

Colloquium · USF · Tampa

Jan'16

Graph Polynomials motivated by Gene Assembly

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with Robert Brjder, Hasselt B

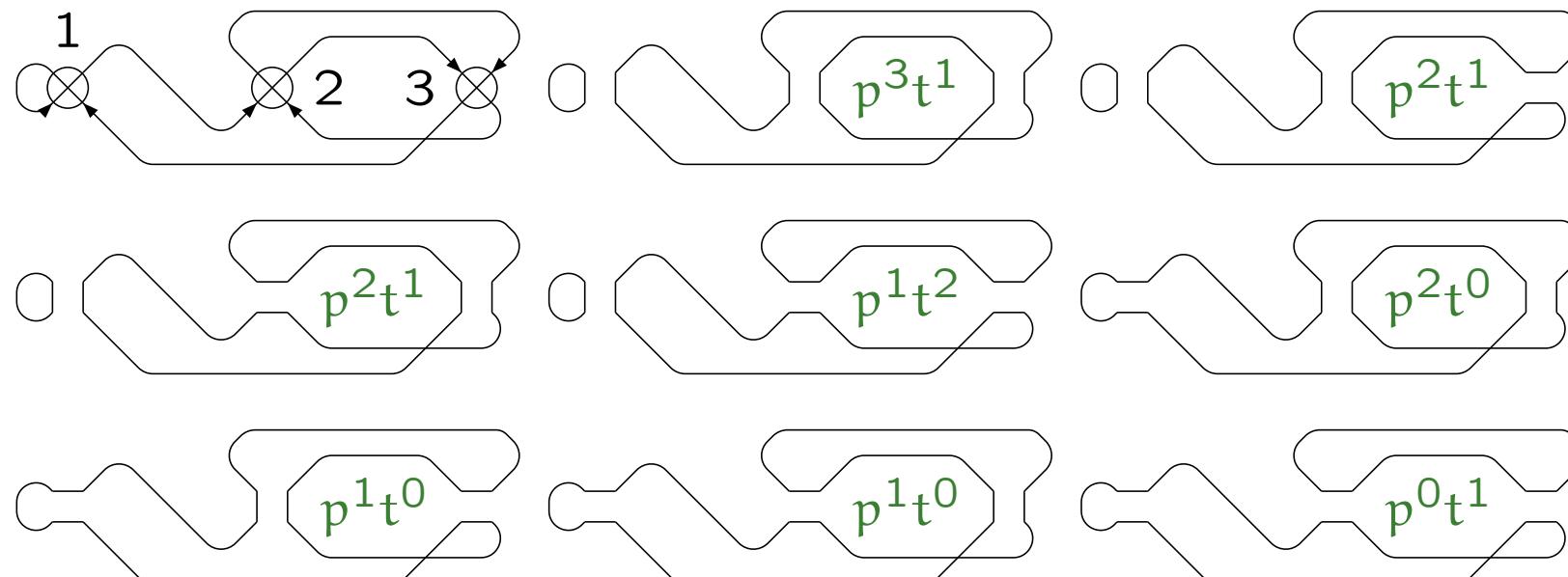
assembly polynomial of G_w for doc-word w

$$S(G_w)(p, t) = \sum_s p^{\pi(s)} t^{c(s)-1},$$

\otimes follow / \circlearrowleft consistent π / \circlearrowright inconsistent
 never p

$w = 1 1 2 3 2 3$

$$p^3t + 2p^2t + p^2 + pt^2 + 2p + t$$



Burns, Dolzhenko, Jonoska, Muche, Saito:
 Four-regular graphs with rigid vertices associated to DNA recombination (2013)

motivation: models for gene recombination

- ▶ ciliates:
4-regular graphs + Euler tours
- ▶ graph polynomials

concept: interlacing $p\ q\ p\ q$

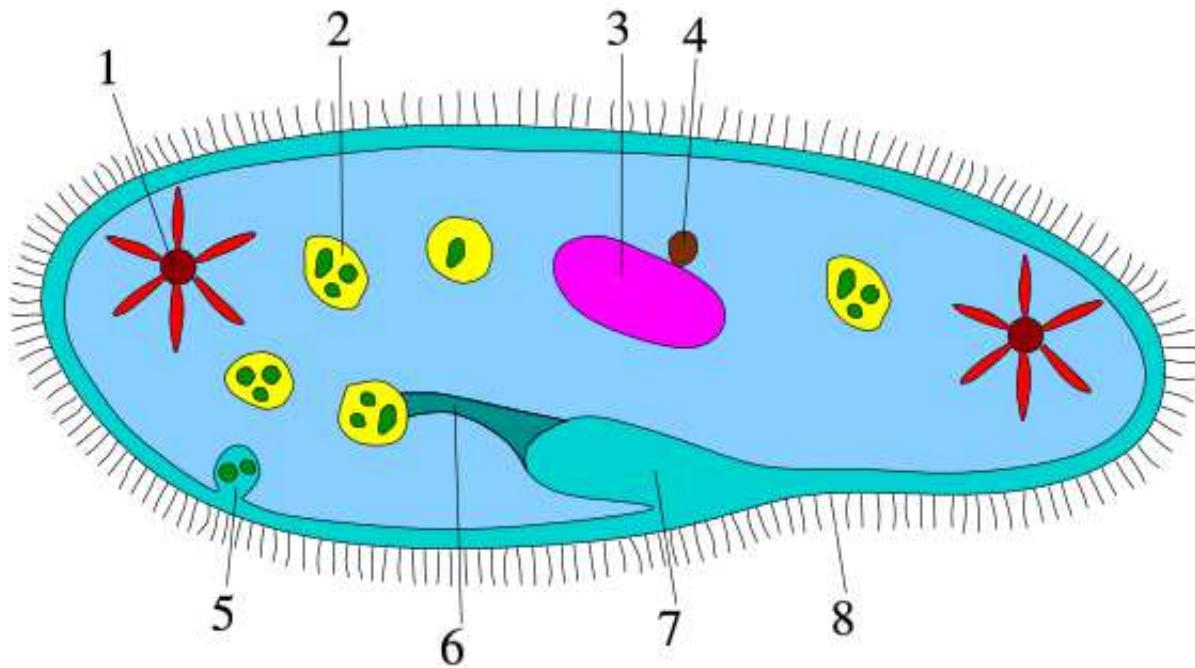
- ▶ four worlds, getting more abstract
 - strings – rewriting
 - graphs – combinatorics
 - matrices – linear algebra
 - (set systems) – symm diff ‘XOR’

‘same’ operation (**pivot**), different tools

Ciliates

cell structure:

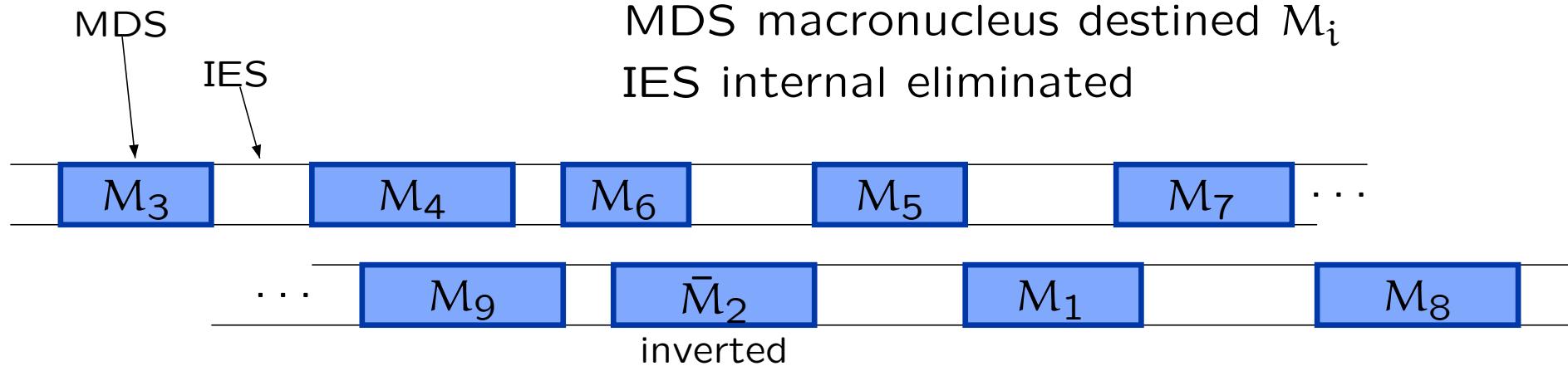
- 3. macronucleus
- 4. micronucleus
- 8. cilium



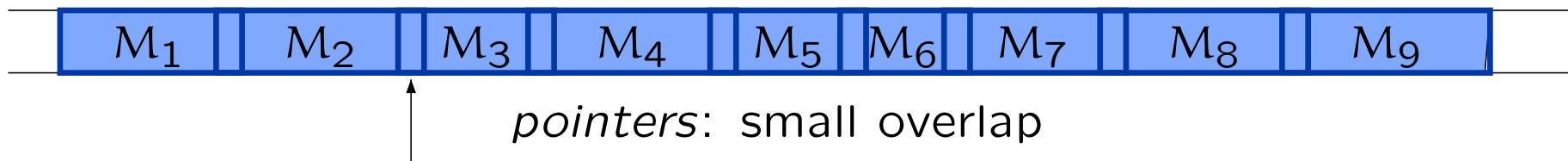
Unlike most other eukaryotes, ciliates have two different sorts of nuclei: a small, diploid *micronucleus* (reproduction), and a large, polyploid *macronucleus* (general cell regulation). The latter is generated from the micronucleus by amplification of the genome and *heavy editing*.

Ciliates: two types of nucleus
gene assembly: splicing and recombination

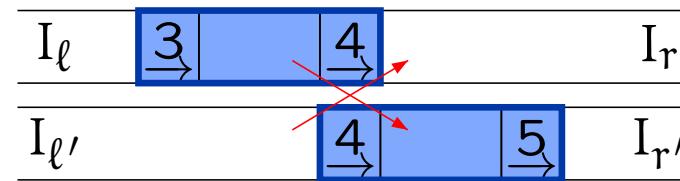
MIC *micronucleus*

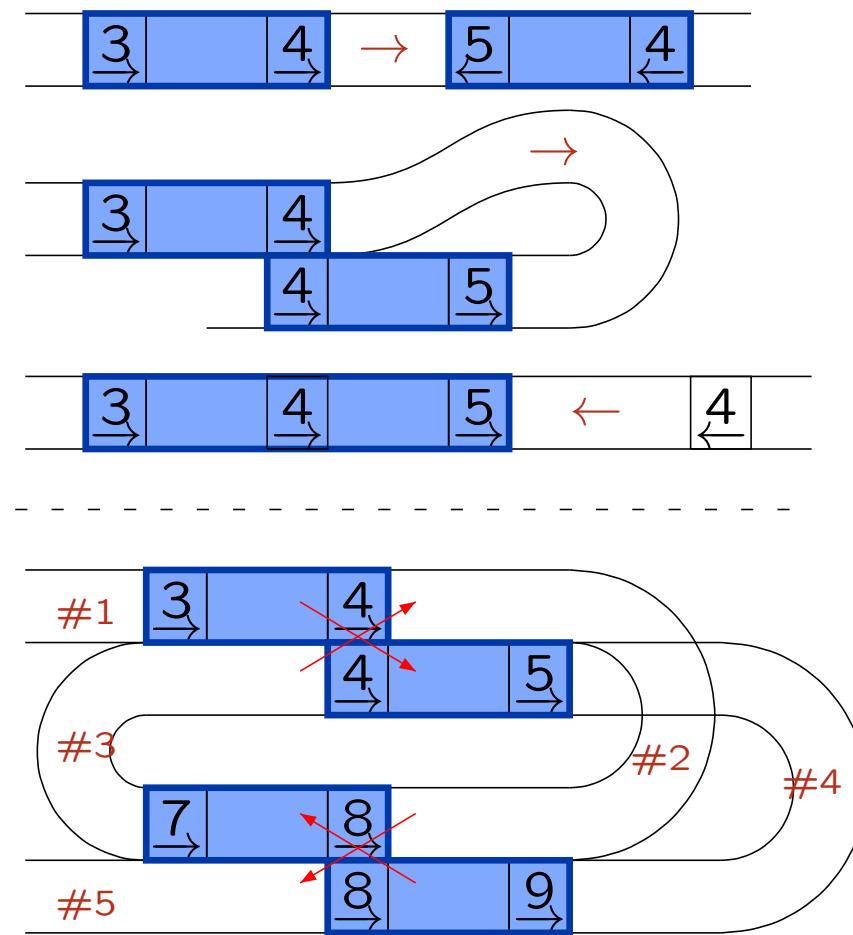
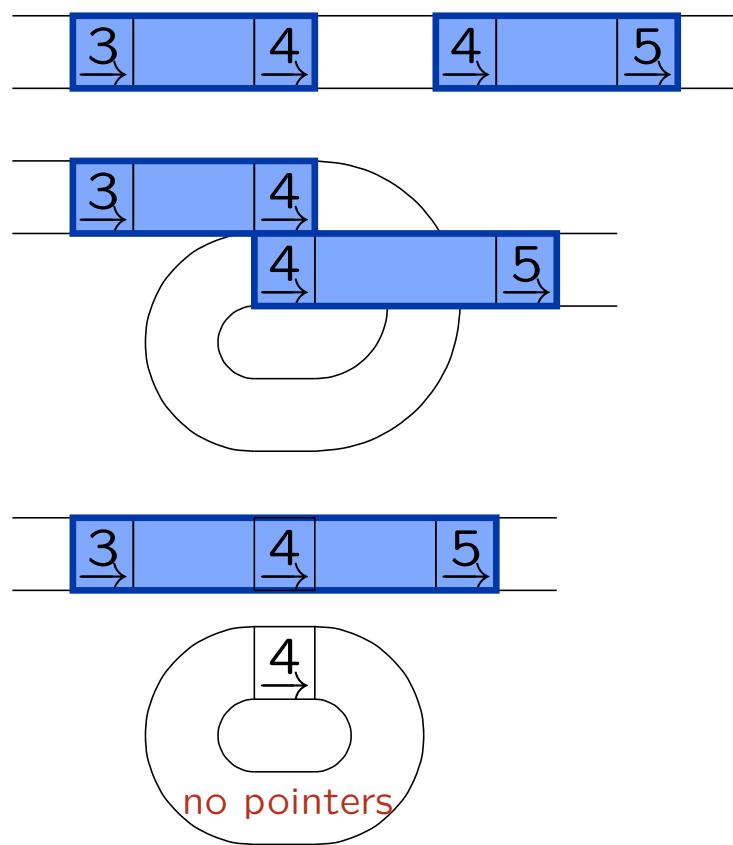


MAC *macronucleus*



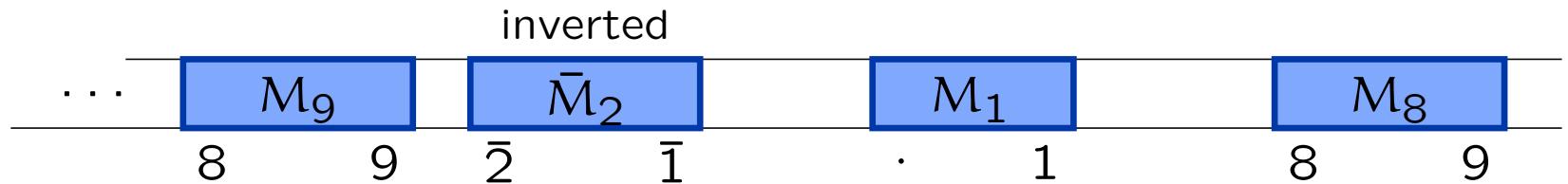
merge consecutive MDS's
align pointers & swap





Ehrenfeucht, Harju, Petre, Prescott, Rozenberg:
Computation in Living Cells – Gene Assembly in Ciliates (2004)

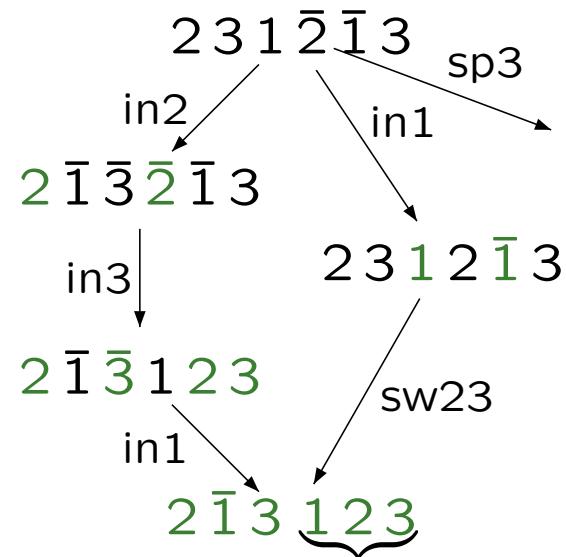
goal: sorting [deleting] pointers



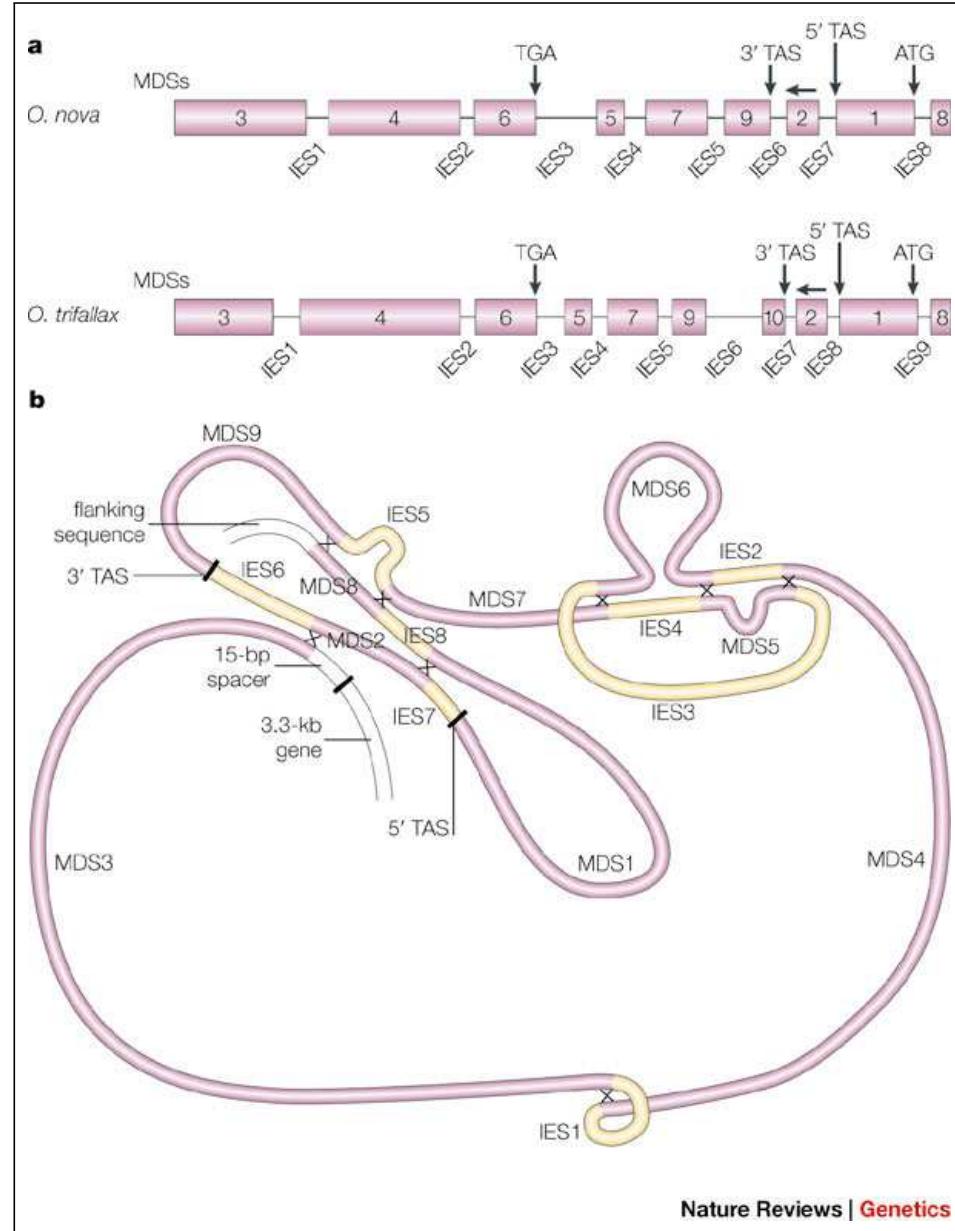
split $u_1 \textcolor{blue}{p} \textcolor{blue}{p} u_2 \xrightarrow{p} u_1 \textcolor{green}{p} \textcolor{green}{p} u_2$

invert $u_1 \textcolor{blue}{p} u_2 \bar{p} u_3 \xrightarrow{p} u_1 \textcolor{green}{p} \bar{u}_2 \bar{p} u_3$

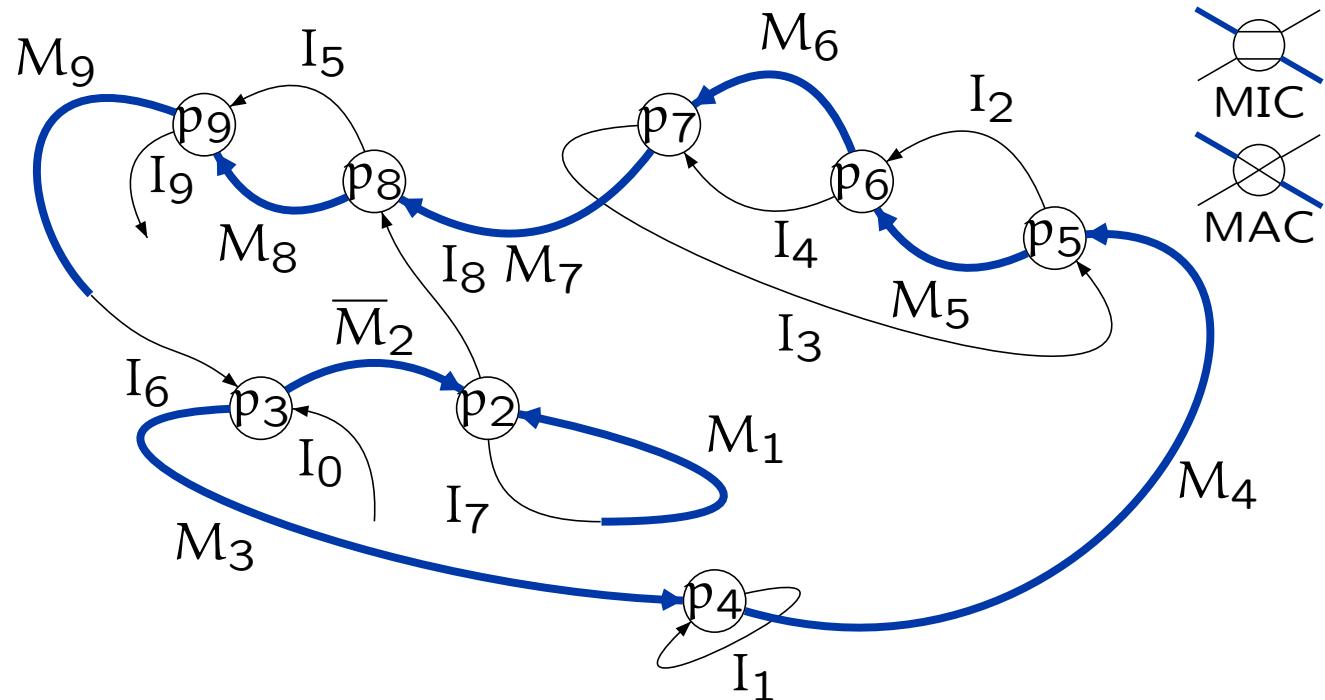
swap $u_1 \textcolor{blue}{p} u_2 \textcolor{blue}{q} u_3 \textcolor{blue}{p} u_4 \textcolor{blue}{q} u_5 \xrightarrow{p,q} u_1 \textcolor{green}{p} u_4 \textcolor{green}{q} u_3 \textcolor{green}{p} u_2 \textcolor{green}{q} u_5$



▷ result depends on operations?



David M. Prescott. Genome gymnastics: unique modes of dna evolution and processing in ciliates. Nature Reviews Genetics (December 2000)



MIC $I_0 M_3 I_1 M_4 I_2 M_6 I_3 M_5 I_4 M_7 I_5 M_9$
 $I_6 \bar{M}_2 I_7 M_1 I_8 M_8 I_9$

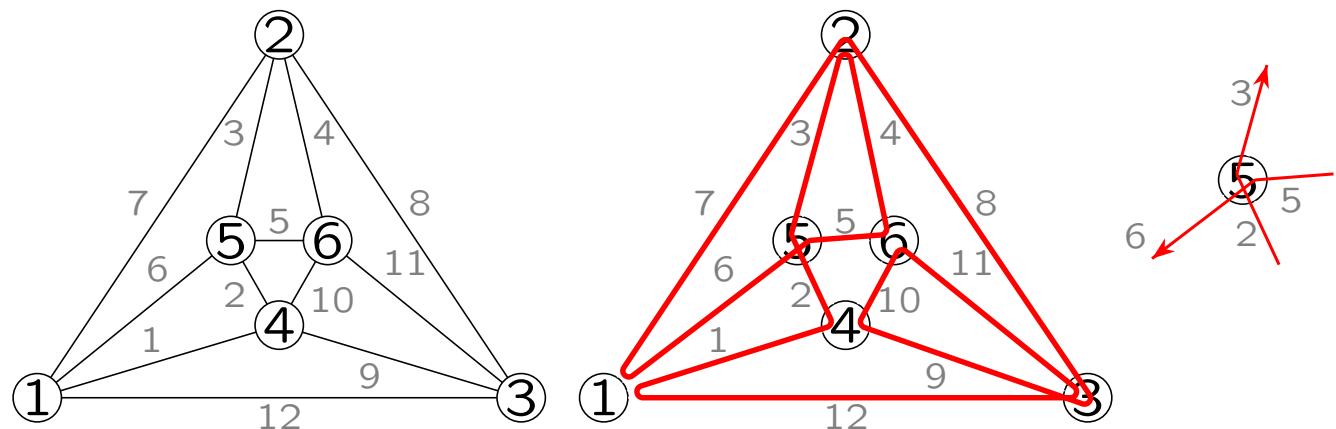
MAC $\bar{I}_9 \bar{I}_5 \bar{I}_8 I_7 \underbrace{M_1 M_2 \cdots M_8 M_9}_{I_6 \bar{I}_0, I_1 \text{ and } I_2 I_4 I_3}$

4-regular graph with Euler circuit

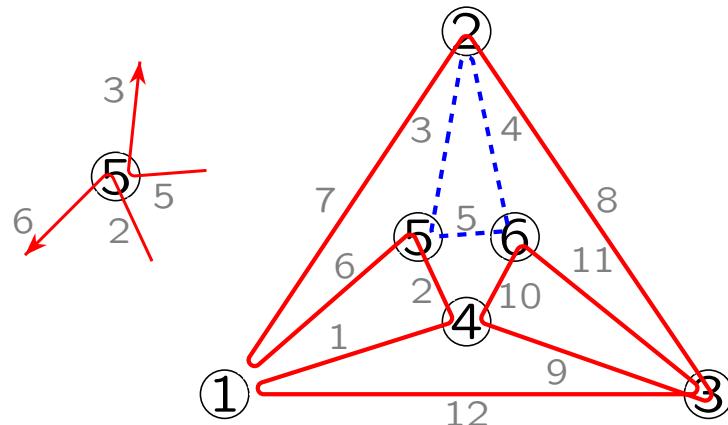
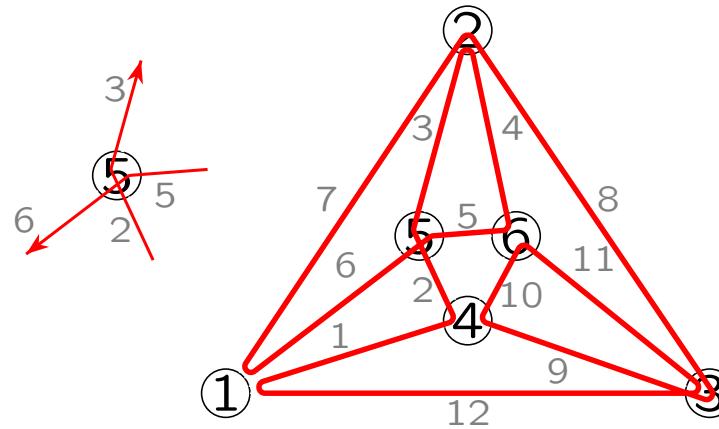
double occurrence string w defines

4-regular graph G_w + Euler circuit C_w
or 2-in 2-out graph + directed circuit

$$w = 1\ 4\ 5\ 2\ 6\ 5\ 1\ 2\ 3\ 4\ 6\ 3$$

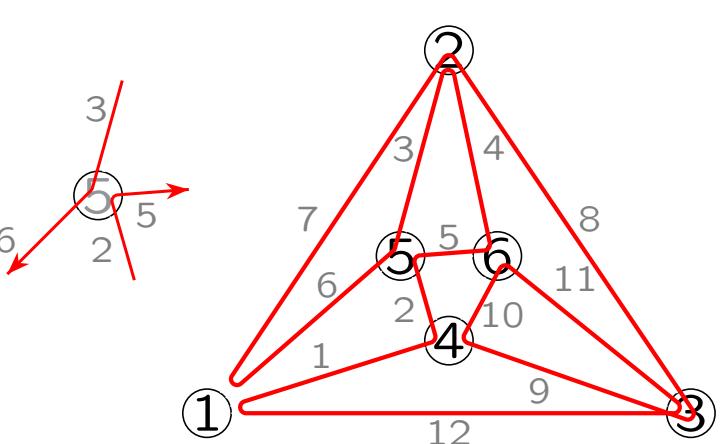


$w = 1 \ 4 \ \textcolor{red}{5} \ 2 \ 6 \ \textcolor{red}{5} \ 1 \ 2 \ 3 \ 4 \ 6 \ 3$



segment **split**

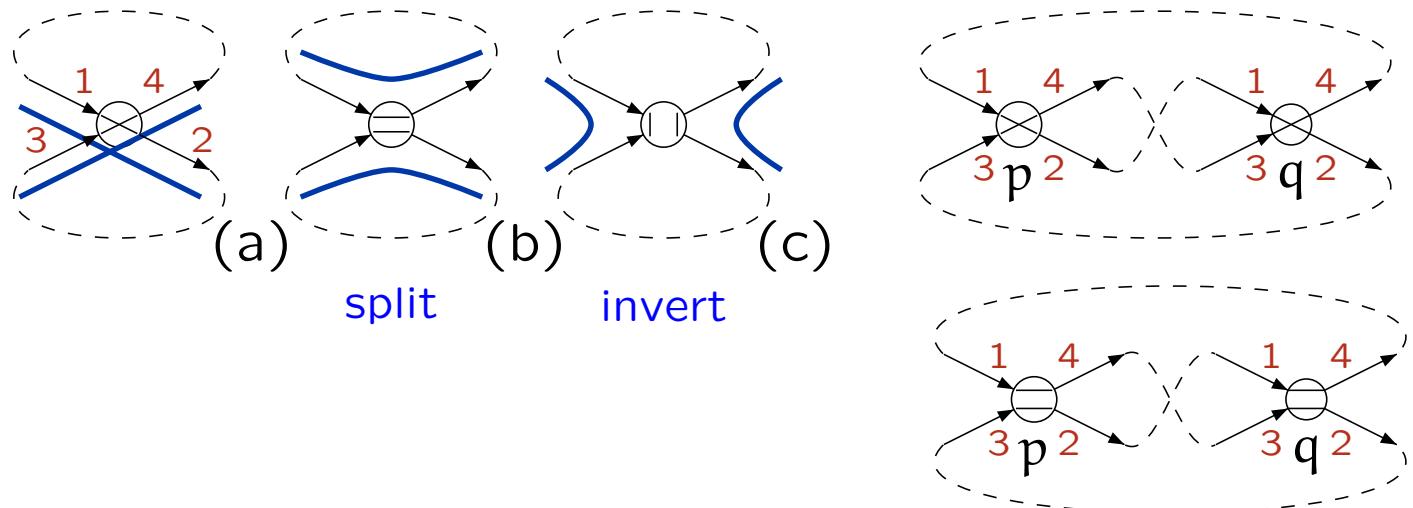
$1 \ 4 \ \textcolor{red}{5} \ 1 \ 2 \ 3 \ 4 \ 6 \ 3 \quad \& \quad \textcolor{blue}{5} \ 2 \ 6$



segment **inverted**

$1 \ 4 \ \textcolor{red}{5} \ \underline{6} \ 2 \ \underline{5} \ 1 \ 2 \ 3 \ 4 \ 6 \ 3$

- (a) follows C
- (b) orientation consistent
- (c) orientation inconsistent



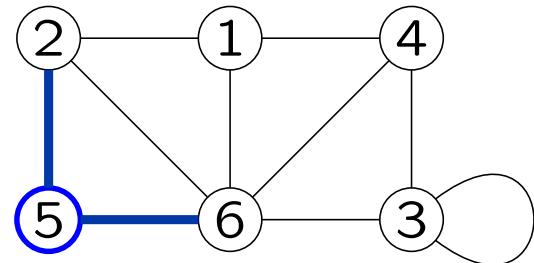
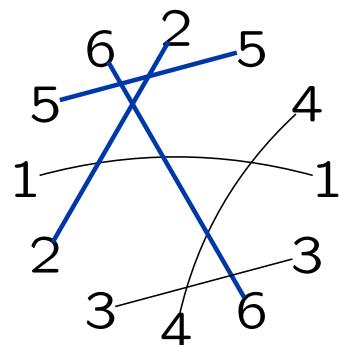
Kotzig. Eulerian lines in finite 4-valent graphs (1966)

rearrangements should not break genome

... $\underbrace{p \dots q}$... $\underbrace{p \dots q}$...

interlace graph $I(C_w)$

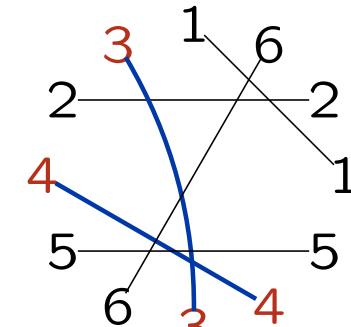
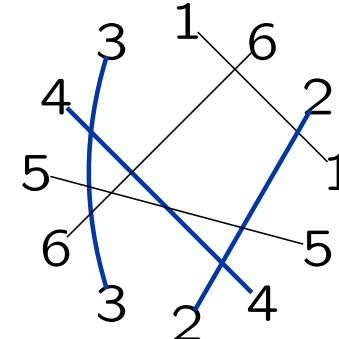
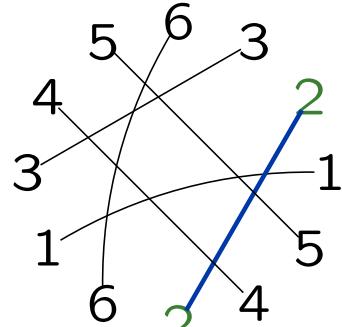
$$w = 1 \ 4 \ \underline{\textcolor{blue}{5} \ 2 \ 6 \ \textcolor{blue}{5}} \ 1 \ 2 \ \bar{3} \ 4 \ 6 \ 3$$



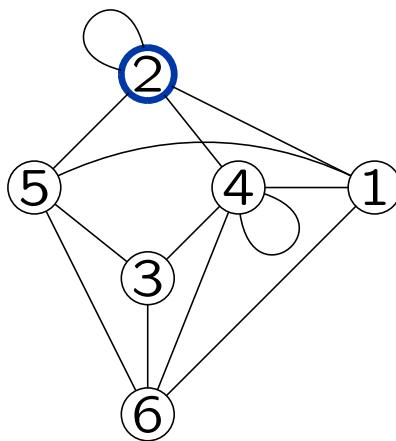
circle graph

(bar + loop for orientation)

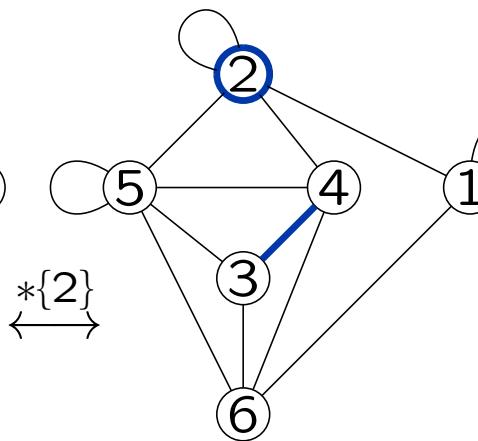
circular
string



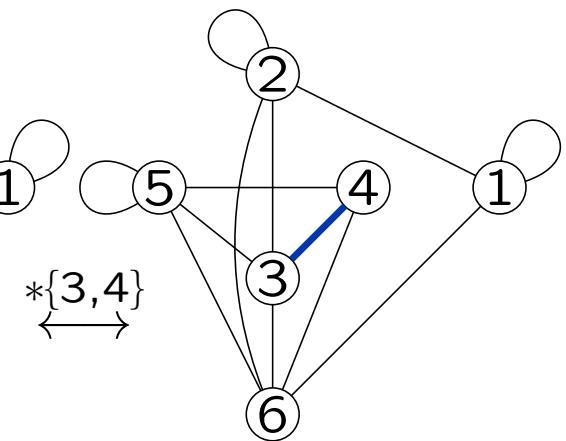
interlace



$\ast\{2\}$



$\ast\{3,4\}$



doc string

$w * \{2\}$

1 2 3 6 5 4 3 1 6 2 4 5

invert

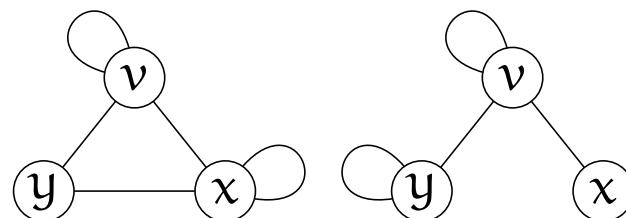
$w = 1 \text{ } 2 \text{ } 6 \bar{1} \text{ } 3 \text{ } 4 \bar{5} \text{ } 6 \text{ } 3 \bar{2} \text{ } 4 \text{ } 5$

$w * \{3, 4\}$
1 2 6 1 3 2 4 5 6 3 4 5

swap

$$\begin{array}{ccc}
 \text{4-regular graph} & & \text{(circle graph)} \\
 + \text{ Euler cycle} & & \text{interlace graph} \\
 C & \longrightarrow & I(C) \\
 \text{invert } \downarrow & & \downarrow \text{local complement} \\
 C * v & \longrightarrow & I(C) * v
 \end{array}$$

$\dots \bar{x} \dots v \xrightarrow{\dots y \dots x \dots} \bar{v} \dots y$ interleaved
 $\dots \bar{x} \dots v \xleftarrow{\dots \bar{x} \dots \bar{y} \dots v \dots y}$ not interleaved

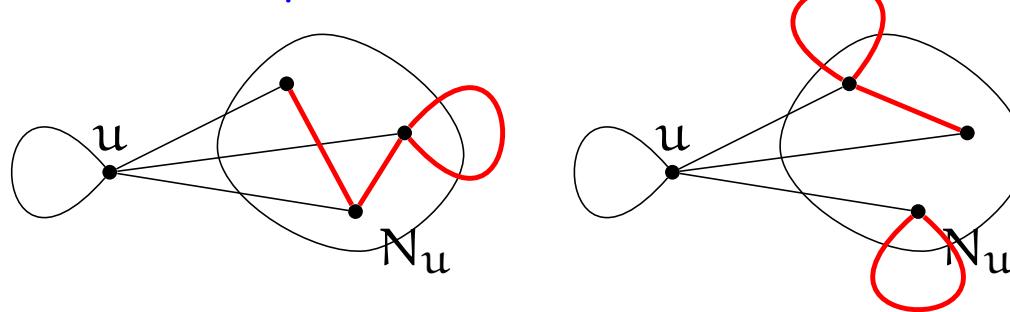


$G \mapsto G * u$

looped vertex u

$$N_u = N_G(u) \setminus \{u\}$$

local complementation



$G \mapsto G * \{u, v\}$

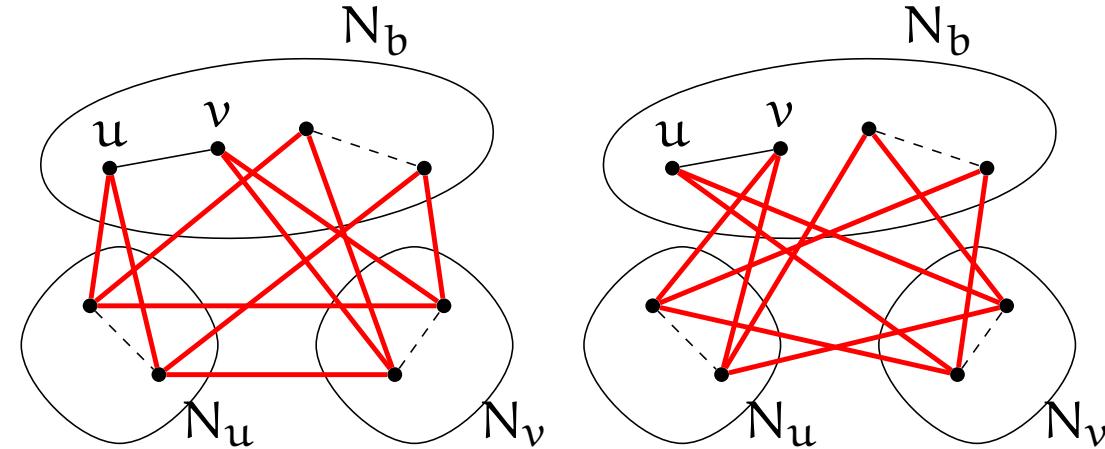
unlooped edge $\{u, v\}$

$$N_u = N_G(u) \setminus N_G(v)$$

$$N_v = N_G(v) \setminus N_G(u)$$

$$N_b = N_G(u) \cap N_G(v)$$

edge complementation



invert $I(C * u) = I(C) * v$

swap $I(C * \{u, v\}) = I(C) * \{u, v\}$

when defined

how do these operations interact?

dependent on (order) operations chosen?

what are the intermediate products?

$$\begin{array}{c}
 \text{Graph: } \\
 \begin{array}{c} \text{2} \\ \text{5} \quad \text{4} \quad \text{1} \\ \text{3} \quad \text{6} \end{array}
 \end{array}
 \leftrightarrow
 \left(\begin{array}{cccccc}
 1 & 1 & 0 & 0 & 0 & 1 \\
 1 & 1 & 0 & 1 & 1 & 0 \\
 0 & 0 & 0 & 1 & 1 & 1 \\
 0 & 1 & 1 & 0 & 1 & 1 \\
 0 & 1 & 1 & 1 & 1 & 1 \\
 1 & 0 & 1 & 1 & 1 & 0
 \end{array} \right)$$

$\downarrow *\{2\}$ $\downarrow ?? \text{ PPT}$

$$\begin{array}{c}
 \text{Graph: } \\
 \begin{array}{c} \text{2} \\ \text{5} \quad \text{4} \quad \text{1} \\ \text{3} \quad \text{6} \end{array}
 \end{array}
 \leftrightarrow
 \left(\begin{array}{cccccc}
 0 & 1 & 0 & 1 & 1 & 1 \\
 1 & 1 & 0 & 1 & 1 & 0 \\
 0 & 0 & 0 & 1 & 1 & 1 \\
 1 & 1 & 1 & 1 & 0 & 1 \\
 1 & 1 & 1 & 0 & 0 & 1 \\
 1 & 0 & 1 & 1 & 1 & 0
 \end{array} \right)$$

$$A = \begin{pmatrix} X & V \setminus X \\ P & Q \\ R & S \end{pmatrix}$$

$$A * X = \begin{pmatrix} X & V \setminus X \\ P^{-1} & -P^{-1}Q \\ RP^{-1} & S - RP^{-1}Q \end{pmatrix}$$

partial inverse

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

PPT matches edge & local complement

$$P = \begin{pmatrix} p \\ 1 \end{pmatrix}, \quad P = \begin{pmatrix} p & q \\ 0 & 1 \\ q & 0 \end{pmatrix}$$

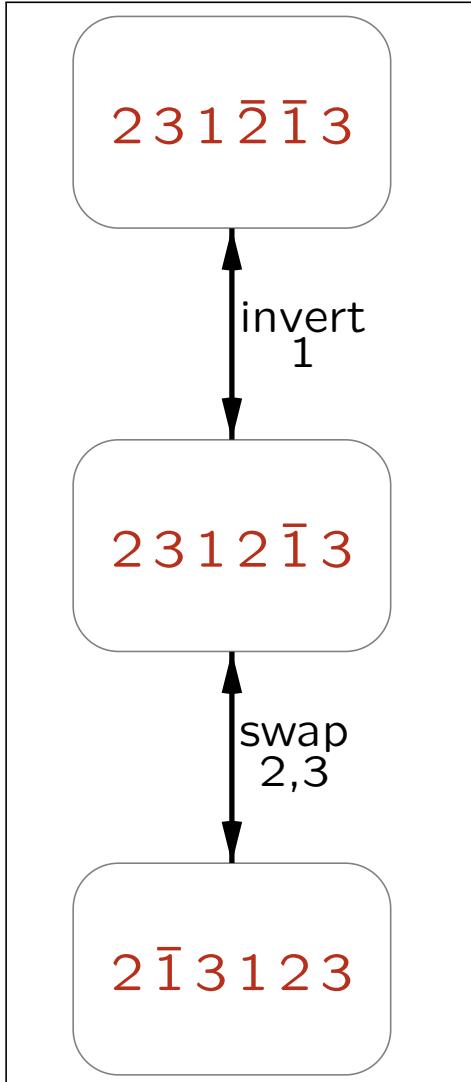
(partial inverse) $A \begin{pmatrix} x_1 \\ y_1 \end{pmatrix} = \begin{pmatrix} x_2 \\ y_2 \end{pmatrix}$ iff $A * X \begin{pmatrix} x_2 \\ y_1 \end{pmatrix} = \begin{pmatrix} x_1 \\ y_2 \end{pmatrix}$

Thm. $(A * X) * Y = A * (X \Delta Y)$ when defined
symmetric difference

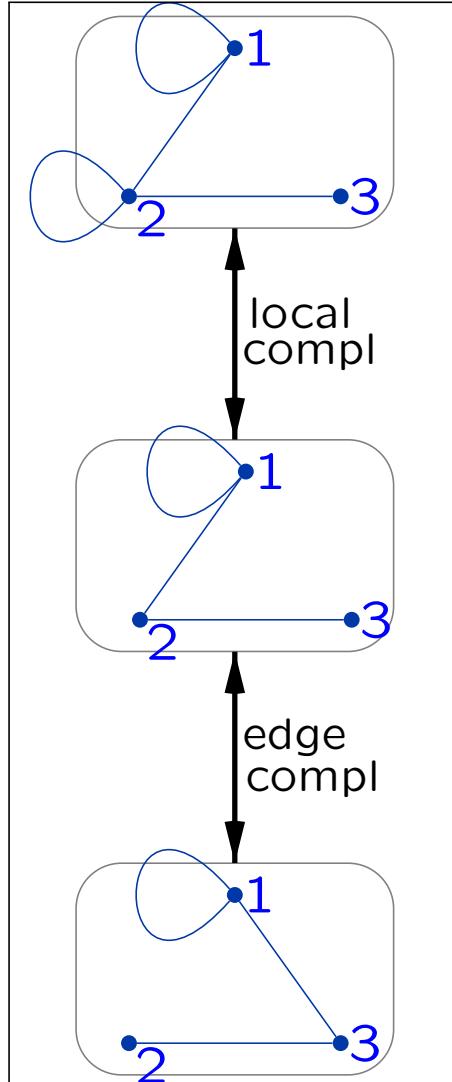
any sequence involving all pointers:
 $A * \{p_1, p_2\} \cdots * \{p_n\} = A * V = A^{-1}$

Cor. does not depend on order of operations (!)

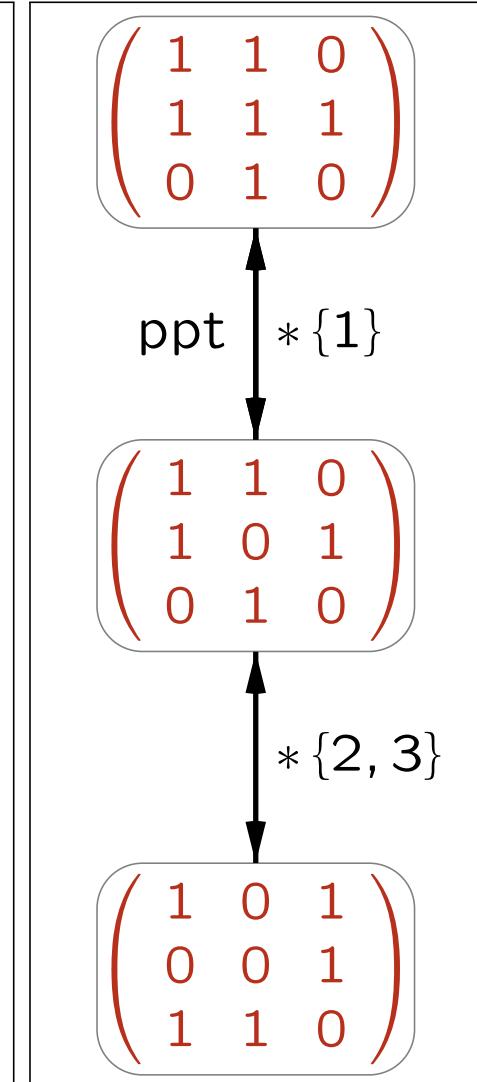
doc strings



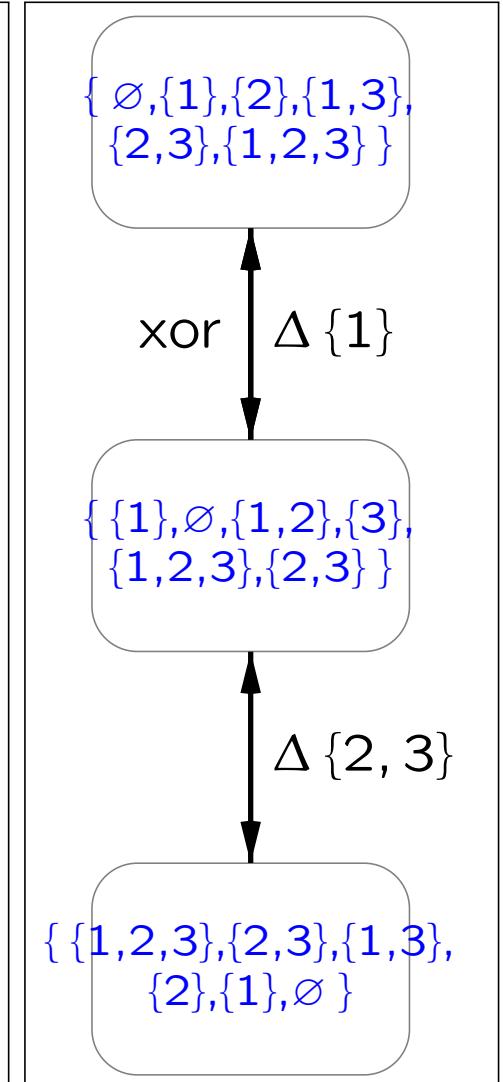
circle graphs



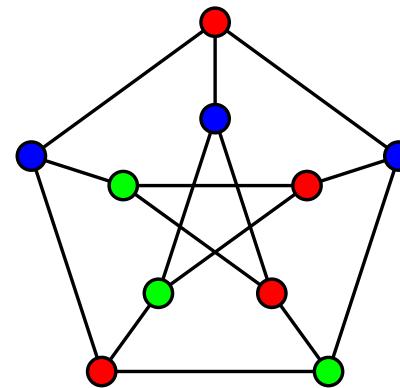
binary matrices



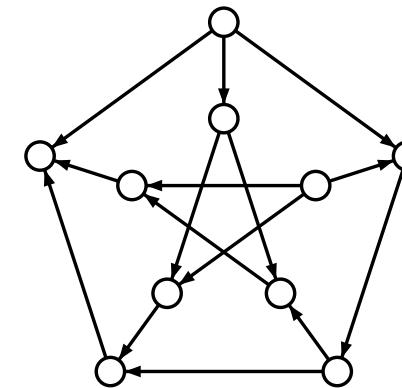
set systems



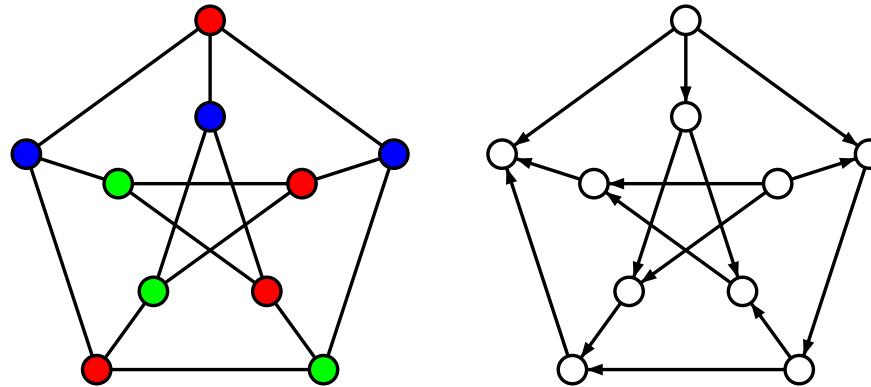
Graph Polynomials



3 colours



16680 acyclic orientations



chromatic polynomial

$$\begin{aligned} \chi_G(t) = t(t-1)(t-2) \cdot & (t^7 - 12t^6 + 67t^5 \\ & \dots - 230t^4 + 529t^3 - 814t^2 + 775t - 352) \end{aligned}$$

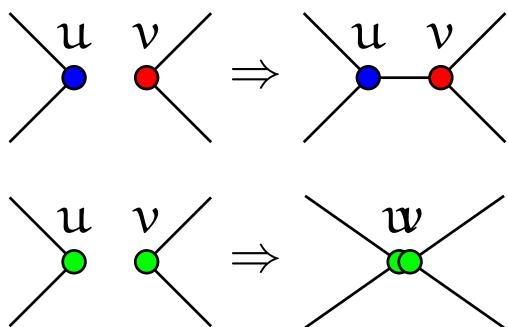
$$\chi_G(t) = \chi_{G+uv}(t) + \chi_{G/uv}(t)$$

$$\chi_G(t) = \chi_{G-e}(t) - \chi_{G/e}(t)$$

deletion & contraction

acyclic orientations

$$16680 = (-1)^{|V_G|} \chi_G(-1)$$



definitions

recursive / closed form

combinatorial / algebraic

evaluations

combinatorial interpretation

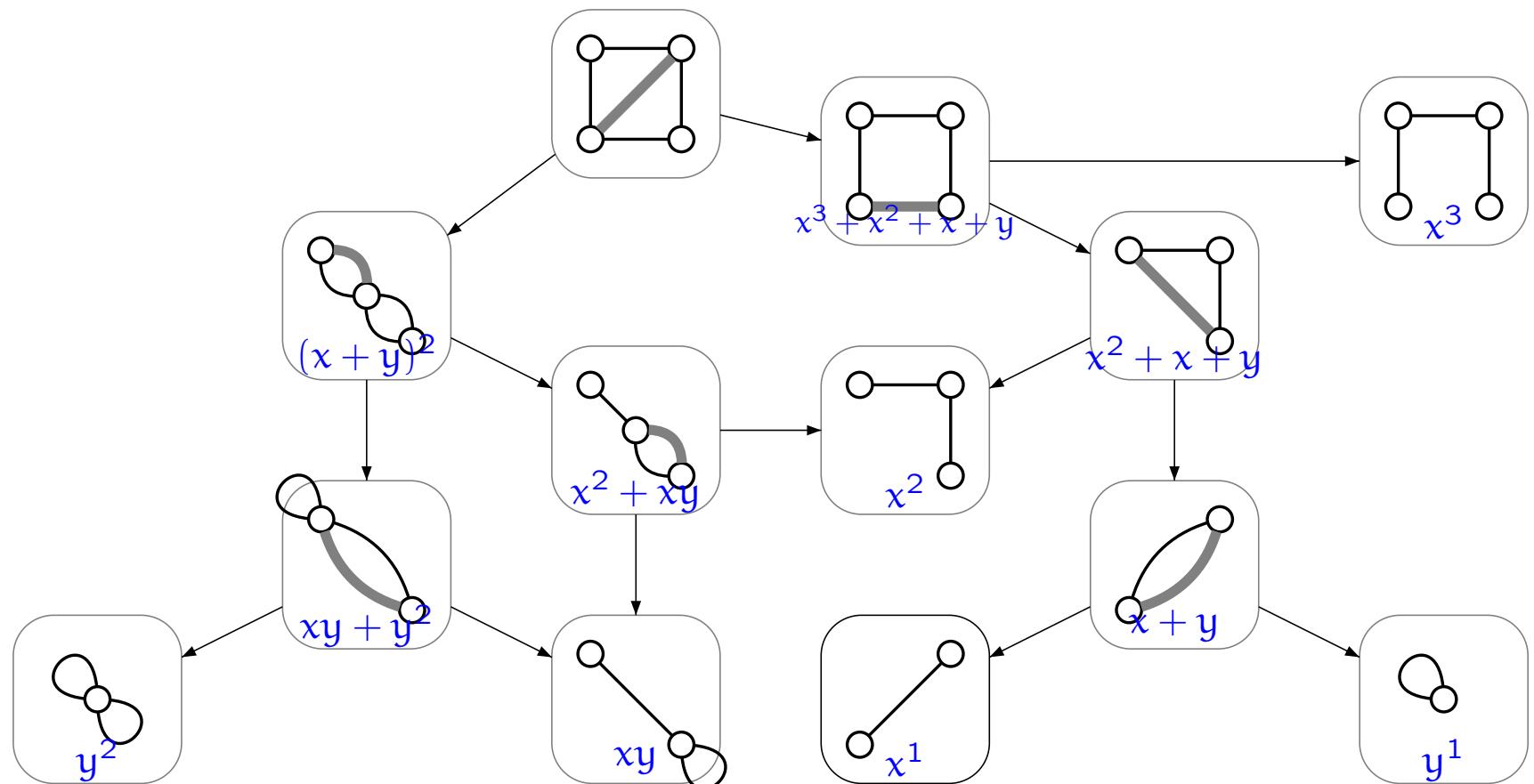
polynomials

- Tutte (*one to rule them all...*)
- Martin (on 2-in 2-out graphs)
- assembly (Ciliates) 'transition pol'
- interlace (DNA reconstruction)

and their **relations!**

loops and parallel edges
diamond graph:

$$T_D = x^3 + 2x^2 + 2xy + x + y^2 + y$$



$$G = (V, E), \quad G[A] = (V, A)$$

$k(A)$ connected components in $G[A]$

$$T_G(x, y) = \sum_{A \subseteq E} (x - 1)^{k(A) - k(E)} (y - 1)^{k(A) + |A| - |V|}$$

rank nullity ‘circuit rank’

deletion & contraction

$$T_G(x, y) = \begin{cases} 1 & \text{no edges} \\ x T_{G/e}(x, y) & \text{bridge } e \\ y T_{G-e}(x, y) & \text{loop } e \\ T_{G-e}(x, y) + T_{G/e}(x, y) & \text{other} \end{cases}$$

$$T_G(x, y) = x^i y^j \quad \text{with } i \text{ bridges and } j \text{ loops}$$

extended to matroids

recipe theorem:

deletion-contraction implies Tutte evaluation
(Tutte-Grothendieck invariant)

$$\chi_G(t) = (-1)^{|V|-c(G)} t^{c(G)} T_G(1-t, 0)$$

$$T_D = x^3 + 2x^2 + 2xy + x + y^2 + y$$

$$\chi_D(t) = t(t-1)(t-2)^2$$

(check Wolfram alpha)

evaluations:

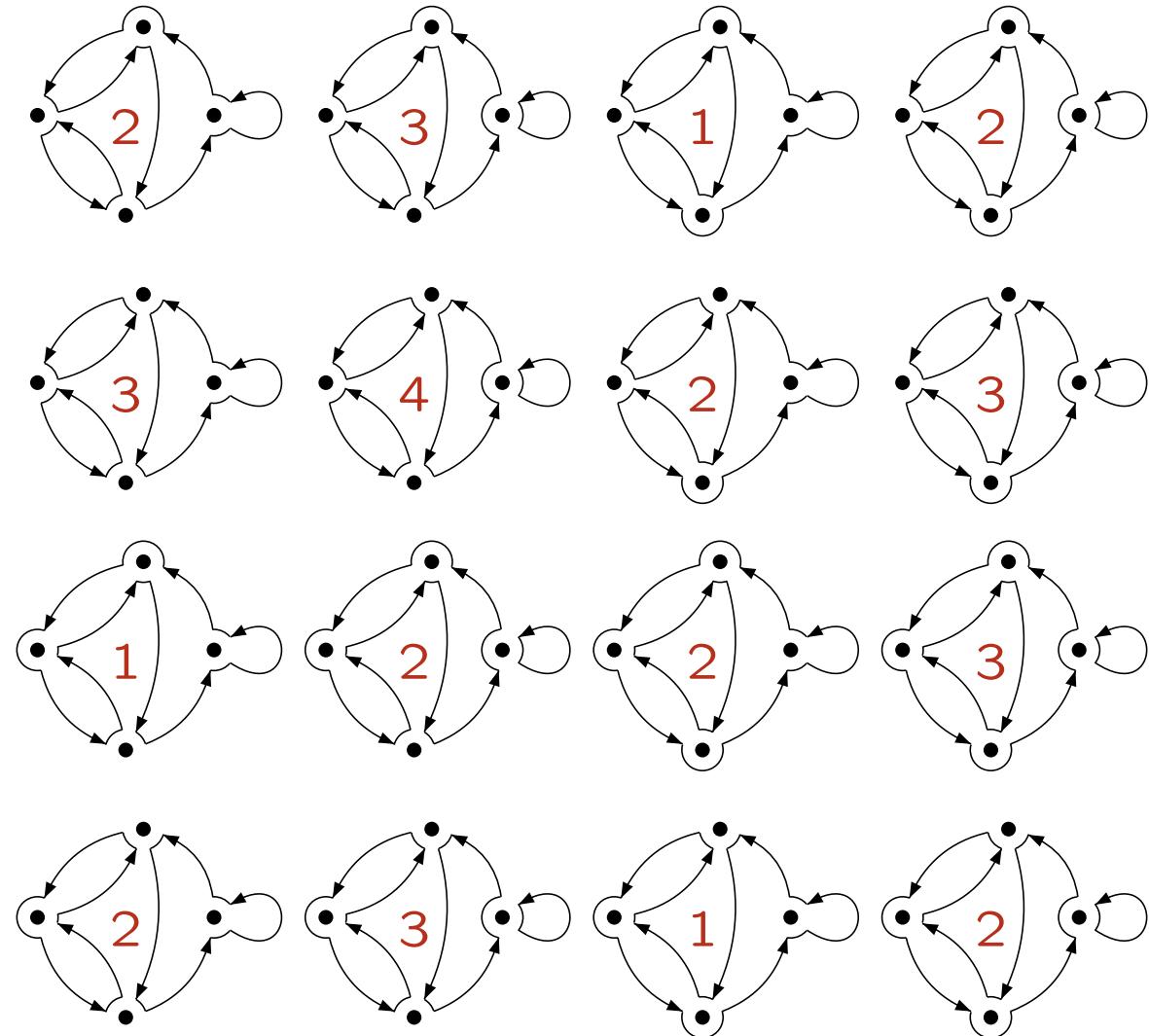
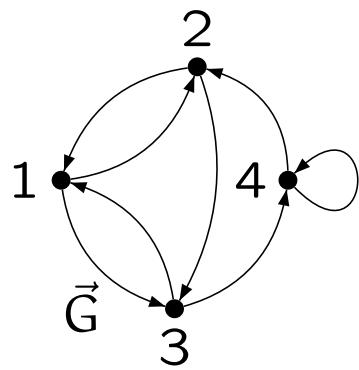
$$T_G(2, 0) \text{ acyclic orientations} = (-1)^{|V|} \chi_G(-1)$$

$$T_G(2, 1) \text{ forests}$$

$$T_G(1, 1) \text{ spanning forests}$$

$$T_G(1, 2) \text{ spanning subgraphs}$$

$$T_G(0, 2) \text{ strongly connected orientations}$$

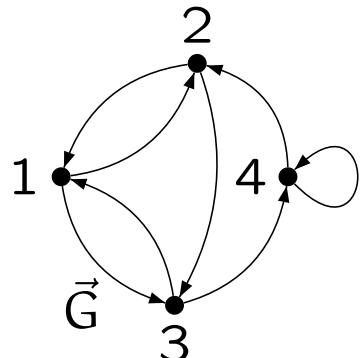


counting components: $3 \times 1, 7 \times 2, 5 \times 3, 1 \times 4$.

transition system $\mathcal{T}(\vec{G})$ (graph state)
 half-edge connections at vertices

Martin polynomial of 2-in 2-out digraph \vec{G}

$$m(\vec{G}; y) = \sum_{T \in \mathcal{T}(\vec{G})} (y - 1)^{k(T) - c(\vec{G})}$$

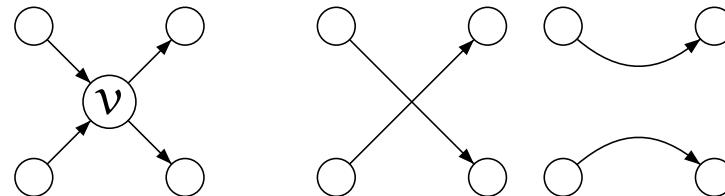


$c(\vec{G})$ components
 $k(T)$ circuits for transition system T

$k : 3 \times 1, 7 \times 2, 5 \times 3, 1 \times 4.$

$$3(y - 1)^0 + 7(y - 1)^1 + 5(y - 1)^2 + 1(y - 1)^3$$

Thm. (1) recursive form (2) Tutte connection
 (3) evaluations



graph reductions: glueing edges

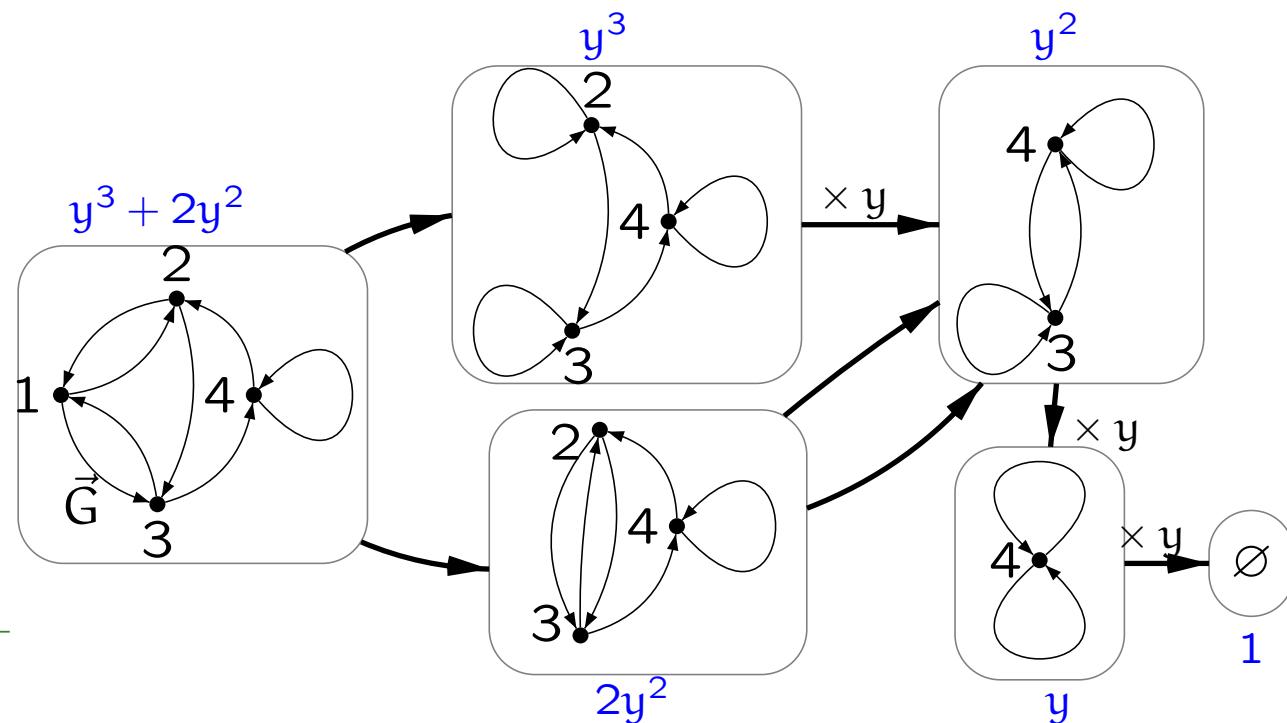
Def. $m(\vec{G}; y) = 1$ for $n = 0$

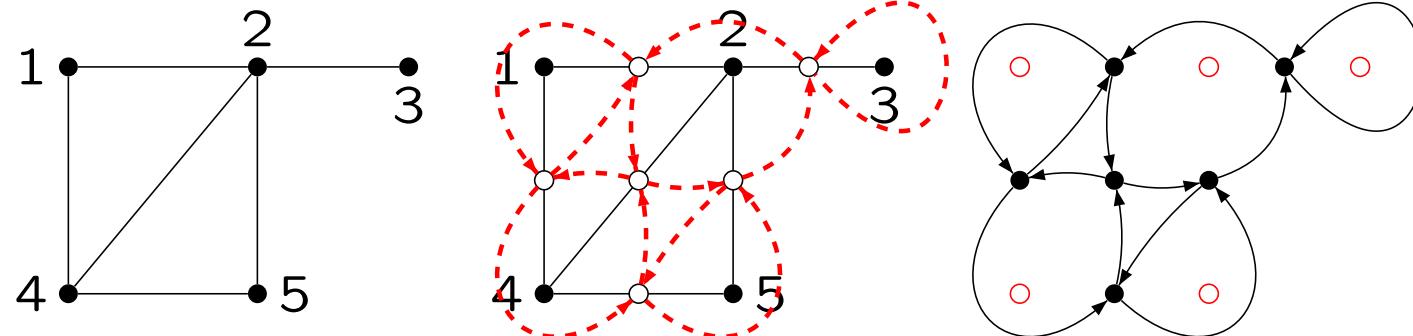
$m(\vec{G}; y) = y m(\vec{G}'; y)$

cut vertex

$m(G; y) = m(\vec{G}'_v; y) + m(\vec{G}''_v; y)$

without loops

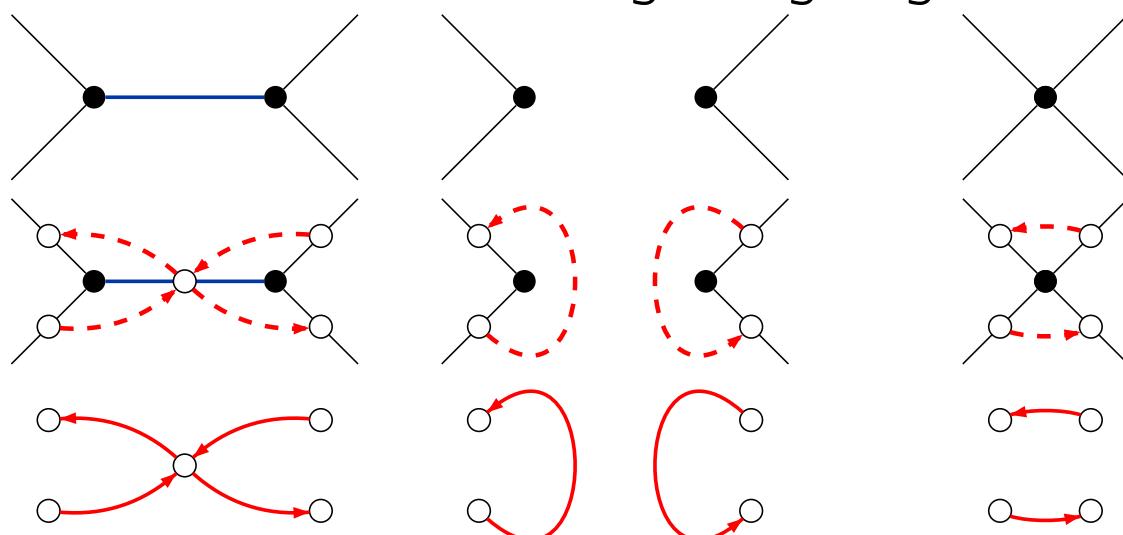




plane graph G , with medial graph \vec{G}_m

$$\textbf{Thm. } m(\vec{G}_m; y) = T(G; y, y)$$

proof: deletion-contraction \equiv glueing edges



$$m(\vec{G}; y) = \sum_{T \in \mathcal{T}(\vec{G})} (y - 1)^{k(T) - c(\vec{G})}$$

\vec{G} 2-in 2-out digraph and $n = |V(\vec{G})|$

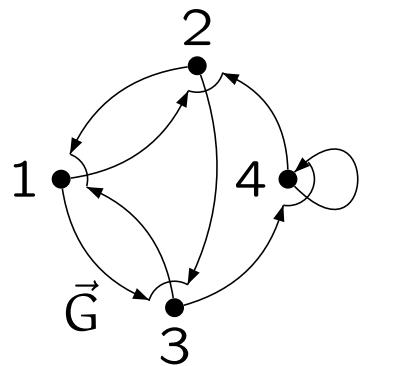
Thm. $m(\vec{G}; -1) = (-1)^n (-2)^{a(\vec{G}) - 1}$ ‘third connection’

$m(\vec{G}; 0) = 0$, when $n > 0$

$m(\vec{G}; 1)$ number of Eulerian systems

$m(\vec{G}; 2) = 2^n$

$m(\vec{G}; 3) = k |m(\vec{G}; -1)|$ for odd k



$a(\vec{G})$ anti circuits

$$m(\vec{G}; y) = y^3 + 2y^2$$

$$m(\vec{G}; -1) = 1$$

Rearrangement Polynomials

Assembly polynomial

Interlace polynomial

connected to Martin polynomial

interlace graph

local and edge complement

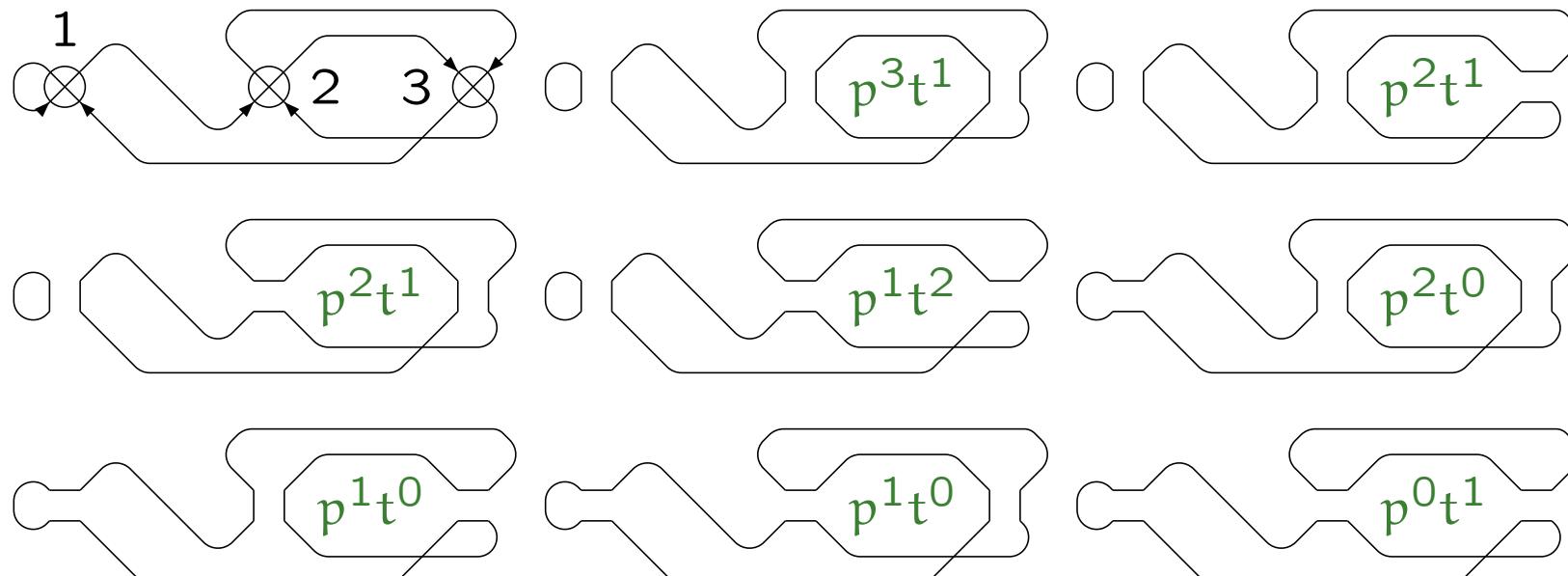
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 never p

$w = 1 1 2 3 2 3$

$$p^3t + 2p^2t + p^2 + pt^2 + 2p + t$$



Burns, Dolzhenko, Jonoska, Muche, Saito:
 Four-regular graphs with rigid vertices associated to DNA recombination (2013)

transition polynomials

$$W = (a, b, c)$$

transition T defines partition V_1, V_2, V_3

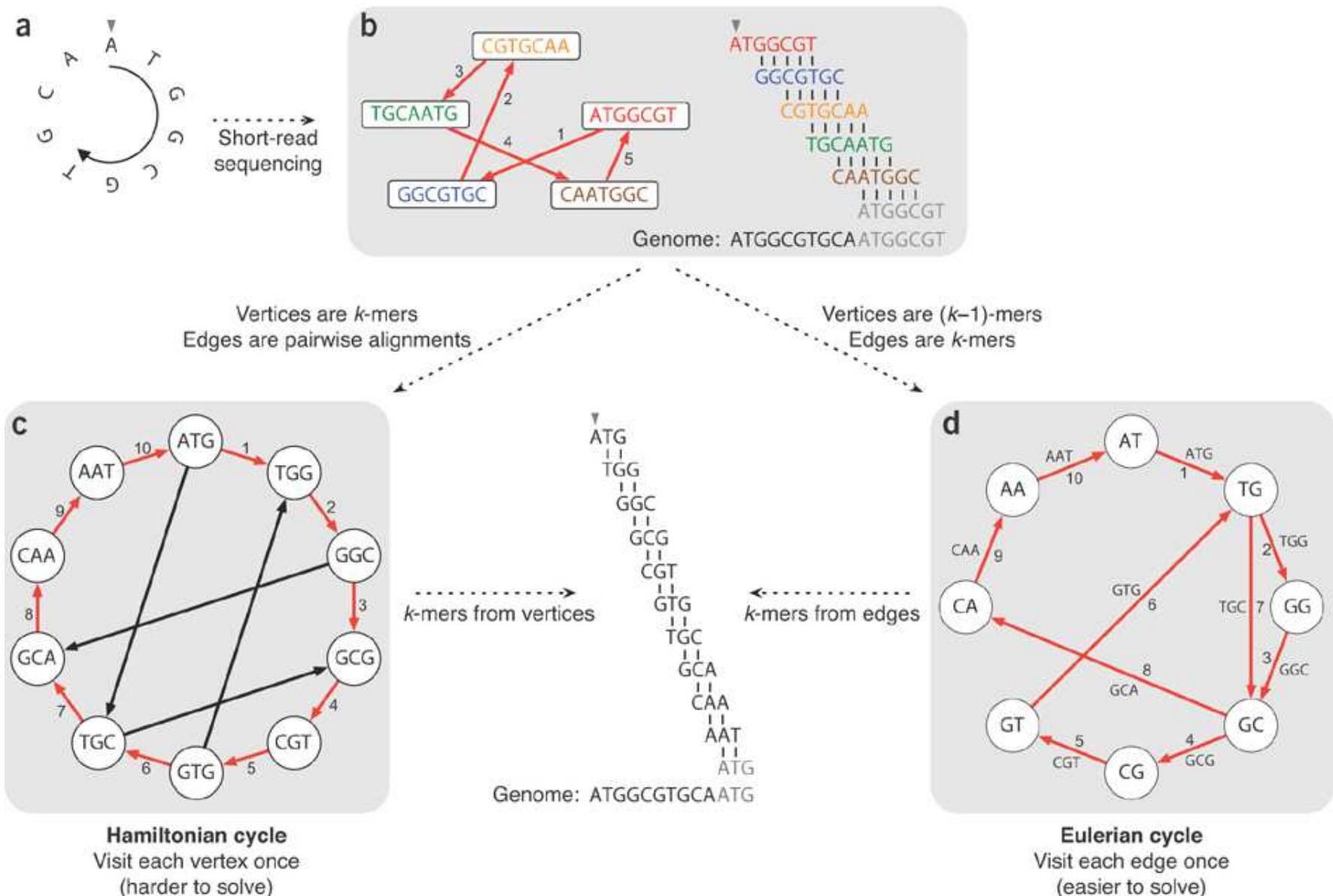
eg wrt fixed cycle

$$\text{weight } W(T) = a^{|V_1|} b^{|V_2|} c^{|V_3|}$$

$$M(G, W; y) = \sum_{T \in \mathcal{T}(\vec{G})} W(T) y^{k(T) - c(\vec{G})}$$

polynomial	a	b	c
Martin	1	1	0
(3-way)	1	1	1
assembly	0	p	1
Penrose	0	1	-1

$$\begin{aligned}
 \text{Diagram} &= \text{Diagram} = \text{Diagram} - \text{Diagram} - \text{Diagram} - \text{Diagram} + \text{Diagram} + \text{Diagram} + \text{Diagram} - \text{Diagram} \\
 &= 3^3 - 3^2 - 3^2 - 3^2 + 3 + 3 + 3 - 3
 \end{aligned}$$



How to apply de Bruijn graphs to genome assembly, Compeau, Pevzner & Tesler

de Bruijn Graphs for DNA Sequencing
originally recursive definition

simple graph G (with loops)

interlace polynomial

(single-variable, vertex-nullity)

$$q(G; y) = \sum_{X \subseteq V(G)} (y - 1)^{n(A(G)[X])}$$

as Tutte, but: vertices vs. edges,
algebraic vs. combinatorial

Arratia, Bollobás, Sorkin: The interlace polynomial: a new graph polynomial (2000)

Aigner, van der Holst: Interlace polynomials (2004)

Bouchet: TutteMartin polynomials and orienting vectors of isotropic systems (1991)

Def. $q(G; y) = 1$ if $n = 0$

$q(G; y) = y q(G \setminus v; y)$ v isolated (unlooped)

$q(G; y) = q(G \setminus v; y) + q((G * v) \setminus v; y)$

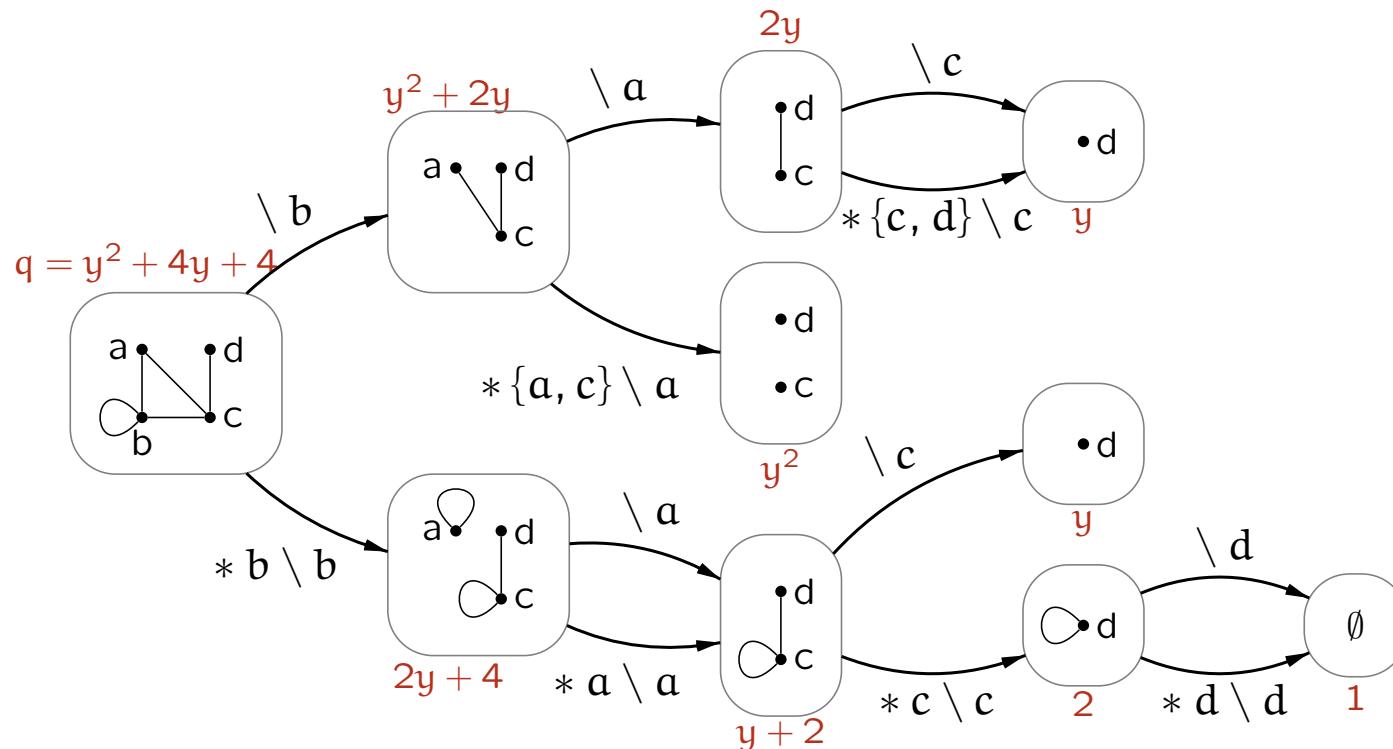
local &

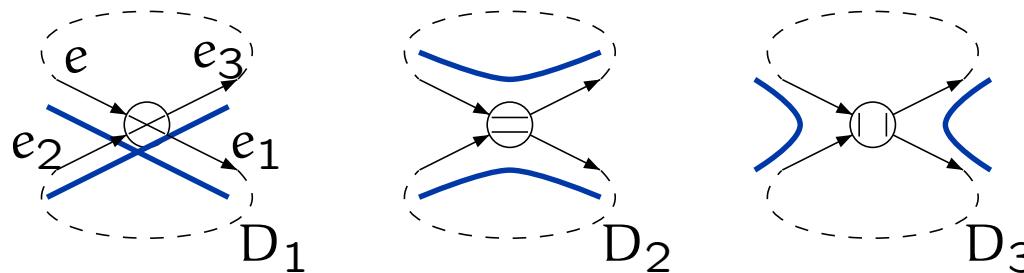
v looped

edge complement

$q(G; y) = q(G \setminus v; y) + q((G * e) \setminus v; y)$

$e = \{v, w\}$ unlooped edge





4-regular graph G with Eulerian system C

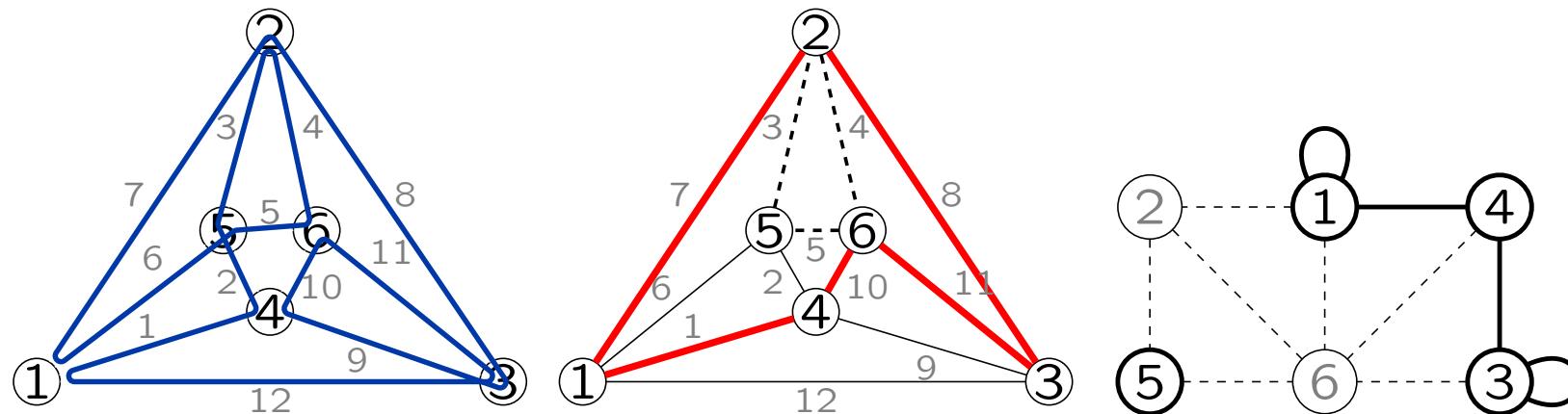
k circuit partition of $E(G)$, partition vertices:

D_1 follows C

D_2 orientation consistent

D_3 orientation inconsistent

Thm. Then $k - c(G) = n((\text{I}(C) + D_3) \setminus D_1)$



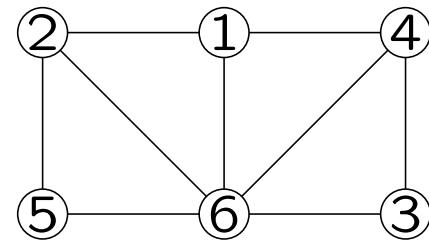
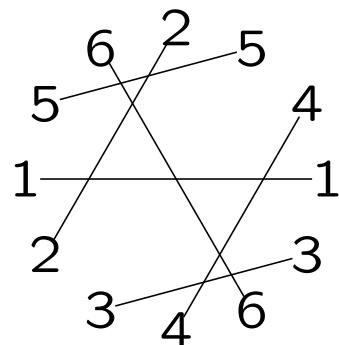
$$\begin{pmatrix} 1 & 3 & 4 & 5 \\ 1 & 1 & 0 & 1 \\ 3 & 0 & 1 & 1 \\ 4 & 1 & 1 & 0 \\ 5 & 0 & 0 & 0 \end{pmatrix}$$

$$q(I(C); y) = \sum_{X \subseteq V(G)} (y-1)^{\textcolor{red}{n}(A(I(C))[X])}$$

$$k - c(G) = n((I(C) + D_3) \setminus \underset{=\emptyset}{D_1})$$

$$m(\vec{G}; y) = \sum_{T \in \mathcal{T}(\vec{G})} (y-1)^{\textcolor{red}{k}(T) - c(\vec{G})}$$

Thm. $m(\vec{G}; y) = q(I(C); y)$



$$w = 1 \ 4 \ \underline{5} \ 2 \ 6 \ \underline{5} \ 1 \ 2 \ 3 \ 4 \ 6 \ 3$$

Thm.	$q(G; y) = q(G * v; y)$	v looped
	$q(G; y) = q(G * e; y)$	e unlooped edge
	$q(G; y) = q(G * X; y)$	$G[X]$ nonsingular

Thm.

$$m(\vec{G}; -1) = (-1)^n (-2)^{a(\vec{G}) - 1}$$

$$m(\vec{G}; 0) = 0, \text{ when } n > 0$$

$m(\vec{G}; 1)$ #Eulerian systems

$$m(\vec{G}; 2) = 2^n$$

$$m(\vec{G}; 3) = k |m(\vec{G}; -1)| \text{ odd } k$$

$$q(G; -1) = (-1)^n (-2)^{n(A(G) + I)}$$

$q(G; 0) = 0$ if $n > 0$, no loops

$q(G; 1)$ #induced subgraphs with
odd number of perfect matchings

$$q(G; 2) = 2^n$$

$$q(G; 3) = k |q(G; -1)| \text{ odd } k$$

defined and studied these polynomials for
 Δ -matroids

(some things become less complicated that way)

nullity corresponds to minimal ‘size’

two directions \Leftrightarrow deletion and contraction

need another ‘minor’ for third direction

thank you ciliates!

when studying new polynomials

look back at old ones

connections to recursive formulations, and

special evaluations

THANKS