Pattern avoiding permutations in genome rearrangement problems: the transposition model

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Permutation Patterns 2017, Reykjavik, 25-30 June 2017.

The genome rearrangement problem

Given a set of rearrangement events, find (and describe) an optimal scenario transforming one genome to another via these rearrangement events.

Here *optimal* refers to the fact that, in view of the parsimony principle, the sequence of rearrangements to transform one genome into another is required to have minimum cost.

Depending on the models, this often allow to introduce a notion of *distance* between two genomes, by counting the number of elementary operations needed to transform one genome into the other.

Main goal: study properties of these distances.

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Genomes and permutations

A proper formalization of the genome rearrangement problem usually consists of

- representing genomes as *permutations*;
- representing rearrangements using suitable *combinatorial operations* on the entries of the related permutation.

For biological reasons, several models have been proposed, corresponding to several sets of combinatorial operations on permutations. Among them:

- the reversal model: $37\boxed{1942}685 \rightsquigarrow 37\boxed{2491}685$;
- the tandem duplication-random loss model: $37\boxed{1942}685 \rightsquigarrow 37\boxed{1\ \cancel{9}\ \cancel{4}2\cancel{1}94\ \cancel{2}}685 \rightsquigarrow 37\boxed{1294}685$;
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General problems

Given permutations ρ, σ, define $d(\rho, \sigma)$ as the minimum number of elementary operations needed to transform ρ into σ in the chosen model.

If we are lucky, d is a *distance*.

If we are luckier, d is *left-invariant*, which implies that computing d is equivalent to sorting permutations using the minimum number of allowed operations.

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General problems

For d left-invariant distance on S_n, define

$$B_k^{(d)}(n) = \{\rho \in S_n \mid d(\rho, id_n) \leq k\}.$$

Main questions:

- compute the diameter of $B_k^{(d)}(n)$;
- compute the diameter of S_n;
- characterize the permutations of $B_k^{(d)}(n)$ having maximum distance from the identity;
- characterize the permutations of S_n having maximum distance from the identity;
- characterize and enumerate the permutations of $B_k^{(d)}(n)$;
- design sorting algorithms and study the related complexity issues.

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The case of the tandem duplication-random loss model

As a matter of fact, in several cases $B_k^{(d)} = \bigcup_{n\geq 0} B_k^{(d)}(n)$ is a *permutation class*; as such, it can be characterized in terms of *pattern avoidance*.

This has been done, for instance, for the whole duplication-random loss model by Bouvel and Rossin [2009].

Subsequent works by Bouvel and Pergola [2010], Mansour and Yan [2010], Chen, Gu and Ma [2011], Bouvel and F. [2013] explored properties of the bases of the related permutation classes, in particular concerning the enumeration of such bases.

We suggest that a systematic investigation of the evolution models of genomes using the permutation pattern paradigm would be very interesting to be carried out. Here we just scratch the surface of a single case, which is the classical transposition model.

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Transposition model and pattern avoidance

Proposition

Given $\pi \in S_n$ and $\sigma \in S_m$, if $\sigma \leq \pi$ then $dt(\sigma) \leq dt(\pi)$. As a consequence, if $B_k = \{\pi \mid dt(\pi) \leq k\}$ is the ball of radius k, then B_k is a class of pattern avoiding permutations, for all k.

Main goals:

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Some notations

A *strip* of $\pi = \pi_1\pi_2\cdots\pi_n \in S_n$ is a maximal consecutive substring $\pi_i\cdots\pi_{i+k-1}$ such that, for all $j = i,\ldots i+k-2$, $\pi_{j+1} = \pi_j + 1$.
Every permutation can be factored into strips: 12567834.

A permutation π is said to be *reduced* when, for all $i = 1,\ldots,n-1$, $\pi_{i+1} \neq \pi_i + 1$. In other words, π is a reduced permutation when it does not have points that are adjacent both in positions and values, i.e. all of its strips have length 1.

$red(\pi)$: (unique) reduced permutation obtained from π by contracting strips of length ≥ 2.

Clearly

- $red(\pi) \leq \pi$;
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More notations

For $\pi \in S_n$ and $v_1, \ldots v_n$ nonnegative integers, the *monotone inflation* of π through $v = (v_1, \ldots v_n)$ is

$$\pi[v] = \pi[id_{v_1}, \ldots, id_{v_n}].$$

$\pi = 41352$, $v = (0, 2, 1, 3, 2)$, $\pi[v] = \underbrace{\ldots}_{4}\underbrace{12}_{1}\underbrace{5}_{3}\underbrace{678}_{5}\underbrace{34}_{2}.$

$MI(\pi)$: set of all monotone inflations of π.
$MI(C) = \bigcup_{\pi \in C} MI(\pi)$.

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Monotone inflations and grid classes

Lemma

Given a $\{-1, 0, 1\}$-matrix M, denote with $Geom(M)$ the geometric grid class of permutations determined by M. Given a permutation π, let M_π be its permutation matrix. Then:

1. $Geom(M_\pi) = Geom(M_{red(\pi)})$;
2. $MI(\pi) = Geom(M_\pi)$;
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Corollary

If C is a set of reduced permutations, then $MI(C)$ is a class of pattern avoiding permutations. Moreover, $MI(C)$ is strongly rational and finitely based.

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Permutations at transposition distance ≤ 1 from the identity

Theorem

1. $B_1 = MI(1324)$;
2. $\pi \in B_1$ *if and only if* π *avoids the patterns* $321, 2143, 2413, 3142$;
3. *For every* $n \geq 1$, *let* $f_n = B_1 \cap S_n$ *be the number of permutations of length* n *having distance* 1 *from the identity. Then*

$$f_n = \binom{n+3}{3} - 2\binom{n+2}{2} + \binom{n+1}{1} + \binom{n+0}{0},$$

and its generating function is

$$F(x) = \sum_{n \geq 0} f_n x^n = \frac{1 - 3x + 4x^2 - x^3}{(1-x)^4}.$$

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Permutations at transposition distance $\leq k$ from the identity

Suppose $\pi = \pi_1\pi_2\cdots\pi_n$ is a reduced permutation of length $n = 3h+1$ in the generating set of B_k.

Inflate π by choosing three (not necessarily distinct) indices $1 \leq i \leq j \leq k \leq n$ and replacing π_i, π_j and π_k by strips of suitable lengths, as follows:

- if the three indices are all distinct, take strips of length 2;
- if two of the indices are equal, take the associated strip of length 3;
- if all indices are equal, take a strip of length 4.

Interchange the two (adjacent) blocks obtained by breaking the nontrivial strips we got by the previous inflation.

$\pi = 1324$, $I = \{2,2,4\} \rightsquigarrow \pi_I = 13\underbrace{\ 4\ }\underbrace{526}7 \rightsquigarrow \tilde{\pi}_I = 13\underbrace{526}\underbrace{\ 4\ }7$

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Permutations at transposition distance $\leq k$ from the identity

Suppose $\pi = \pi_1\pi_2 \cdots \pi_n$ is a reduced permutation of length $n = 3h+1$ in the generating set of B_k.

Inflate π by choosing three (not necessarily distinct) indices $1 \leq i \leq j \leq k \leq n$ and replacing π_i, π_j and π_k by strips of suitable lengths, as follows:

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$\mathcal{I}(n)$: set of all 3-multisets of $\{1, \dots n\}$.
$\pi = \pi_1 \cdots \pi_n$: reduced permutation of length n.
For every $I \in \mathcal{I}(n)$:

- $\tilde{\pi}_I$ is a reduced permutation of length $n+3$;
- if $\pi_1 = 1$ and $\pi_n = n$, then $(\tilde{\pi}_I)_1 = 1$ and $(\tilde{\pi}_I)_{n+3} = n+3$.

Proposition

For every reduced permutation $\pi \in S_n$, denote with $MI(\pi)^{+1}$ the set of all permutations which can be obtained with a single block transposition from any permutation of $MI(\pi)$. Then

$$MI(\pi)^{+1} = \bigcup_{I \in \mathcal{I}(n)} MI(\tilde{\pi}_I).$$

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Theorem

Let $k \geq 1$.

1. *There exist $N = N(k)$ reduced permutations $\alpha^{(1)}, \ldots, \alpha^{(N)}$ of length $3k+1$, each at distance k from the identity, such that*

$$B_k = \bigcup_{j=1}^{N} MI(\alpha^{(j)}).$$

2. *B_k is a strongly rational and finitely-based permutation class; moreover, each permutation of its basis has length at most $3k+1$.*

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When $k = 2$, we get

$$B_2 = \bigcup_{\pi \in \Pi} MI(\pi),$$

where

$$\Pi = \{1324657, 1352647, 1354627, 1364257, 1426357, 1436527, 1462537, 1524637, 1536247, 1624357, 1632547\}.$$

But...

Cheyne Homberger, Vincent Vatter

On the effective and automatic enumeration of polynomial permutation classes

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"Give us something to take home!"

Further work:

- Describe the function $N(k)$ (that is, what's the cardinality of the set of reduced permutations that generate B_k by monotone inflation?)
- More to know on the basis of B_k.
- Further models which could probably be approached in the same way: reversal, prefix transposition, prefix reversal,...
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