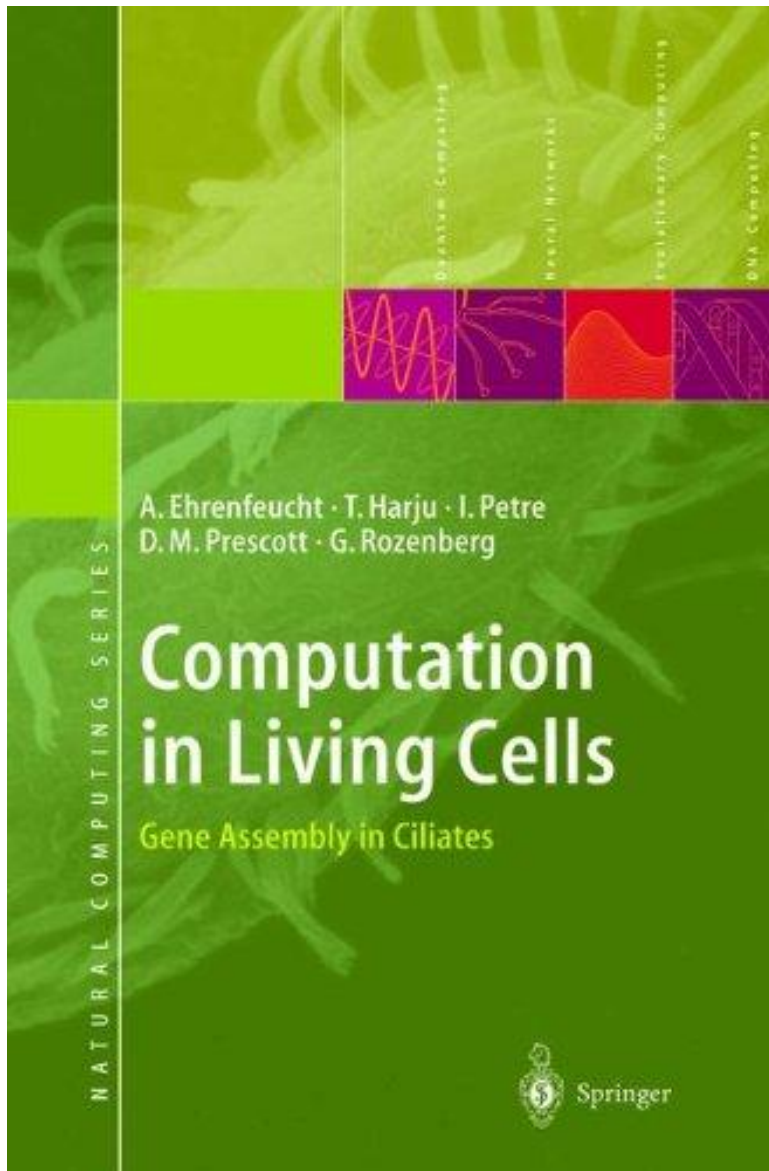
10th International Conference on
Unconventional Computation

Workshop on
**Language Theory in
Biocomputing**
Turku, June 9, 2011

The Algebra of Ciliates

Robert Brijder Hasselt

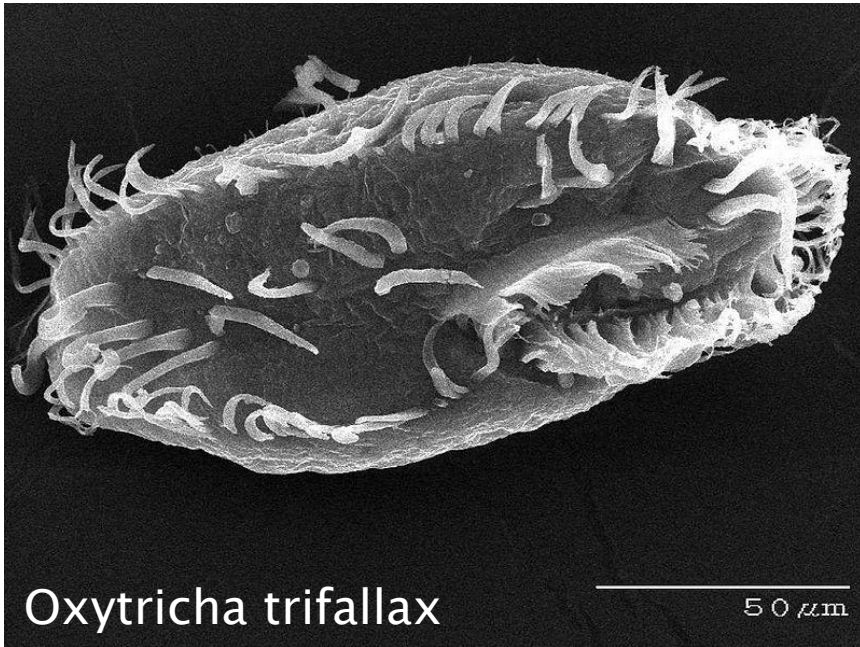
Hendrik Jan Hoogeboom
Leiden



Computation in Living Cells
Gene Assembly in Ciliates

A. Ehrenfeucht, T. Harju, I. Petre,
D.M. Prescott, G. Rozenberg

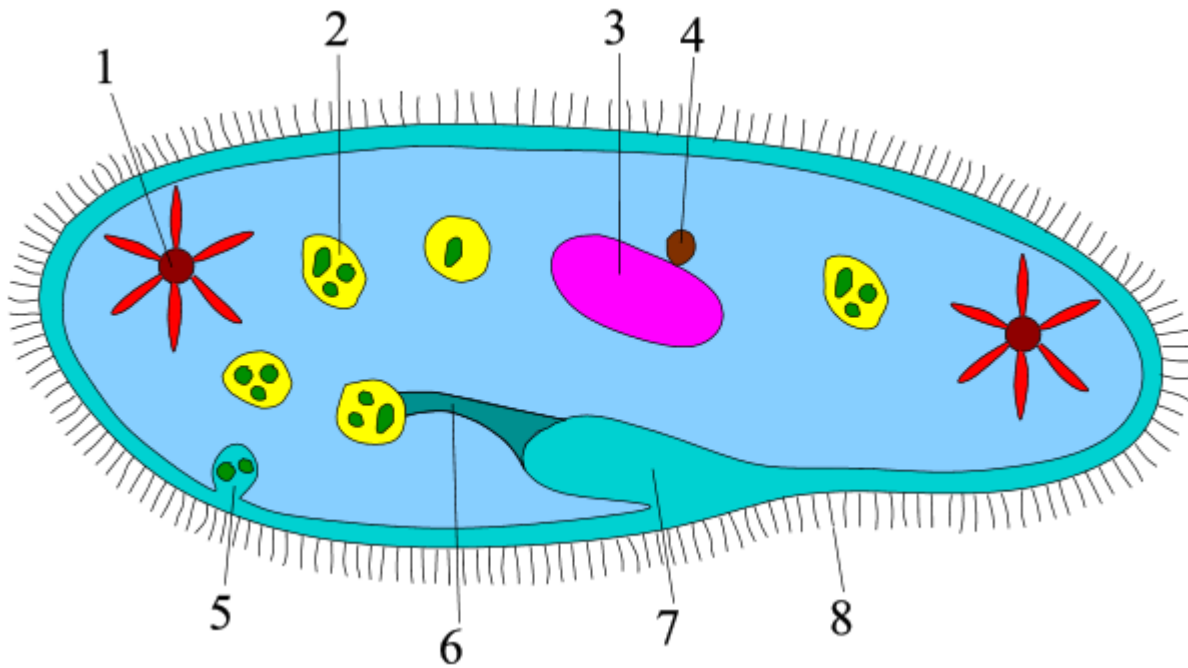
Natural Computing Series, Springer,
2004.



The **ciliates** are a group of protozoans characterized by the presence of hair-like organelles called **cilia**, [...] variously used in swimming, crawling, attachment, feeding, and sensation.

Ciliates are one of the most important groups of protists, common **almost everywhere there is water** — in lakes, ponds, oceans, rivers, and soils. Ciliates have many ectosymbiotic and endosymbiotic members, as well as some obligate and opportunistic parasites. Ciliates tend to be large protozoa, a few reach 2 mm in length, and are some of the **most complex** protozoans in structure

micro and macro



cell structure:

- 3. macronucleus
- 4. micronucleus
- 8. cilium

Unlike most other eukaryotes, ciliates have two different sorts of nuclei: a small, diploid **micronucleus** (reproduction), and a large, polyploid **macronucleus** (general cell regulation). The latter is generated from the micronucleus by amplification of the genome and **heavy editing**.

from micro to macro

http://oxytricha.princeton.edu/cgi-bin/get_MDS_IES_Info.cgi?num=38

micronucleus

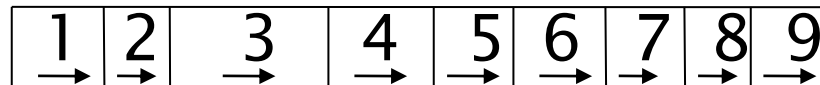
DNA: 2374 bp



recombination

macronucleus

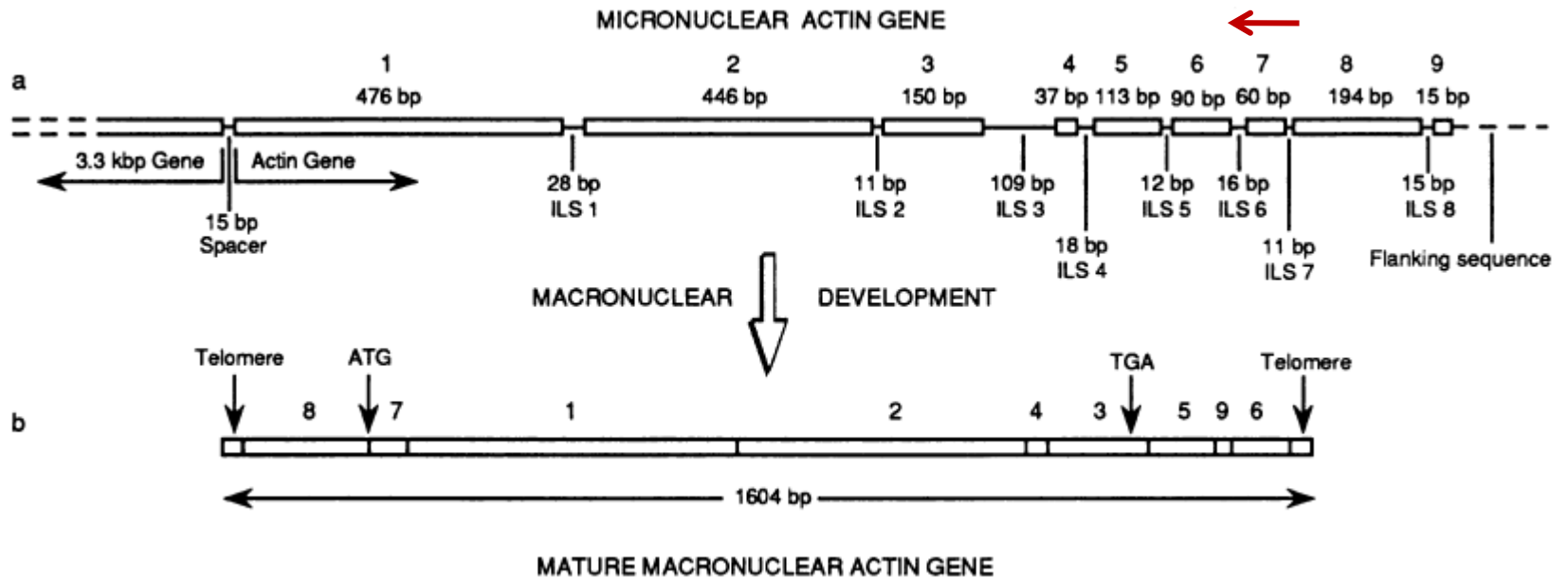
DNA: 1604 bp



here: segment numbers in sorted order

micronucleus

9 exons



macronucleus

Greslin, Prescott et al. Reordering of nine exons is necessary to form a functional actin gene in *Oxytricha nova*. PNAS 86, 6264–6268, Aug 1989.

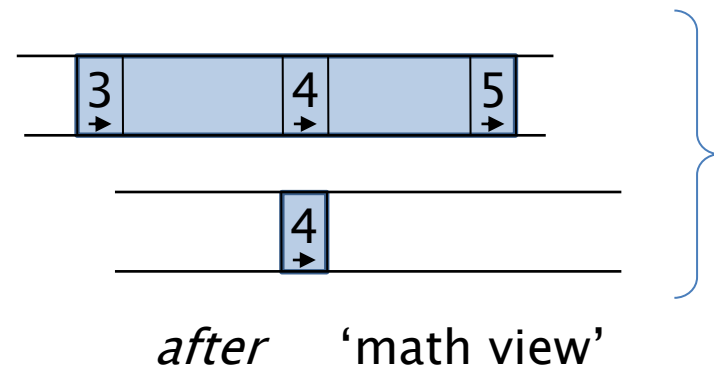
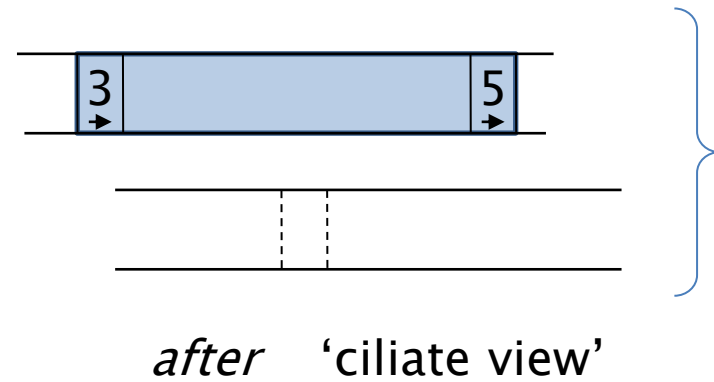
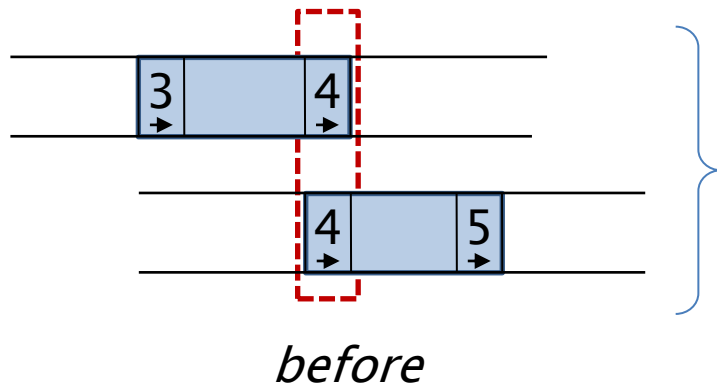


pointers – overlapping segments (for glueing)



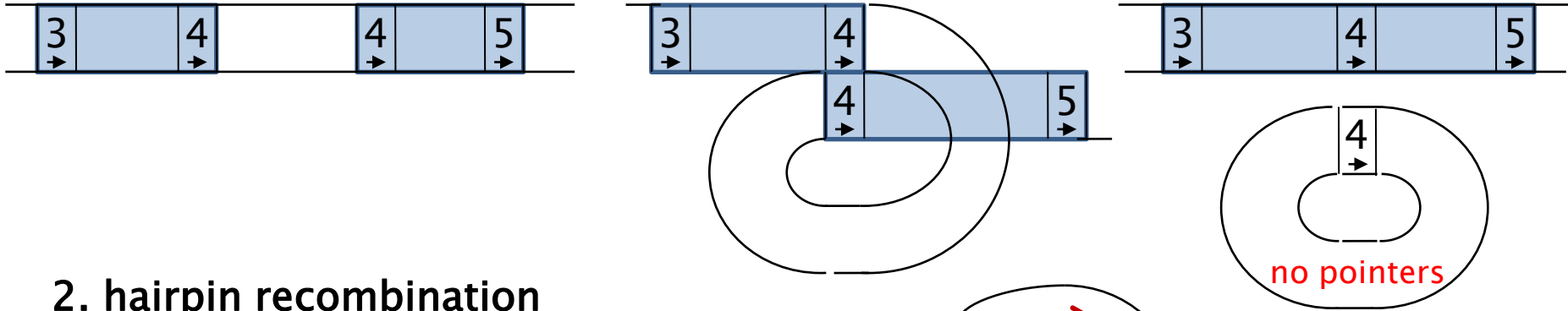
e.g., pointer 5 of actin gene: 13 bp

rc_4 recombination on pointer 4 'generic'

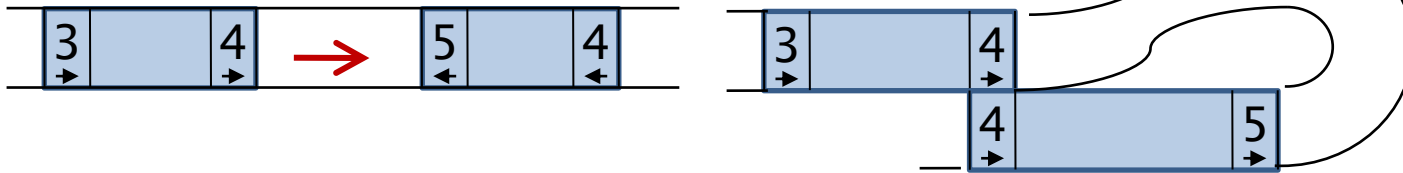


recombination on pointers

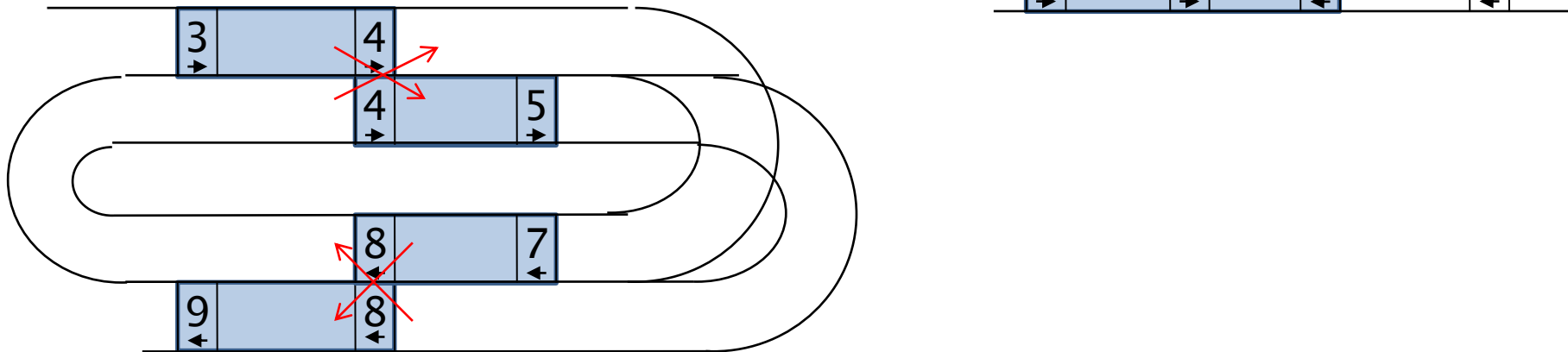
1. loop recombination



2. hairpin recombination



3. double-loop recombination

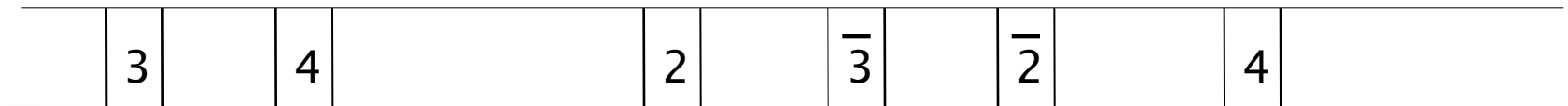


quest for the “right” model

- strings
- graphs
- matrices
- set systems



abstraction: pointers



342 $\bar{3}$ $\bar{2}$ 4

'legal' string

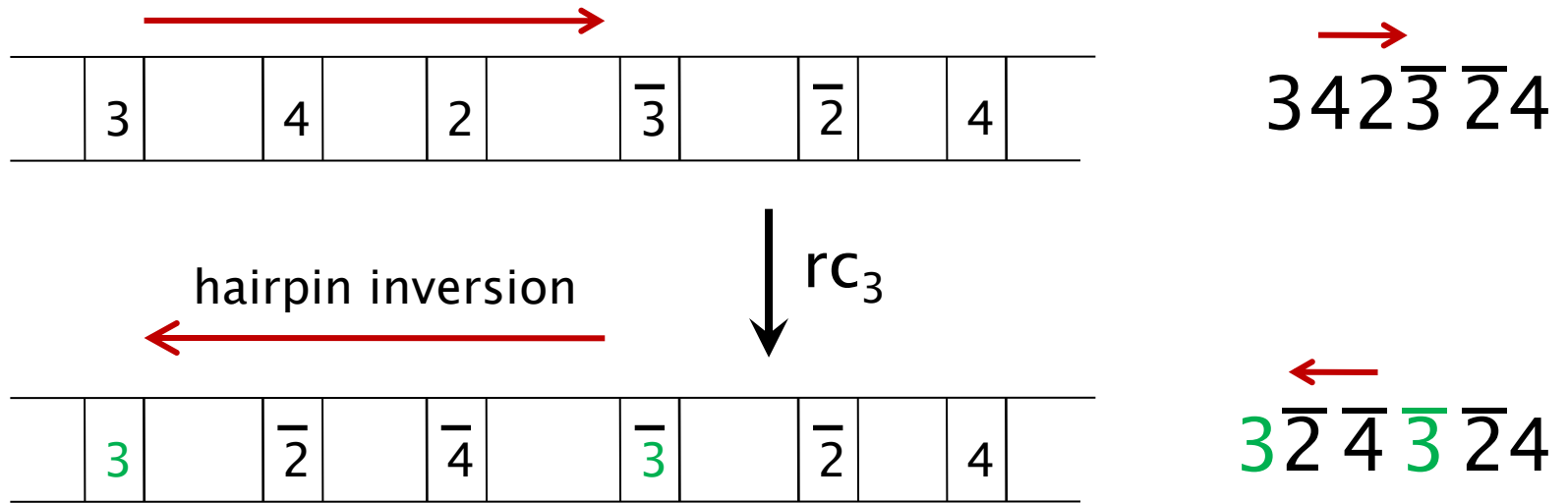
realistic strings

vs. generalizations

... 4774 ...

string positive rule

translating recombinations into string operations




$$rc_p(u_1 p u_2 \bar{p} u_3) = u_1 p \bar{u}_2 \bar{p} u_3$$

string pointer reduction systems

$$rc_p(u_1 p p u_2) = u_1 p p u_2$$

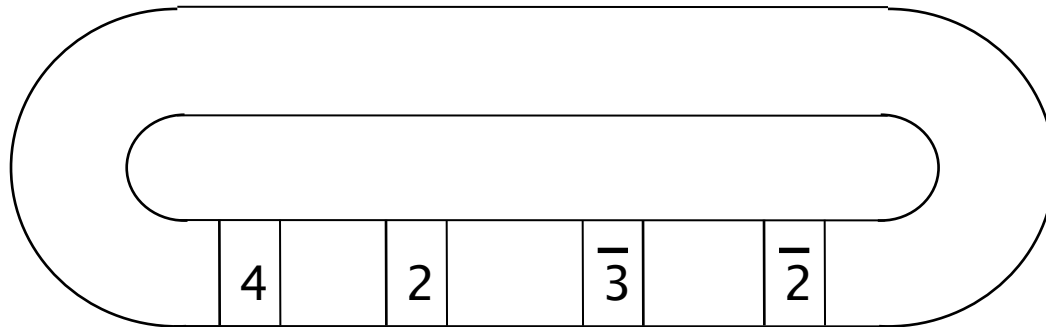
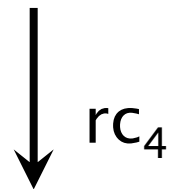
no rearrangement
excision circular molecule

$$rc_p(u_1 p u_2 \bar{p} u_3) = u_1 p \bar{u}_2 \bar{p} u_3$$

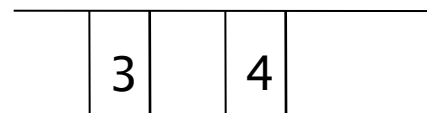
$$rc_{p,q}(u_1 p u_2 q u_3 p u_4 q u_5) = u_1 p u_4 q u_3 p u_2 q u_5$$




342 $\bar{3}$ $\bar{2}$ 4



undefined



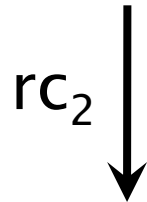
(we will come beack to this)

sorting = reduction

Micronuclear DNA



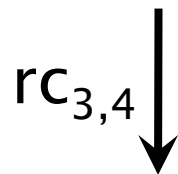
342 $\bar{3}$ $\bar{2}$ 4



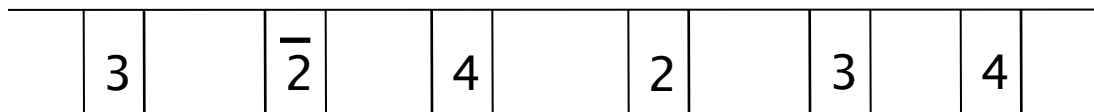
$$rc_p(u_1 p u_2 \bar{p} u_3) = u_1 p \bar{u}_2 \bar{p} u_3$$



3423 $\bar{2}$ 4



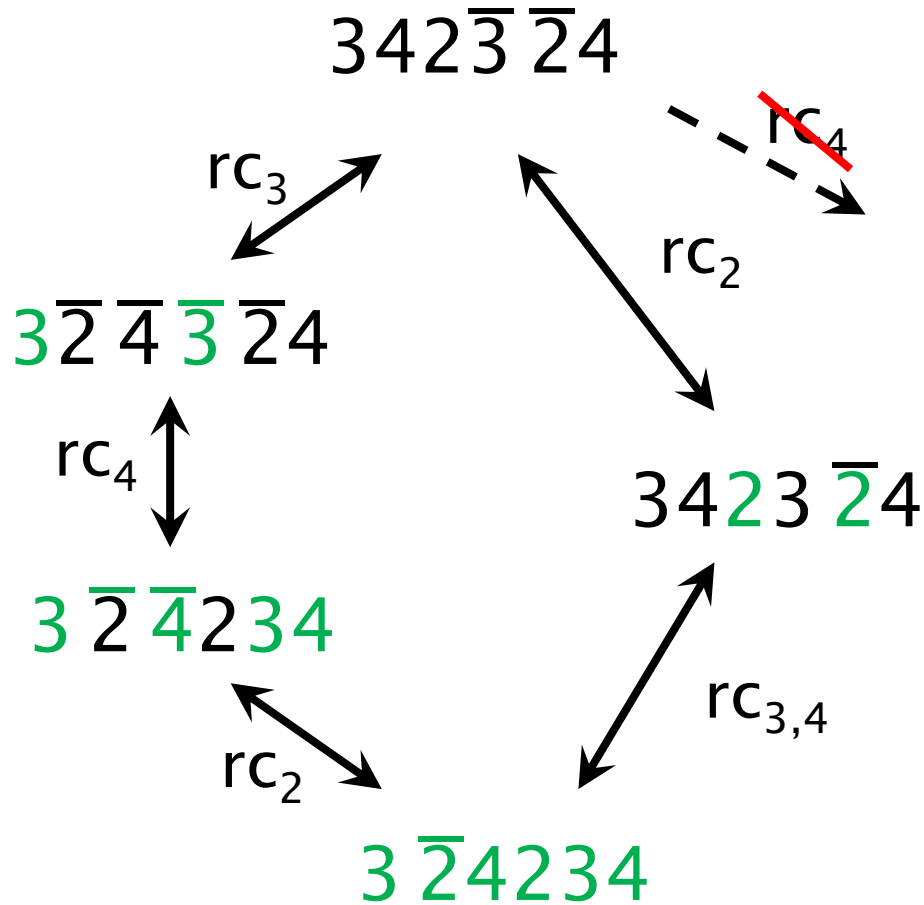
$$rc_{p,q}(u_1 p u_2 q u_3 p u_4 q u_5) = u_1 p u_4 q u_3 p u_2 q u_5$$



3 $\bar{2}$ 4234

Macronuclear DNA

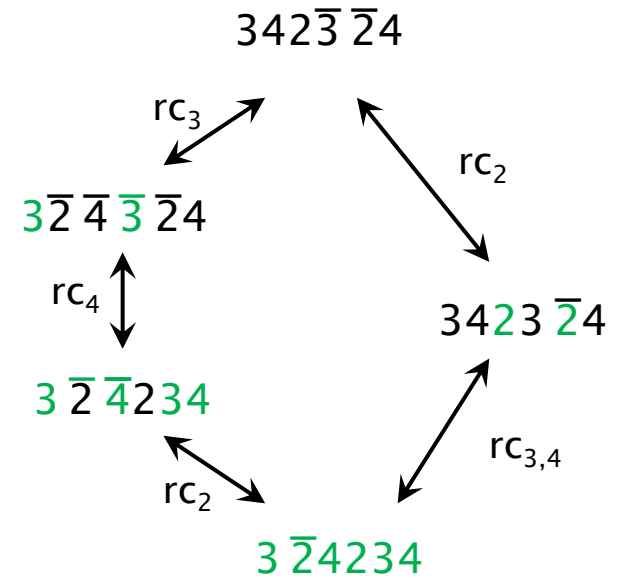
Micronuclear DNA



Macronuclear DNA

$$rc_p(u_1 p u_2 \bar{p} u_3) = u_1 p \bar{u}_2 \bar{p} u_3$$

$$rc_{p,q}(u_1 p u_2 q u_3 p u_4 q u_5) = u_1 p u_4 q u_3 p u_2 q u_5$$



question:

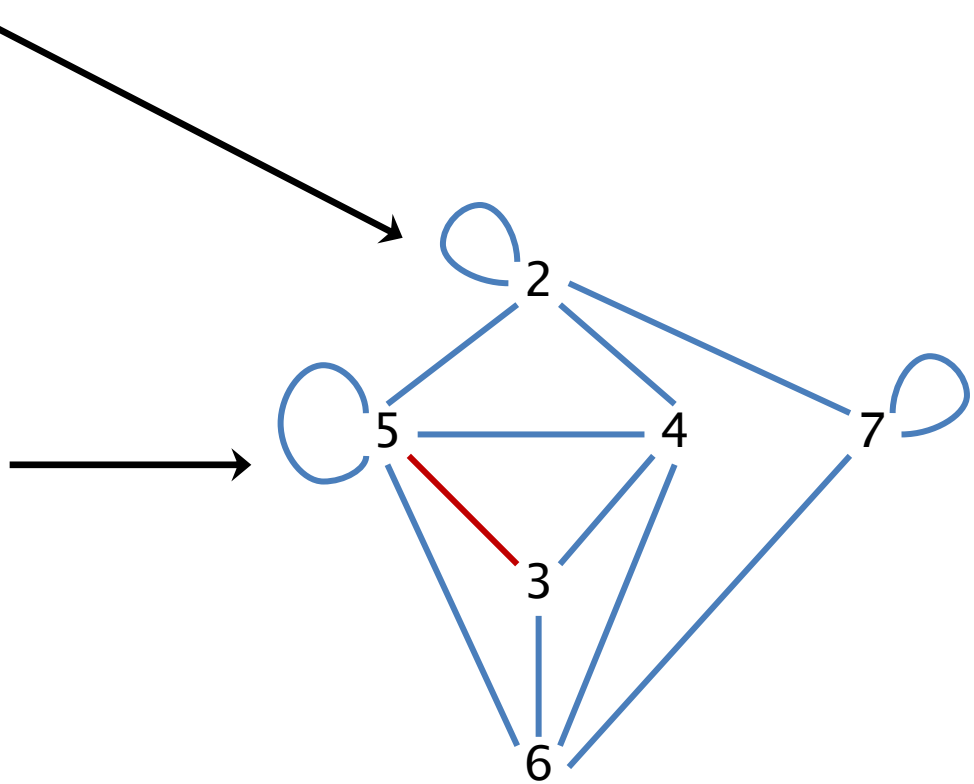
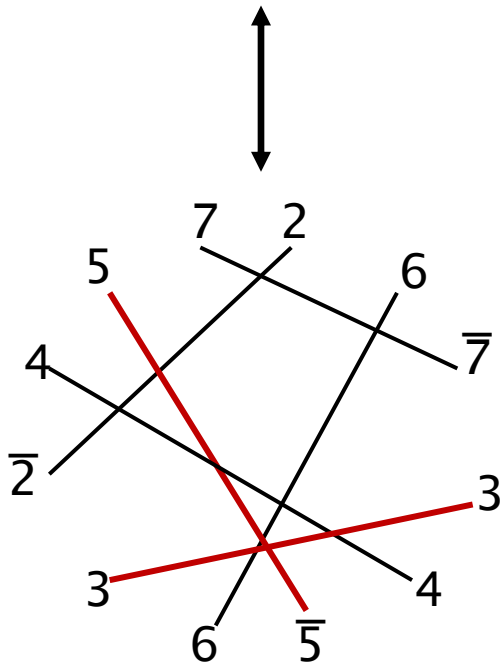
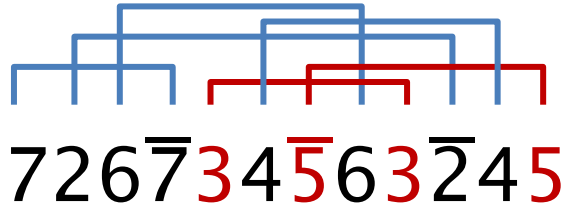
is the result of reductions independent of operations chosen?

quest for the “right” model

- strings
- graphs
- matrices
- set systems



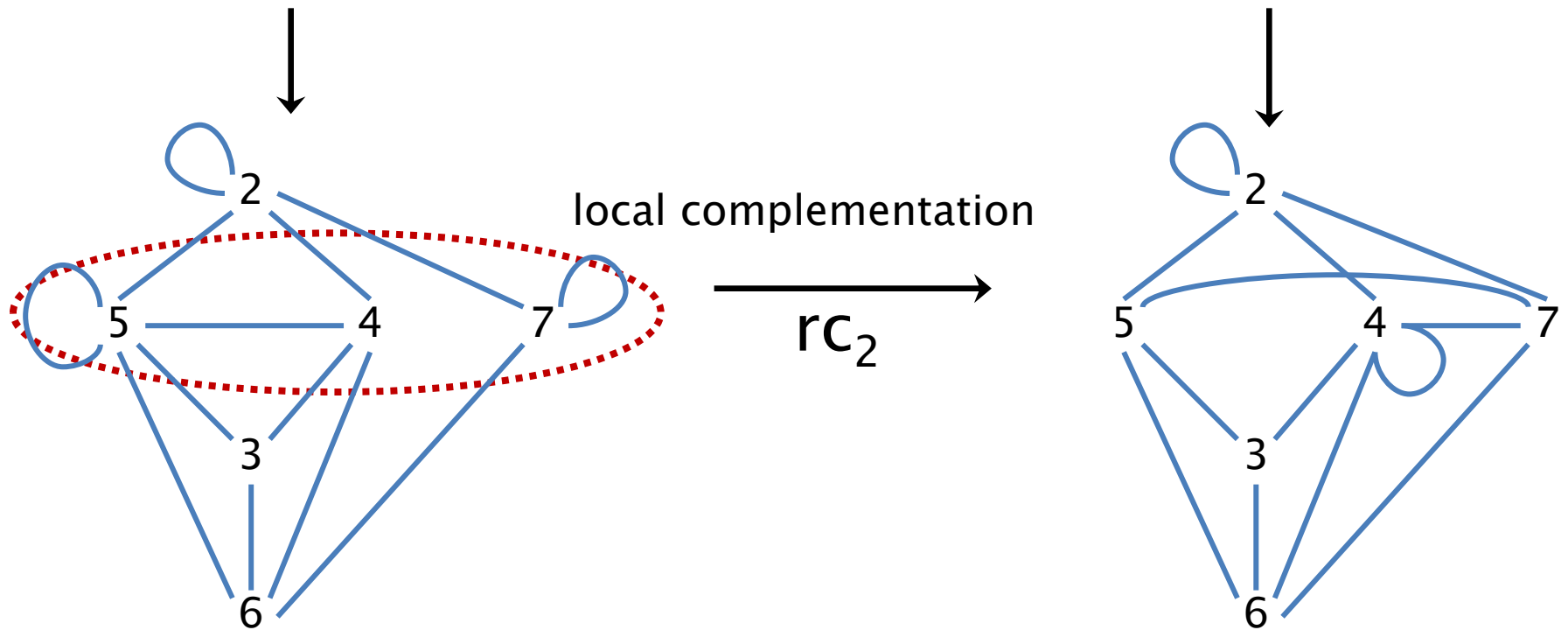
circle & overlap graph



string to overlap graph

real generalization

$726\overline{7}34\overline{5}63\overline{2}45 \xrightarrow{rc_2} 72\overline{3}6\overline{5}4\overline{3}7\overline{6}245$



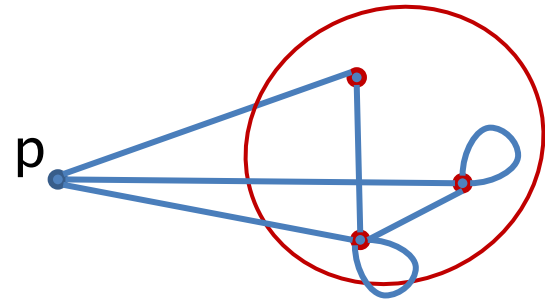
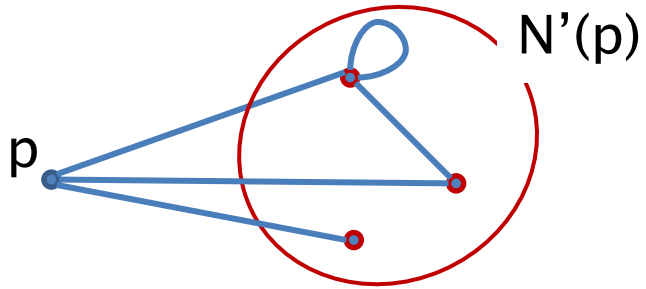
Ehrenfeucht et al, *Theor. Comp. Sci.*, 2003

(for signed graphs instead of looped graphs)

rc_p

local complementation

looped vertex p

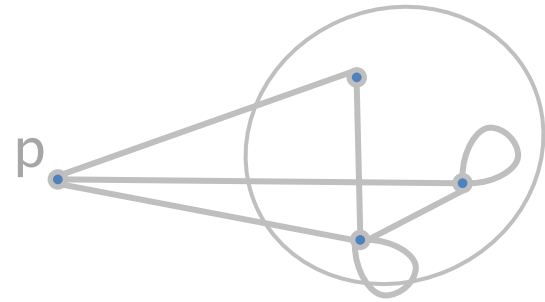
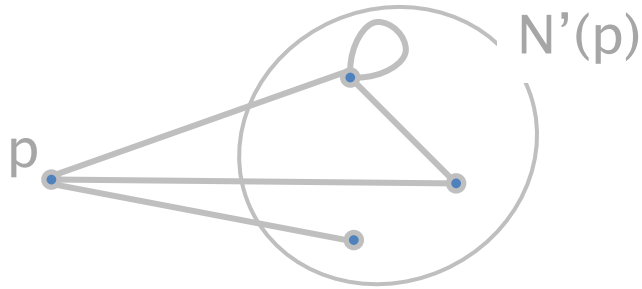


graph operations

rc_p

local complementation

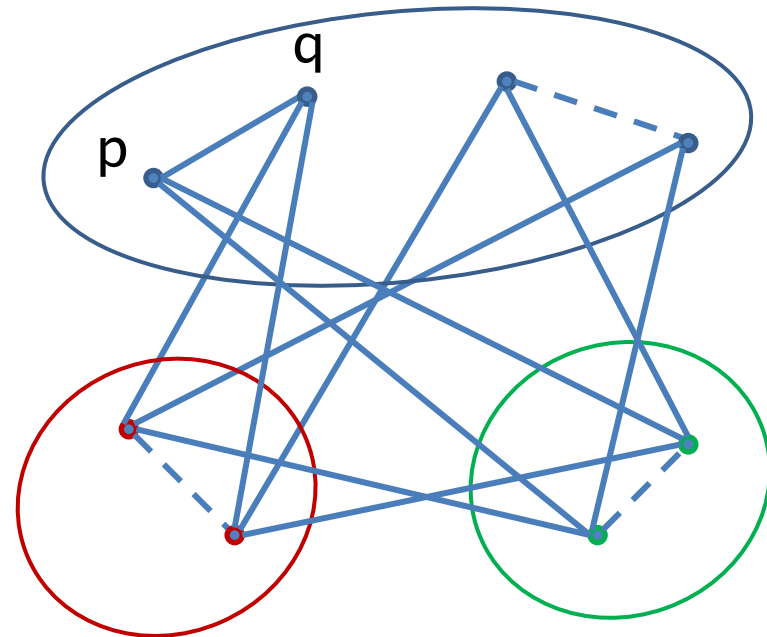
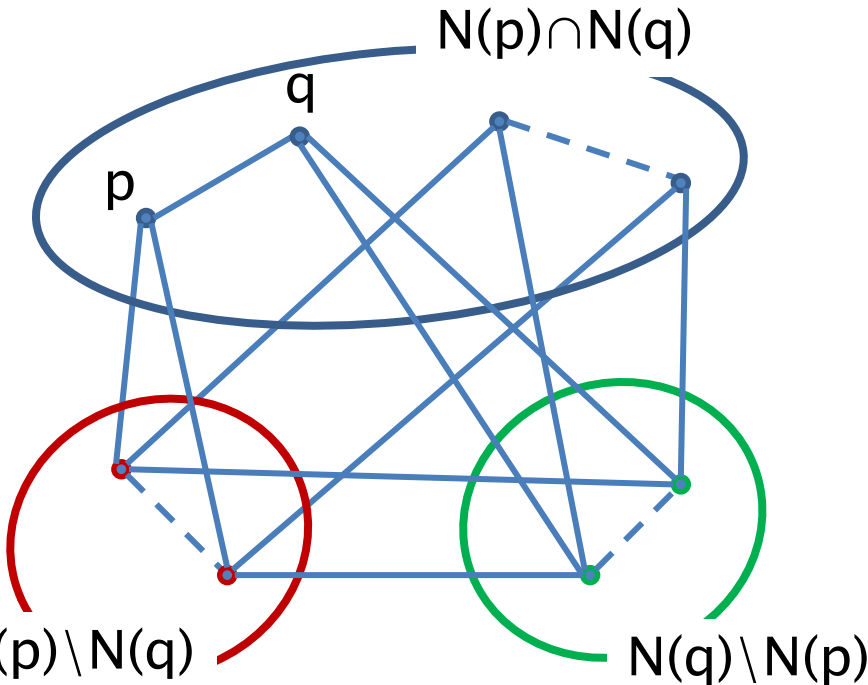
looped vertex p



$rc_{p,q}$

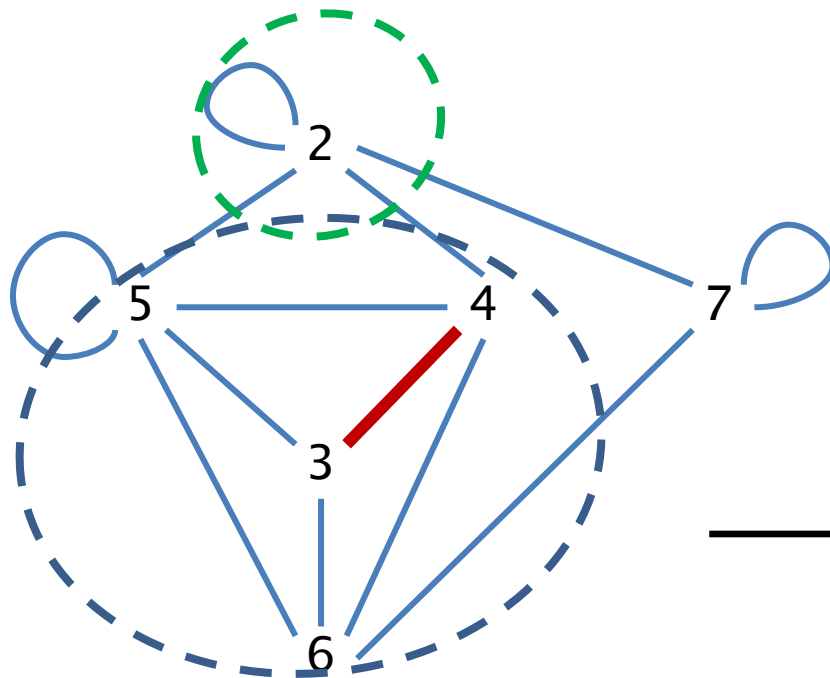
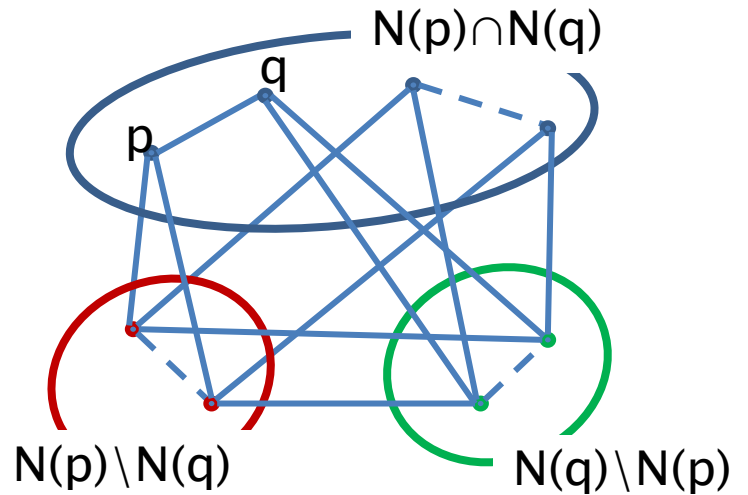
edge complementation

unlooped edge pq

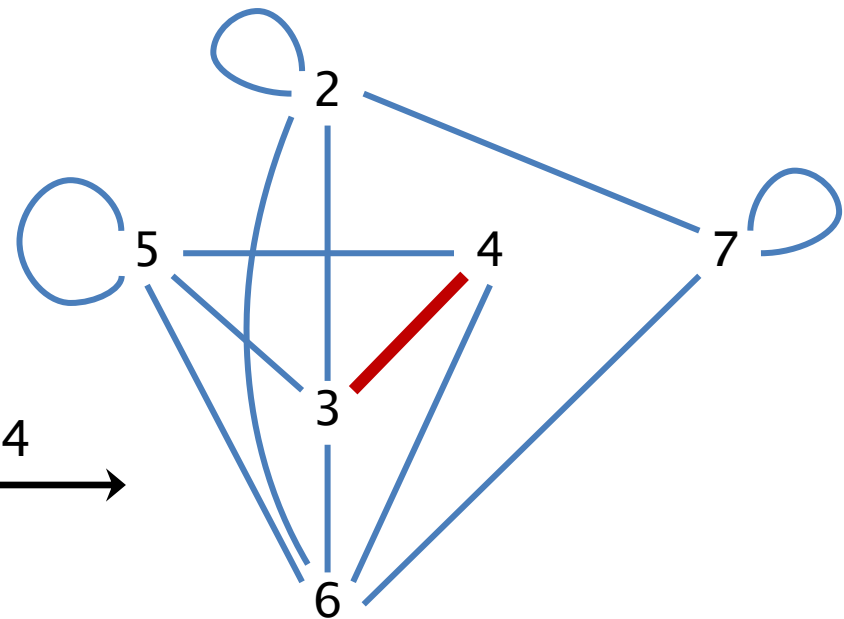


example edge complement

$rc_{3,4}$ on edge 3,4



$rc_{3,4}$



two worlds

Micronuclear DNA

$342\bar{3}\bar{2}4$

rc_3

rc_2

$3\bar{2}\bar{4}\bar{3}\bar{2}4$

rc_4

$3423\bar{2}4$

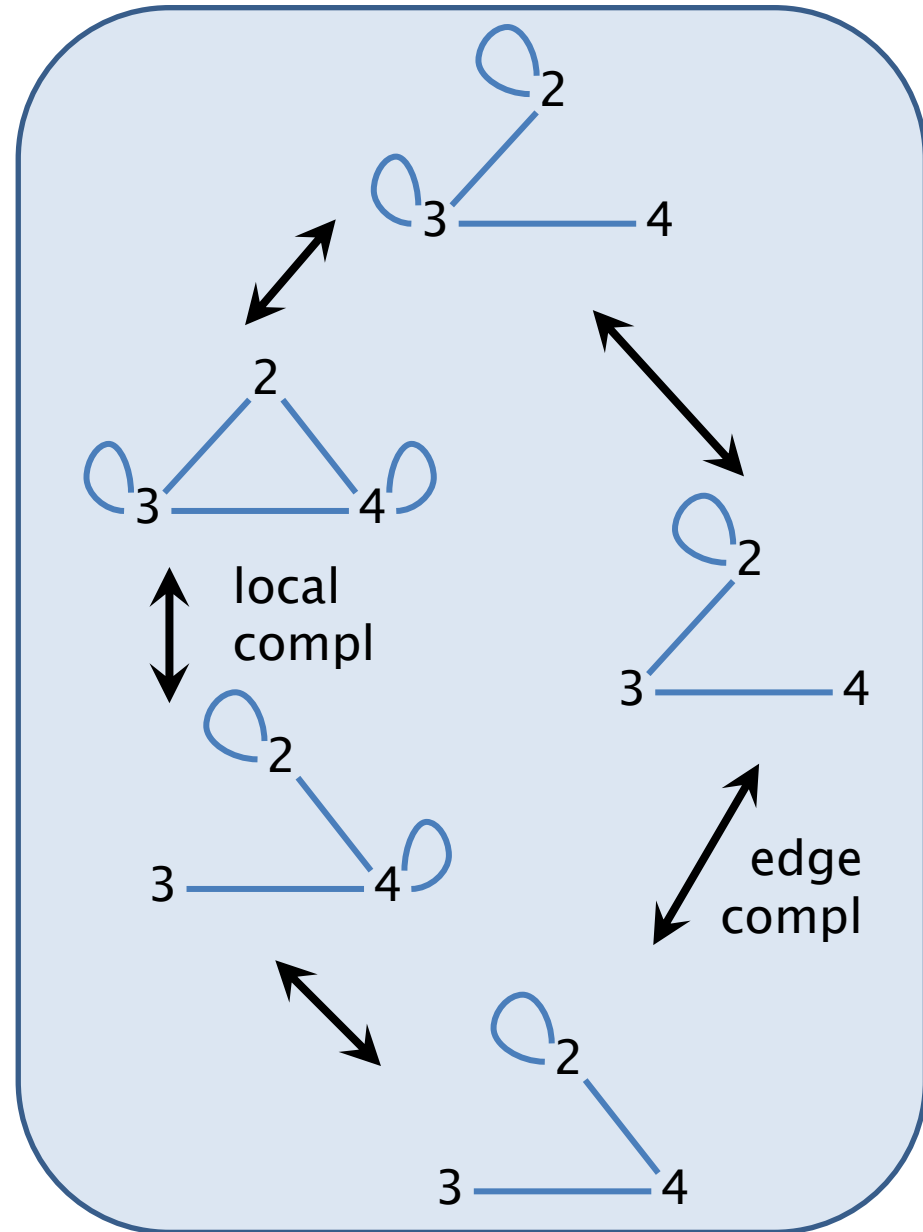
$3\bar{2}\bar{4}234$

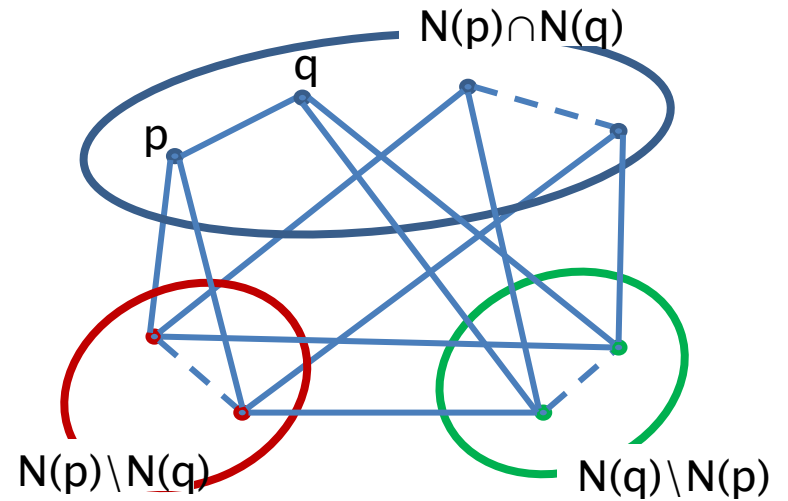
rc_2

$rc_{3,4}$

$3\bar{2}\bar{4}234$

Macronuclear DNA





question:

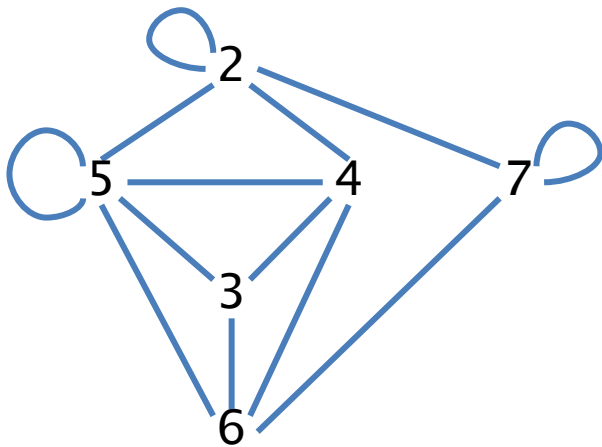
how do $rc_{p,q}$ and $rc_{p',q'}$ interact ?

quest for the “right” model

- strings
- graphs
- matrices
- set systems

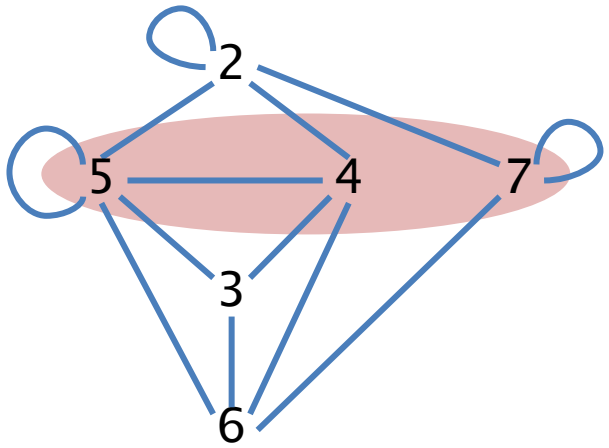


graphs and matrices



	2	3	4	5	6	7
2	1	0	1	1	0	1
3	0	0	1	1	1	0
4	1	1	0	1	1	0
5	1	1	1	1	1	0
6	0	1	1	1	0	1
7	1	0	0	0	1	1

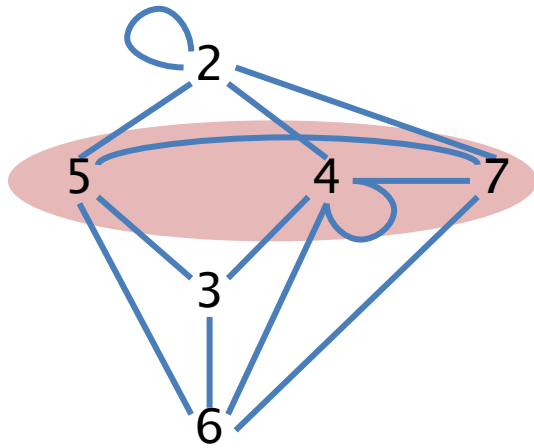
reconsider local/edge complementation



	2	3	4	5	6	7
2	1	0	1	1	0	1
3	0	0	1	1	1	0
4	1	1	0	1	1	0
5	1	1	1	1	1	0
6	0	1	1	1	0	1
7	1	0	0	0	1	1



rc_2



	2	3	4	5	6	7
2	1	0	1	1	0	1
3	0	0	1	1	1	0
4	1	1	1	0	1	1
5	1	1	0	0	1	1
6	0	1	1	1	0	1
7	1	0	1	1	1	0



rc_2



what *is* happening?

$$\begin{array}{c}
 342\bar{3}\bar{2}4 \\
 \begin{array}{c} 2 \\ 3 \\ 4 \end{array} \begin{pmatrix} 2 & 3 & 4 \\ 1 & 1 & 0 \\ 1 & 1 & 1 \\ 0 & 1 & 0 \end{pmatrix}
 \end{array}
 \xrightarrow{rc_3 \ rc_4 \ rc_2}
 \begin{array}{c}
 3\bar{2}4234 \\
 \begin{array}{c} 2 \\ 3 \\ 4 \end{array} \begin{pmatrix} 2 & 3 & 4 \\ 1 & 0 & 1 \\ 0 & 0 & 1 \\ 1 & 1 & 0 \end{pmatrix}
 \end{array}$$

multiply (over the binary numbers)

$$\begin{array}{c} \begin{pmatrix} 1 & 1 & 0 \\ 1 & 1 & 1 \\ 0 & 1 & 0 \end{pmatrix} \\ \text{micro} \end{array}
 \begin{array}{c} \begin{pmatrix} 1 & 0 & 1 \\ 0 & 0 & 1 \\ 1 & 1 & 0 \end{pmatrix} \\ \text{macro} \end{array}
 =
 \begin{array}{c} \begin{pmatrix} \\ \\ 0 \end{pmatrix} \end{array}$$

+ xor \oplus $1+1=0$
 * and \wedge

what *is* happening? inversion

$$\begin{array}{c}
 342\bar{3}\bar{2}4 \\
 \begin{array}{c} 2 \\ 3 \\ 4 \end{array} \begin{pmatrix} 2 & 3 & 4 \\ 1 & 1 & 0 \\ 1 & 1 & 1 \\ 0 & 1 & 0 \end{pmatrix}
 \end{array}
 \xrightarrow{rc_3 \ rc_4 \ rc_2}
 \begin{array}{c}
 3\bar{2}4234 \\
 \begin{array}{c} 2 \\ 3 \\ 4 \end{array} \begin{pmatrix} 2 & 3 & 4 \\ 1 & 0 & 1 \\ 0 & 0 & 1 \\ 1 & 1 & 0 \end{pmatrix}
 \end{array}$$

multiply (over the binary numbers)

$$\begin{array}{c} \begin{pmatrix} 1 & 1 & 0 \\ 1 & 1 & 1 \\ 0 & 1 & 0 \end{pmatrix} \\ \text{micro} \end{array}
 \begin{array}{c} \begin{pmatrix} 1 & 0 & 1 \\ 0 & 0 & 1 \\ 1 & 1 & 0 \end{pmatrix} \\ \text{macro} \end{array}
 =
 \begin{array}{c} \begin{pmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix} \end{array}$$

$$\begin{array}{c} \begin{pmatrix} 1 & 1 & 0 \\ 1 & 1 & 1 \\ 0 & 1 & 0 \end{pmatrix} \\ \text{micro} \end{array}
 =
 \begin{array}{c} \begin{pmatrix} 1 & 0 & 1 \\ 0 & 0 & 1 \\ 1 & 1 & 0 \end{pmatrix} \\ \text{macro} \end{array}
 ^{-1}$$

sorting DNA = computing the inverse

$$A x = y \quad \text{iff} \quad A^{-1} y = x$$

principal pivot transform

$$A \begin{pmatrix} x_1 \\ x_2 \end{pmatrix} = \begin{pmatrix} y_1 \\ y_2 \end{pmatrix} \quad \text{iff} \quad A * X \begin{pmatrix} y_1 \\ x_2 \end{pmatrix} = \begin{pmatrix} x_1 \\ y_2 \end{pmatrix}$$

\leftarrow X pointers
 \leftarrow other

$A * X$ is defined iff $A[X]$ is invertible

real recipe (which we do not need)

$$A = \begin{matrix} & X \\ X & \begin{pmatrix} P & Q \\ R & S \end{pmatrix} \end{matrix} \quad A * X = \left(\begin{array}{c|c} P^{-1} & -P^{-1} Q \\ \hline R P^{-1} & S - R P^{-1} Q \end{array} \right)$$

$P = A[X]$ invertible / nonsingular i.e. $\det P \neq 0$

principal pivot transform

$$A \begin{pmatrix} x_1 \\ x_2 \end{pmatrix} = \begin{pmatrix} y_1 \\ y_2 \end{pmatrix} \text{ iff } A * X \begin{pmatrix} y_1 \\ x_2 \end{pmatrix} = \begin{pmatrix} x_1 \\ y_2 \end{pmatrix}$$

using partial inversion

xor

$$(A * X) * Y = A * (X \oplus Y)$$

(when defined)

$$A * \{p_1, p_2\} \dots * p_n = A * V = A^{-1}$$

(all pointers)

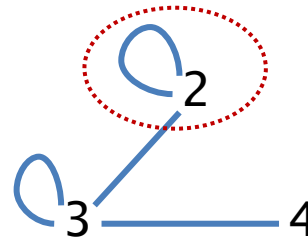
this shows

- how the rc_p and $rc_{p,q}$ interact
- result does not depend on order of operations

$A * X$ is defined iff $A[X]$ is invertible

rc_2

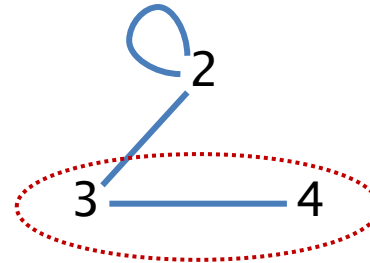
342 $\bar{3}$ $\bar{2}$ 4



$$\begin{pmatrix} 1 & 1 & 0 \\ 1 & 1 & 1 \\ 0 & 1 & 0 \end{pmatrix}$$

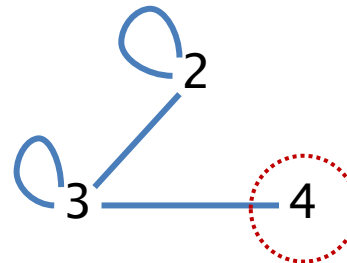
$rc_{3,4}$

3423 $\bar{2}$ 4



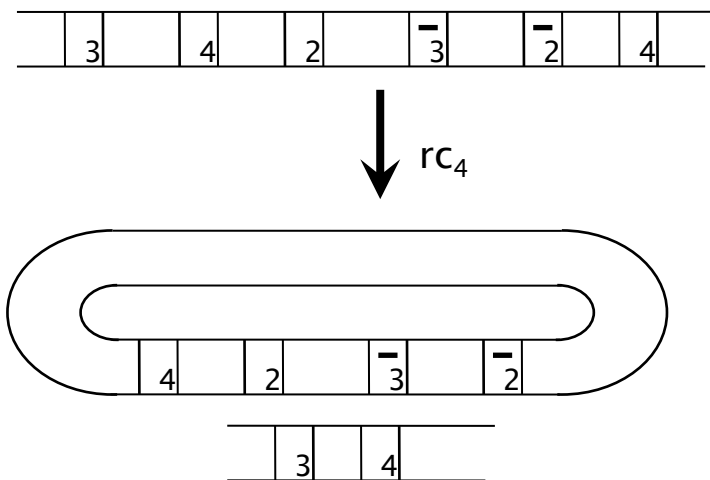
$$\begin{pmatrix} 1 & 1 & 0 \\ 1 & 0 & 1 \\ 0 & 1 & 0 \end{pmatrix}$$

342 $\bar{3}$ $\bar{2}$ 4



$$\begin{matrix} & \begin{matrix} 2 & 3 & 4 \end{matrix} \\ \begin{matrix} 2 \\ 3 \\ 4 \end{matrix} & \begin{pmatrix} 1 & 1 & 0 \\ 1 & 1 & 1 \\ 0 & 1 & 0 \end{pmatrix} \end{matrix}$$

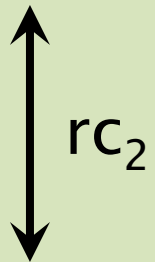
undefined



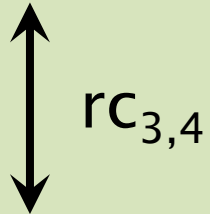
three worlds

Micronuclear DNA

342 $\bar{3}$ $\bar{2}$ 4

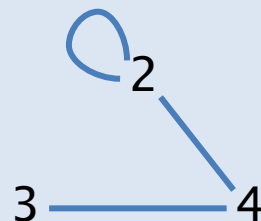
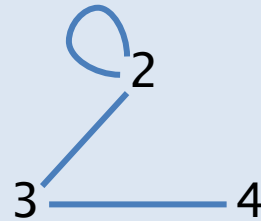
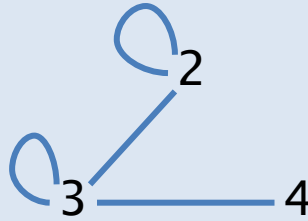


3423 $\bar{2}$ 4

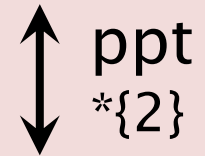


3 $\bar{2}$ 4234

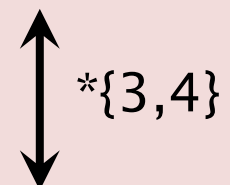
Macronuclear DNA



$$\begin{pmatrix} 1 & 1 & 0 \\ 1 & 1 & 1 \\ 0 & 1 & 0 \end{pmatrix}$$



$$\begin{pmatrix} 1 & 1 & 0 \\ 1 & 0 & 1 \\ 0 & 1 & 0 \end{pmatrix}$$



$$\begin{pmatrix} 1 & 0 & 1 \\ 0 & 0 & 1 \\ 1 & 1 & 0 \end{pmatrix}$$

- by careful modeling we find that gene assembly is *actually* principal pivot transform (ppt)
- we can use results about ppt to know more about gene assembly
 - independent order operations
 - interaction operations

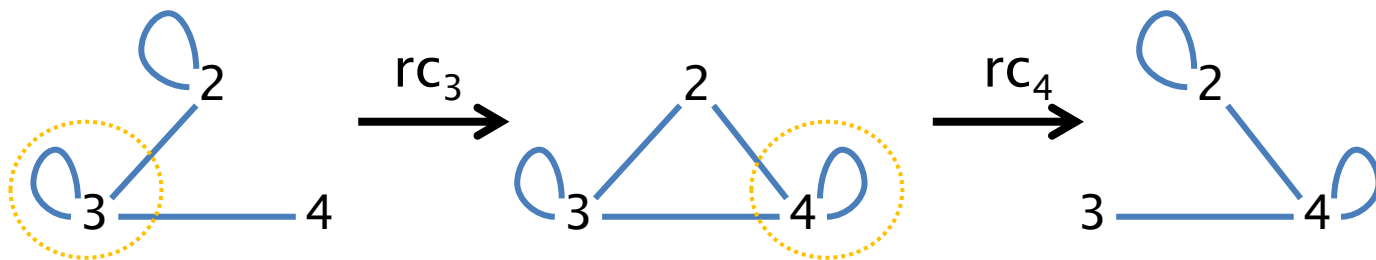
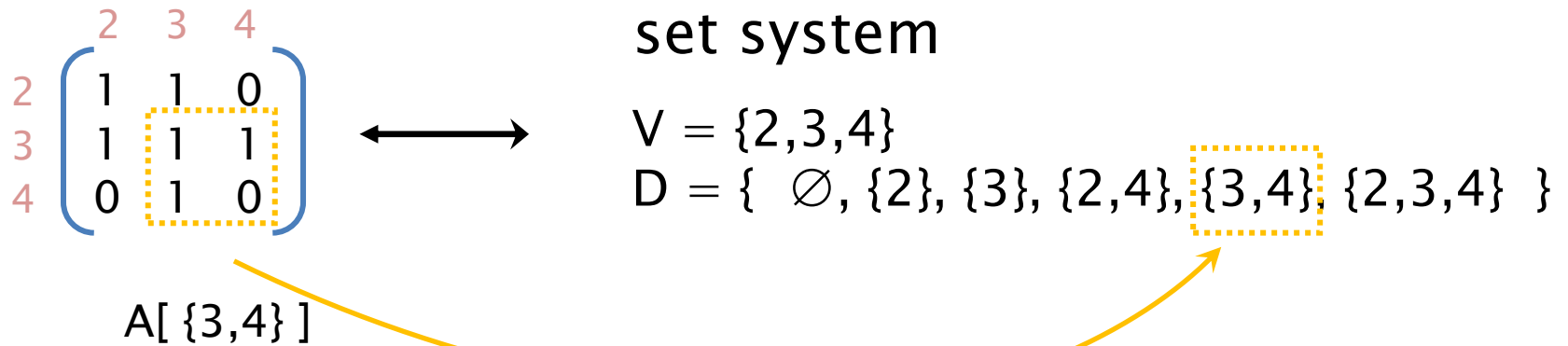
quest for the “right” model

- strings
- graphs
- matrices
- set systems

the most elegant model was hidden

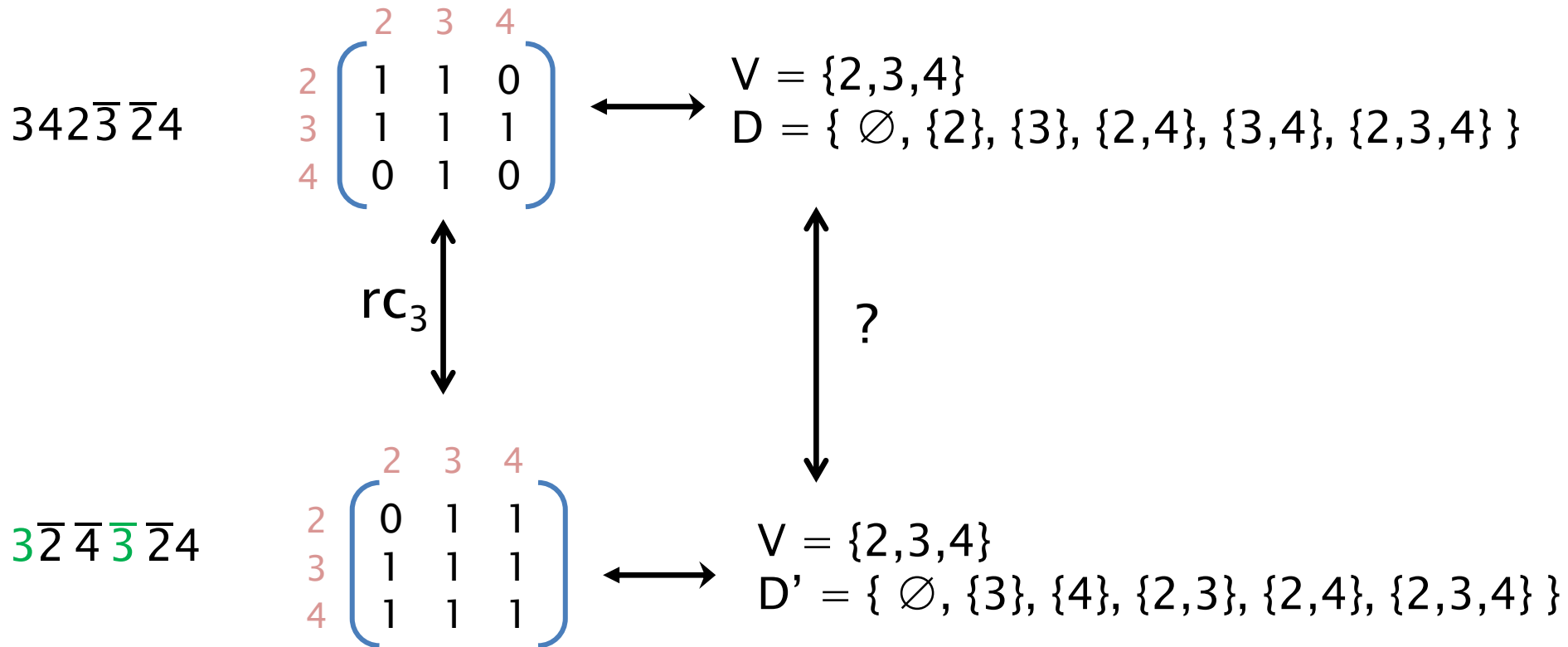


$A * X$ is defined iff $A[X]$ is invertible



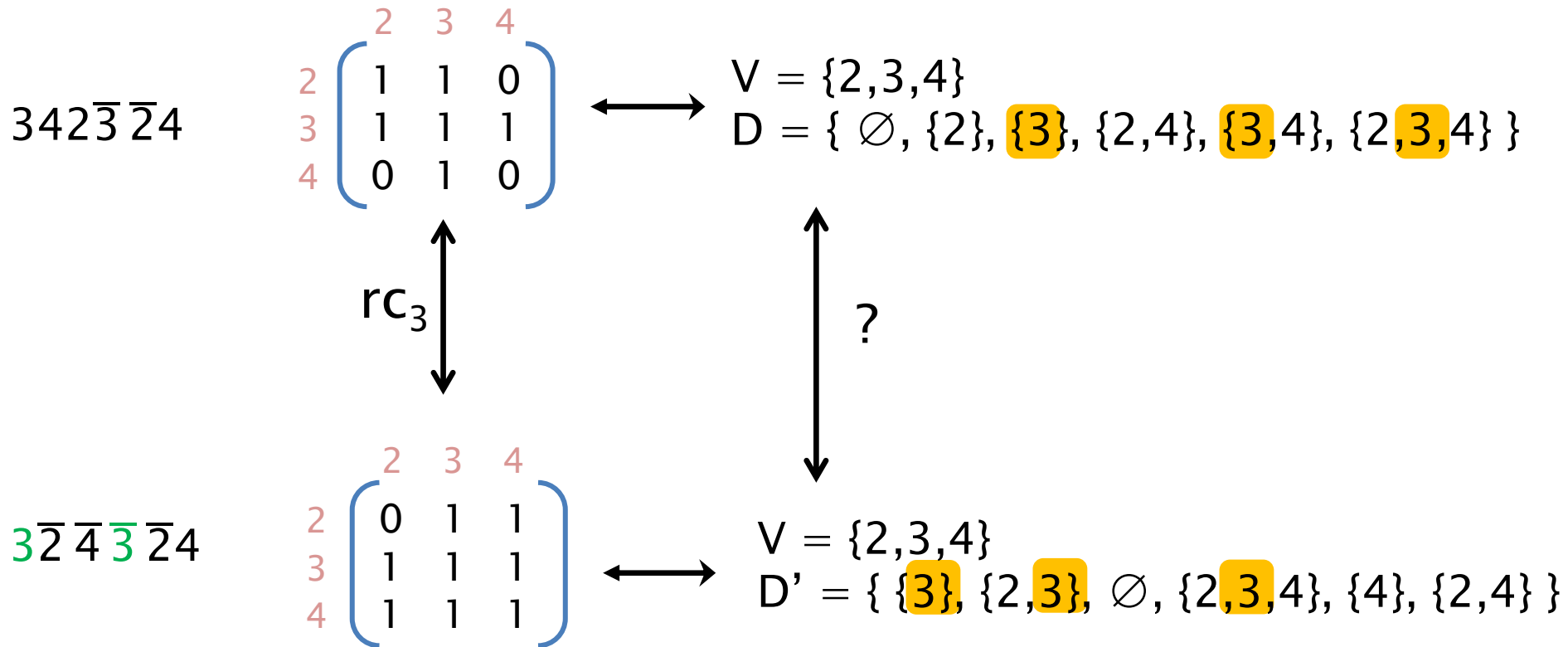
which operation ?

graphs \subseteq set systems (strict)



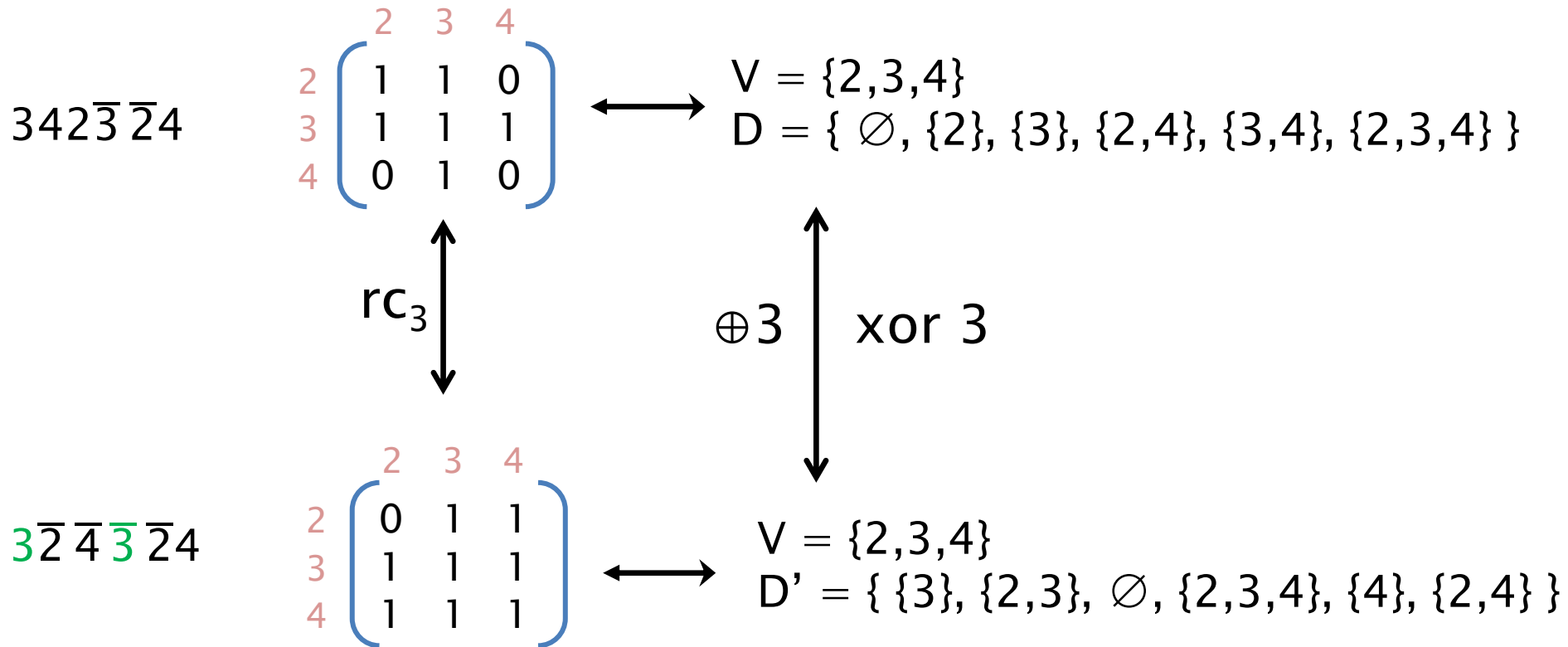
which operation ?

graphs \subseteq set systems (strict)



how simple can it get ...

graphs \subseteq set systems (strict)



applicability (!)

XOR {4} is defined, while rc_4 is not
nb. {4} not in D

four worlds

Micronuclear DNA

342 $\bar{3}$ $\bar{2}$ 4

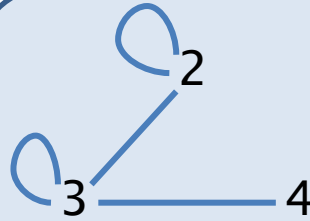
spr \longleftrightarrow rc₂

3423 $\bar{2}$ 4

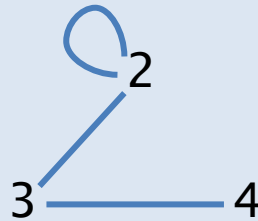
sdr \longleftrightarrow rc_{3,4}

3 $\bar{2}$ 4234

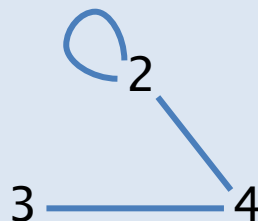
Macronuclear DNA



local compl



edge compl



$$\begin{pmatrix} 1 & 1 & 0 \\ 1 & 1 & 1 \\ 0 & 1 & 0 \end{pmatrix}$$

ppt \longleftrightarrow *{2}

$$\begin{pmatrix} 1 & 1 & 0 \\ 1 & 0 & 1 \\ 0 & 1 & 0 \end{pmatrix}$$

*{3,4}

$$\begin{pmatrix} 1 & 0 & 1 \\ 0 & 0 & 1 \\ 1 & 1 & 0 \end{pmatrix}$$

{ \emptyset , {2}, {3}, {2,4},
{3,4}, {2,3,4}}

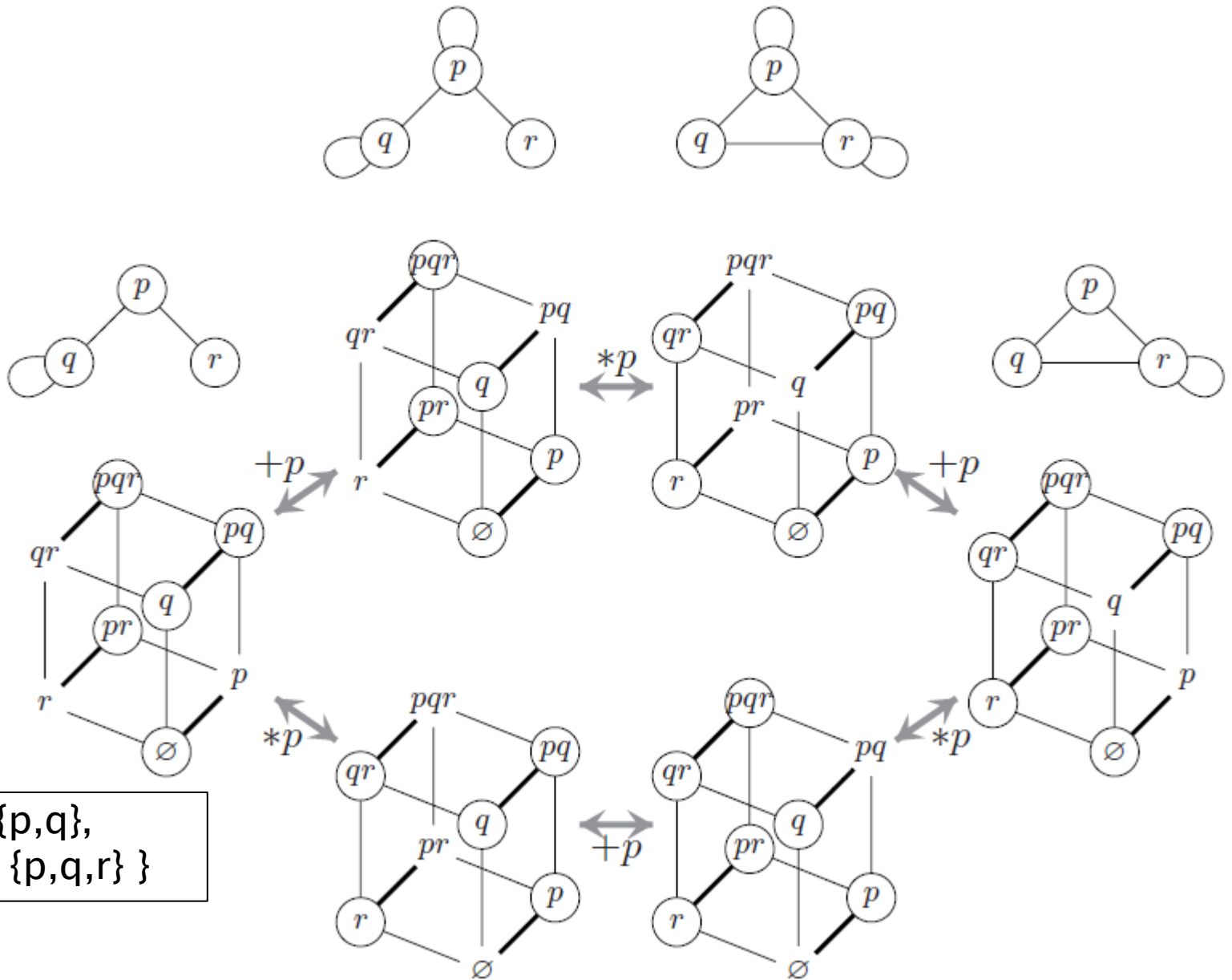
XOR \longleftrightarrow \oplus {2}

{ {2}, \emptyset , {2,3}, {4},
{2,3,4}, {3,4} }

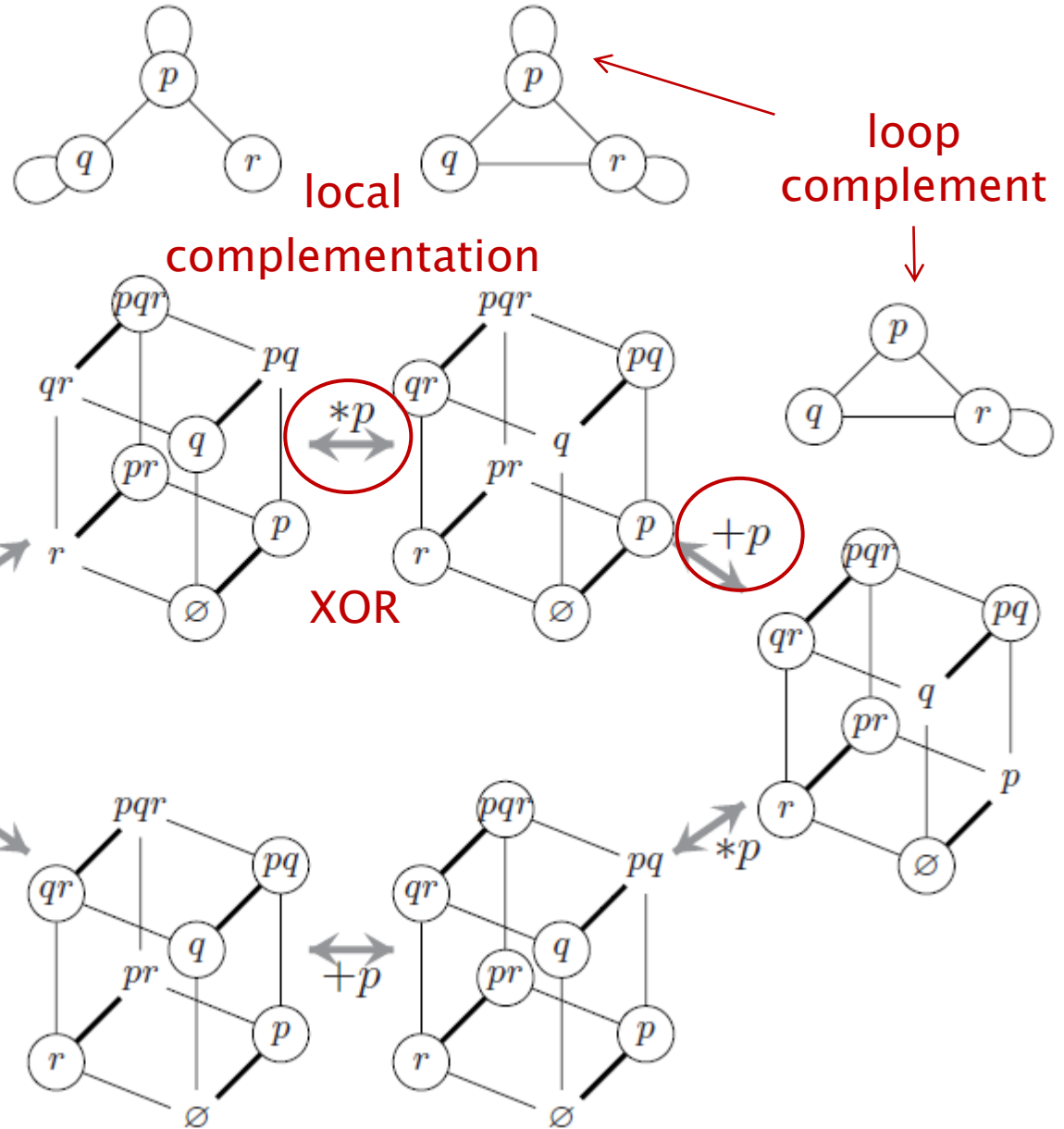
\longleftrightarrow \oplus {3,4}

{ {2,3,4}, {3,4},
{2,4}, {3}, {2}, \emptyset }

algebra of set systems



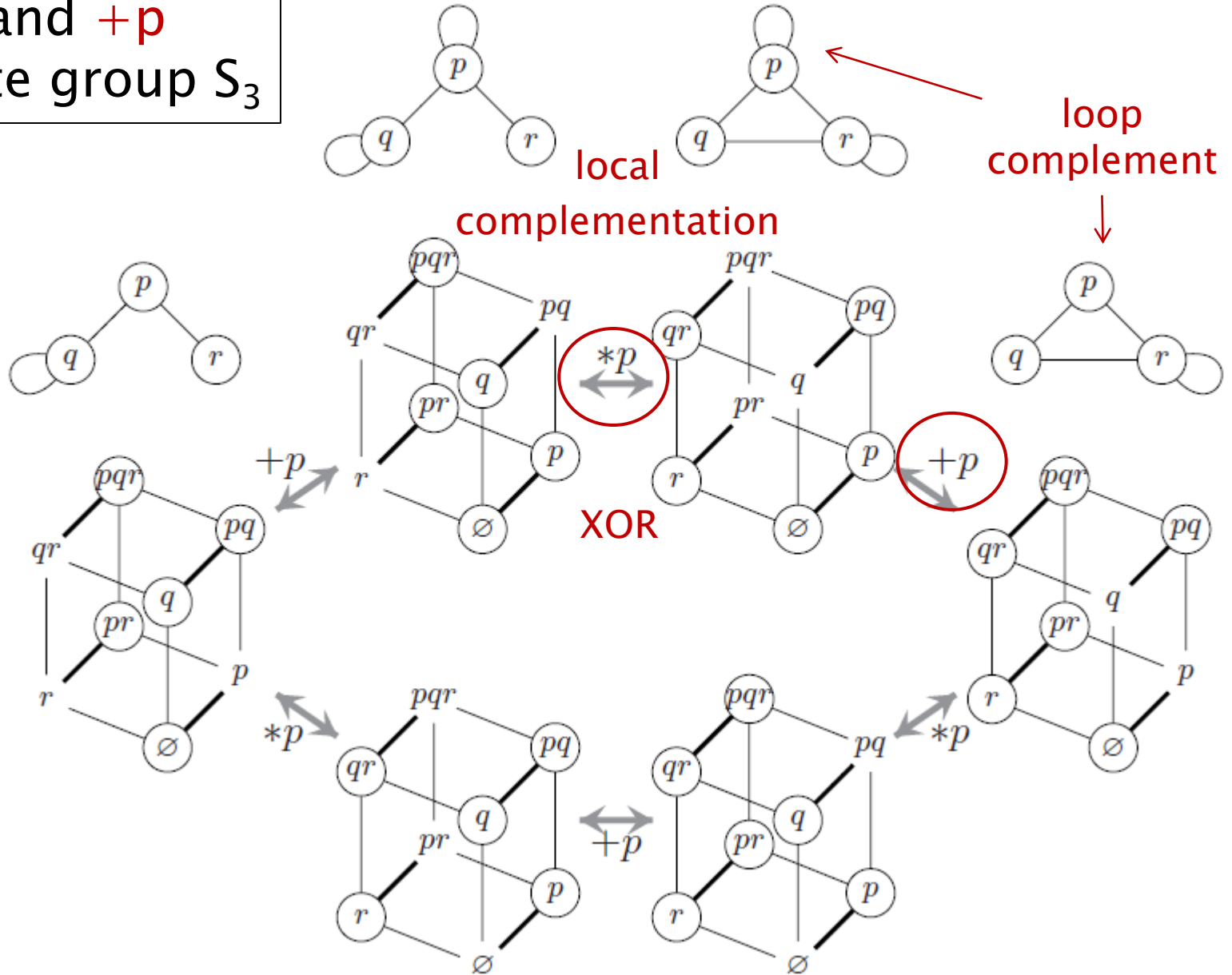
algebra of set systems



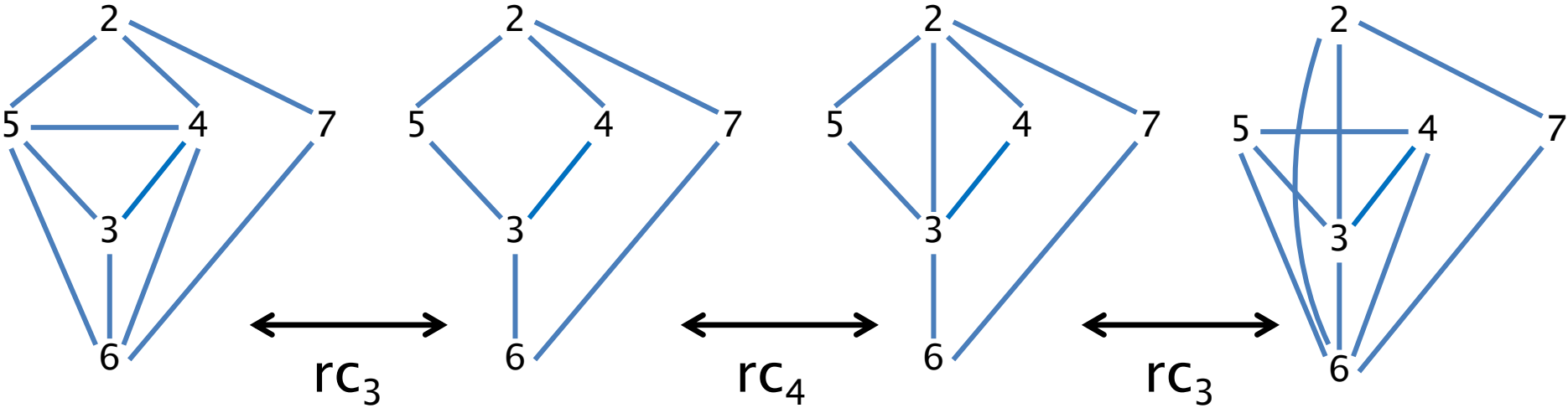
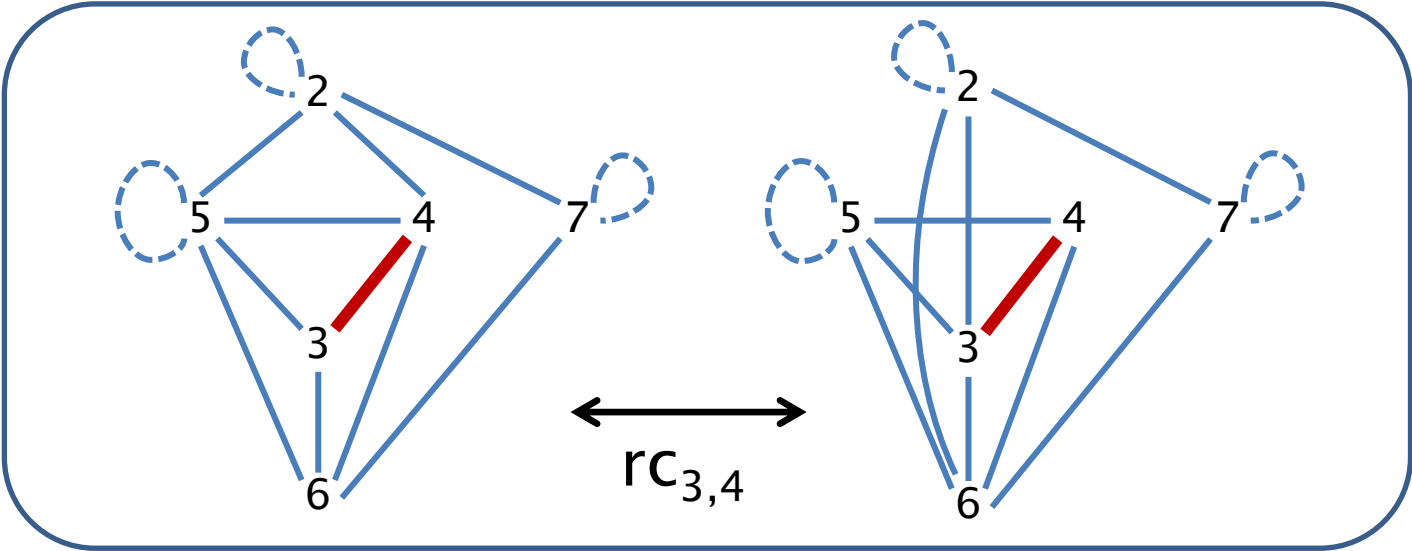
$\{ \emptyset, \{q\}, \{p,q\}, \{p,r\}, \{p,q,r\} \}$

algebra of set systems

***p** and **+p**
generate group S_3

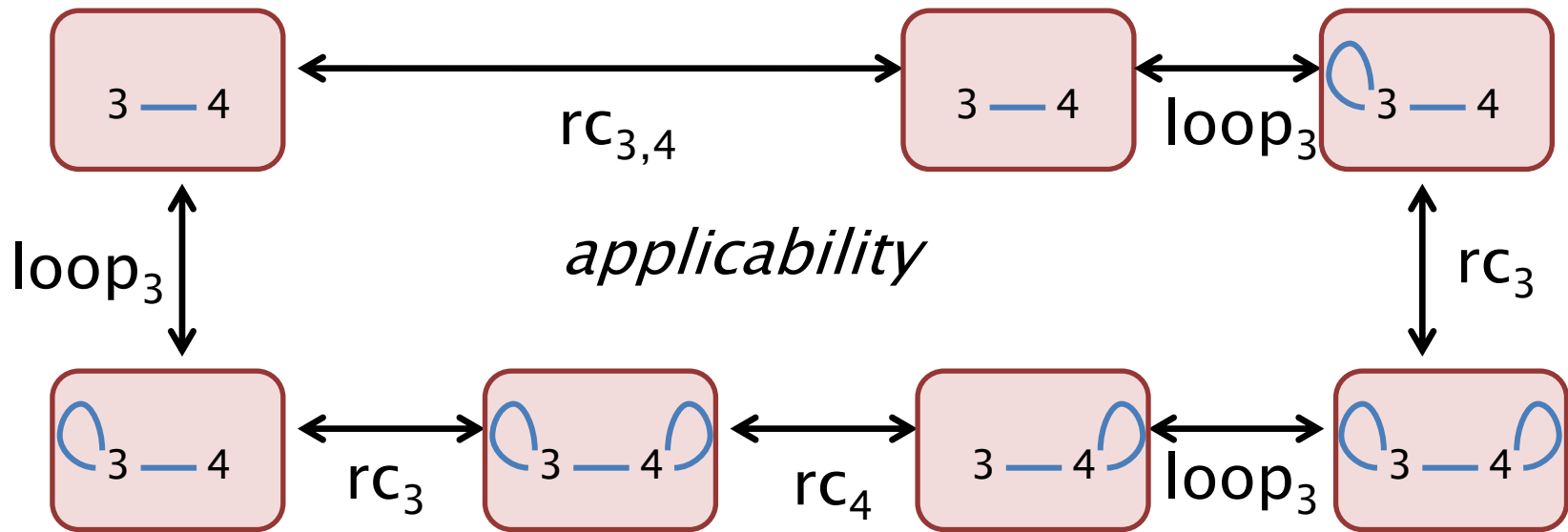


edge complement vs. local complement



ignoring loops

edge complement vs. local complement



basic algebra S_3

$*3 *4 = *4 *3$

$*3 *3 = \text{id} = +3 +3$

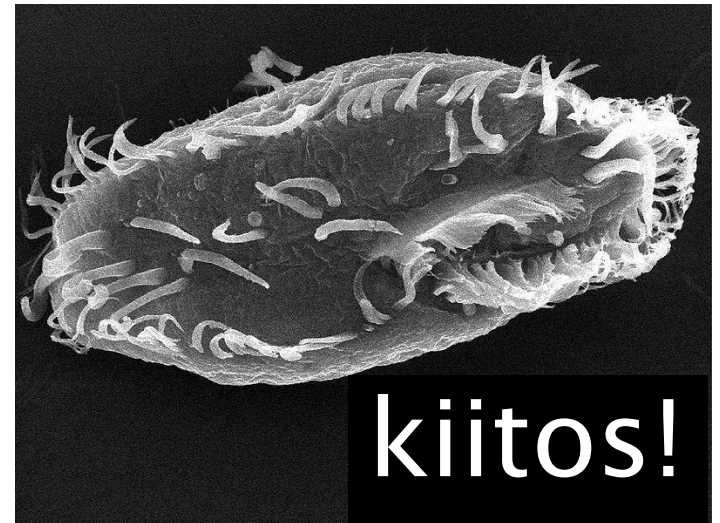
$+3 *3 +3 = *3 +3 *3$

$$\begin{aligned}
 +3 *3 *4 +3 *3 +3 &= \\
 +3 *3 +3 *3 +3 *4 &= \\
 +3 *3 *3 +3 *3 *4 &= \\
 +3 +3 *3 *4 &= \\
 *3 *4 &= \\
 * \{3,4\} &=
 \end{aligned}$$

- by careful modeling we find that gene assembly is *actually* principal pivot transform (ppt) **and XOR**
- we can use results about ppt (on matrices) **and XOR (on set systems)** to know more about gene assembly
- **but also inspiration the other way around ...**

however ...

- parallelism
- 'simple' operations



R. Brijder, H.J. Hoogeboom. The Group Structure of Pivot and Loop Complementation on Graphs and Set Systems. *Eur.J.Comb.* (2011).

R. Brijder, H.J. Hoogeboom. Maximal Pivots on Graphs with an Application to Gene Assembly. *Discr.Appl.Math.* 158 (2010) 1977–1985.

R. Brijder, H.J. Hoogeboom. Reality–and–Desire in Ciliates.
In: *Algorithmic Bioprocesses* (Condon et al, eds.), Natural Computing Series, Springer (2009) pp.99–115.

R. Brijder, T. Harju, H.J. Hoogeboom, Pivots, determinants, and perfect matchings of graphs (2008)
submitted for publication – *really a long time ago now* [arXiv:0811.3500]

A. Ehrenfeucht, T. Harju, I. Petre, D. Prescott, G. Rozenberg, *Computation in Living Cells: Gene Assembly in Ciliates*, Natural Computing Series, Springer (2004)

(this one you know, of course)

