

Category theory for genetics

Rémy Tuyéras

talk by Kenny Courser

February 19, 2019

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DNA sequencing
alignment methods,
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genetic linkage
and more.

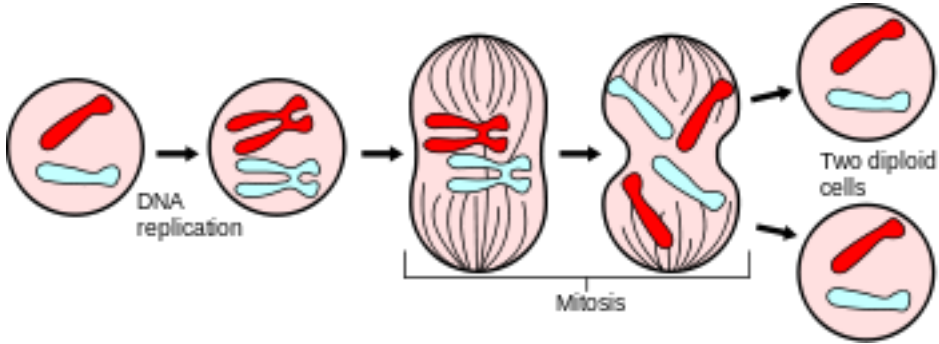
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Our DNA is made of a sequence of nucleobases:

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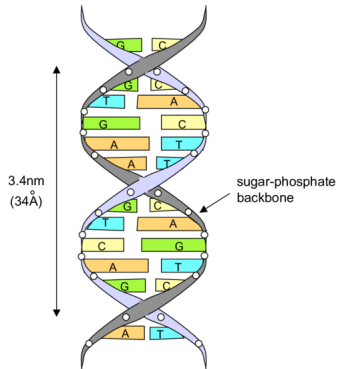
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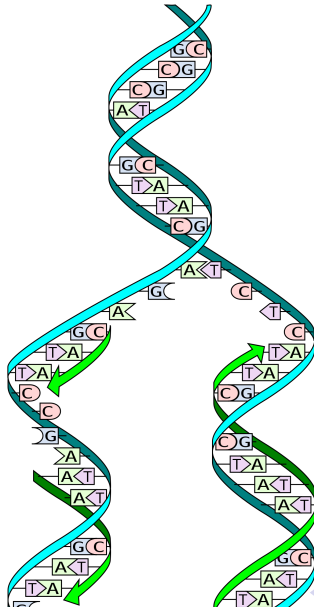
Thymine

intertwined in a double helix shape.



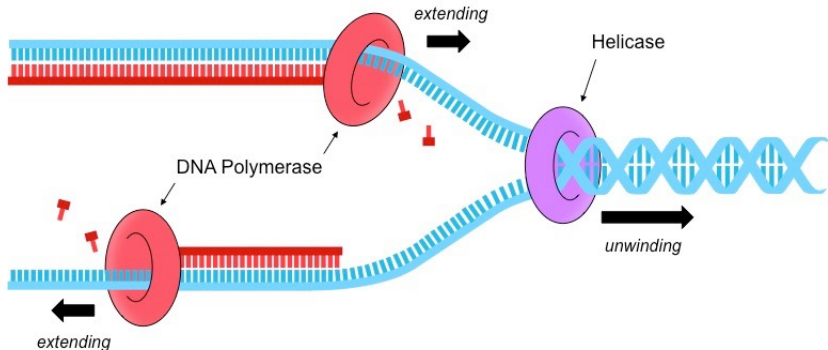
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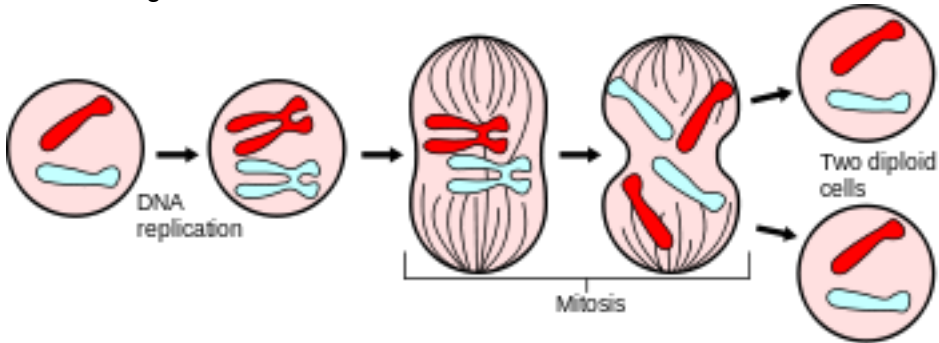


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After the DNA is replicated, the cell undergoes mitosis and splits apart into two copies, each with its own copy of DNA containing one of the strands from the original cell.



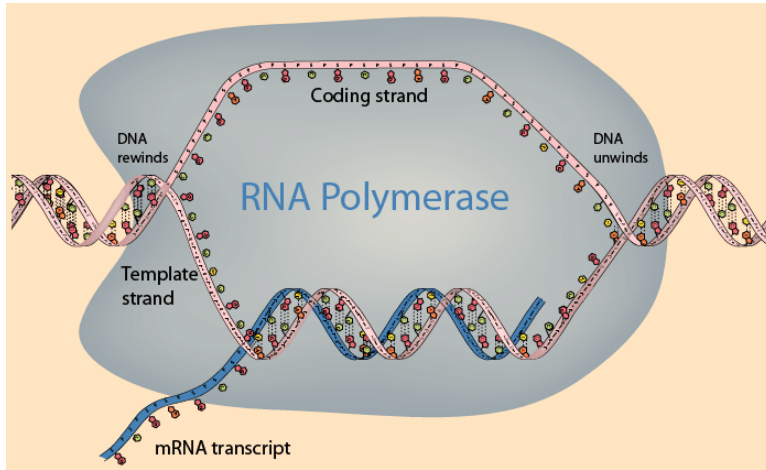
RNA transcription and translation

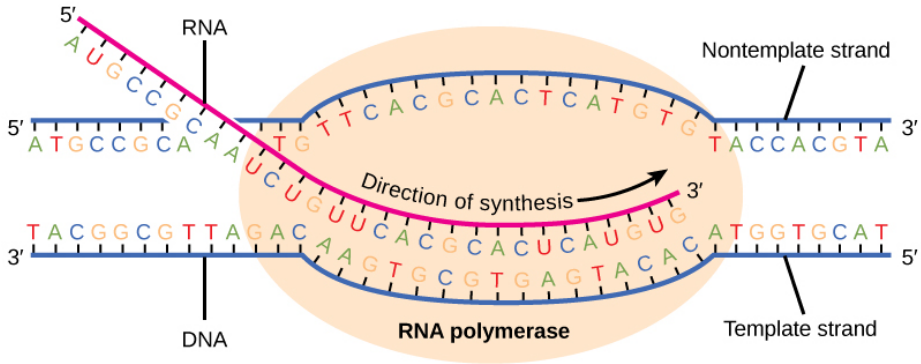
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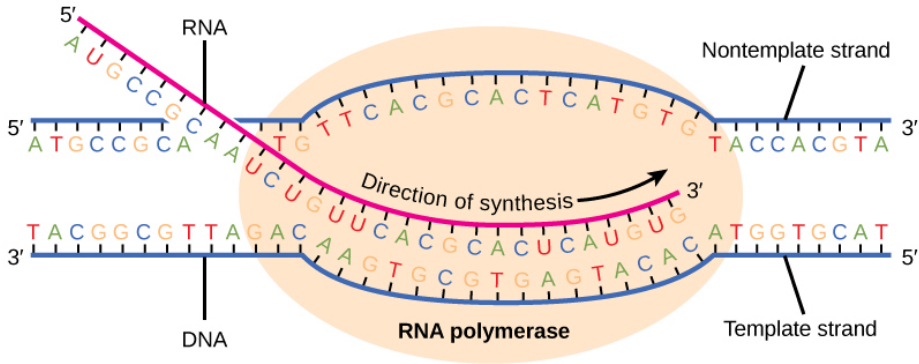
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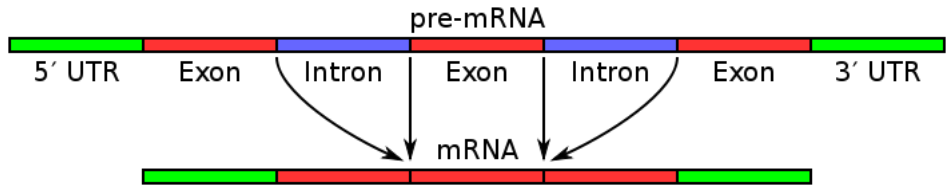
RNA uses **U**racil instead of **T**hymine.

RNA Transcription

Before the mRNA strand exits the nucleus, it has certain regions called 'introns' that are cut out of it.

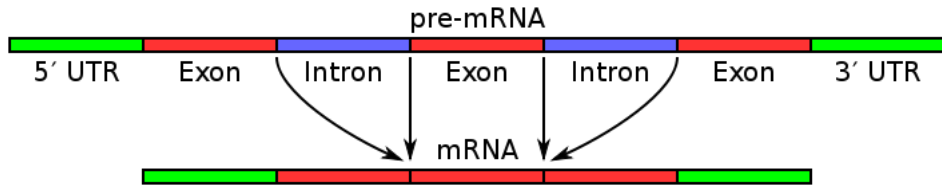
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Now the mRNA strand is ready to leave the nucleus and begin translation.

RNA Translation

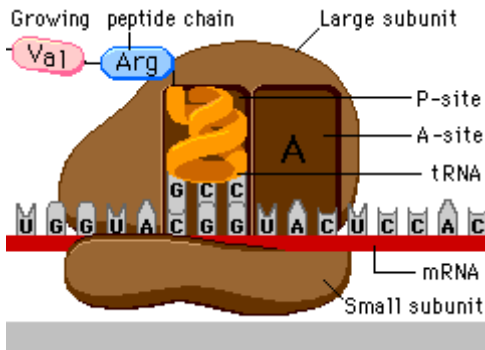
RNA Translation

Now the mRNA strand is outside the nucleus. The mRNA strand is made up of 'codons' which are 3-letter sequences of nucleotides such as AUG, UGA, UAG, UAA, etc.

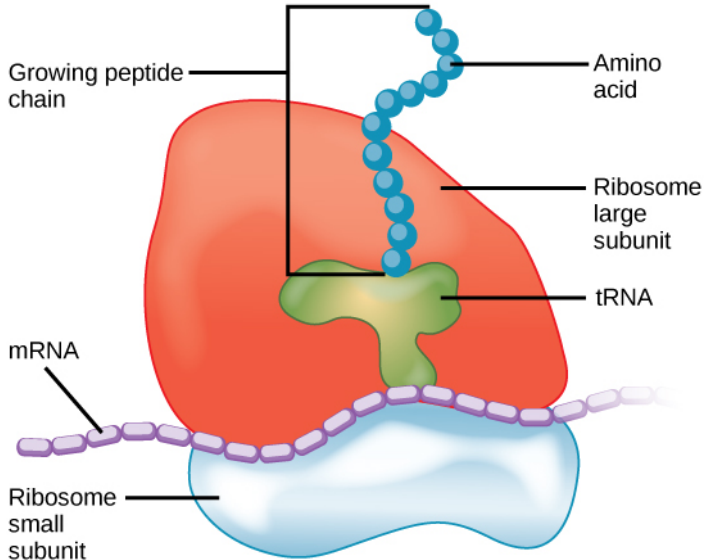
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A 'ribosomal unit' binds to a particular 'start codon' (AUG) which tells the ribosomal unit where to begin translating.



Once the ribosomal unit reaches a 'stop codon' (UGA, UAG, UAA) the unit detaches from the mRNA strand and the sequence of amino acids (blue) created goes off to do stuff.



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The function $c: [n_0] \rightarrow \Omega$ then specifies how each patch is to be interpreted.

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And what about the function $c: [n_0] \rightarrow \Omega$?

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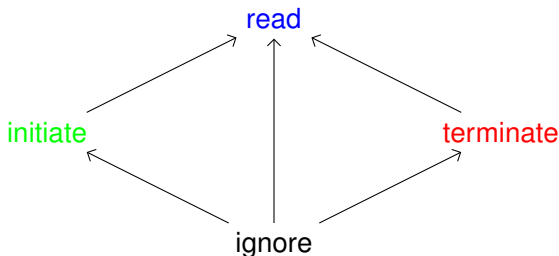
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We will denote a **segment over** Ω simply as $(t, c): [n_1] \rightarrow [n_0]$.

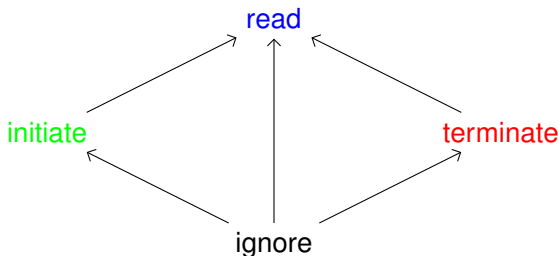
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With this preorder, we can consider segments (t, c) which look something like:

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and such that $c'(f_0(i)) \leq c(i)$ for every $i \in [n_0]$.

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Proposition

*Let (Ω, \leq) be a preordered set. Then there exists a category $\text{Seg}(\Omega)$ with:
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where $c'(f_0(i)) \leq c(i)$ for every $i \in [n_0]$ and f_1 and f_0 are order preserving.

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This says that the way one parses the patches of a segment influences the way that one parses the whole segment, e.g. codons to genes.

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This allows us to insert spaces into the parsing of a segment.

Definition

Let (t, c) and (t', c') be two objects in $\text{Seg}(\Omega)$. Then the two segments (t, c) and (t', c') are said to be **homologous** if their topologies t and t' are equal.

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Proposition

Let (Ω, \leq) be a preorder set and $t: [n_1] \twoheadrightarrow [n_0]$ an order preserving surjection. Then $\text{Seg}(\Omega : t)$ is a preorder category.

Definition

If two segments (t, c) and (t', c') over Ω have the same domain $[n_1]$ then we say that the two segments (t, c) and (t', c') are **quasihomologous**.

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Proposition

Let (Ω, \leq) be a preordered set and let n_1 be a positive integer. Then there exists a preorder category $\text{Seg}(\Omega : n_1)$ whose objects are quasihomologous segments in (Ω, \leq) with domain $[n_1]$ and whose morphisms are pairs $(\text{id}_{[n_1]}, f_0)$.

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and so $Tr_1(t', c') \subset Tr_1(t, c)$.

Proposition

Let $(f_1, f_0): (t, c) \rightarrow (t', c')$ be a morphism in $\text{Seg}(\Omega)$. If $f_1(i) \in \text{Tr}_b(t', c')$, then $i \in \text{Tr}_b(t, c)$.

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This says that if the image of some node is truncated, then its preimage is truncated (remember, colors cannot ‘increase’).

Proposition

For every $b \in \Omega$ and nonnegative integer n_1 , the truncation by b map $(t, c) \rightarrow \text{Tr}_b(t, c)$ extends to a functor $\text{Tr}_b: \text{Seg}(\Omega : n_1) \rightarrow \text{Set}^{\text{op}}$.

Recall there is an adjunction

$$\mathbf{Set} \begin{matrix} \xrightarrow{F} \\ \xleftarrow{U} \end{matrix} \mathbf{Set}_*$$

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$$F(f: X \rightarrow Y) = f+!: X + \{\star\} \rightarrow Y + \{\star\}$$

The functor U is the forgetful functor which forgets the distinguished object.

Proposition

For every element $b \in \Omega$, the map $(t, c) \rightarrow F(Tr_b(t, c))$ extends to a functor $Tr_b^: \text{Seg}(\Omega) \rightarrow \text{Set}_*^{\text{op}}$ defined as:*

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$$Tr_1^*(f_1, f_0) \uparrow$$

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where $\textcolor{red}{4}$ and $\textcolor{red}{5}$ map to the distinguished element \star .

Now let (E, ϵ) be a pointed set and consider the following composition of functors:

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What does E_b^ϵ do to objects?

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as well as many others.

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$$(AG\epsilon)(TCAA)(GC) \mapsto (AG\epsilon\epsilon\epsilon)(TCAA)(\epsilon)$$

$$(GT\epsilon)(\epsilon\epsilon\epsilon C)(TA) \mapsto (GT\epsilon\epsilon\epsilon)(\epsilon\epsilon\epsilon C)(\epsilon)$$

$$(TAA)(GATC)(AA) \mapsto (TAA\epsilon\epsilon)(GATC)(\epsilon)$$

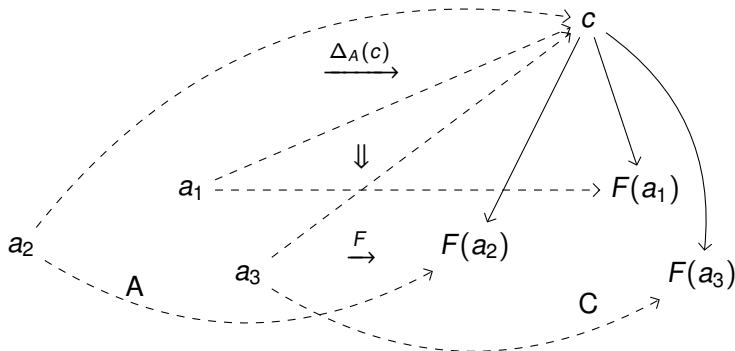
etc.

Definition

A **cone** in a category \mathcal{C} consists of an object $c \in \mathcal{C}$, a functor $F: \mathcal{A} \rightarrow \mathcal{C}$ and a natural transformation $\Delta_{\mathcal{A}}(c) \Rightarrow F$ where $\Delta_{\mathcal{A}}(c)$ is the constant functor mapping every object of \mathcal{A} to $c \in \mathcal{C}$.

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A cone over a discrete diagram A .

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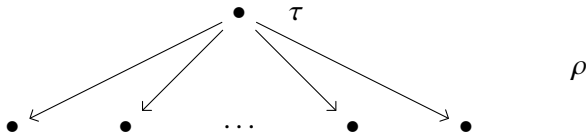
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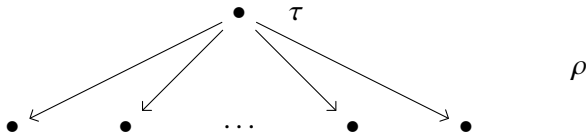
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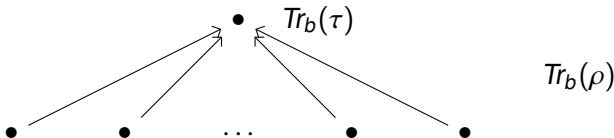


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If we apply the functor $Tr_b : \text{Seg}(\Omega : n) \rightarrow \text{Set}^{\text{op}}$ to the cone ρ , we get a cocone in Set :



From the cocone

$$Tr_b(\rho): Tr_b(\theta) \Rightarrow \Delta_A \circ Tr_b(\tau)$$

in **Set**, we can consider the following composite of maps through the union $\cup_{a \in A} Tr_b \theta(a)$ as follows:

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where m is monic and e is epic.

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Definition

A cone in $\mathbf{Seg}(\Omega : n)$ is **b-distributive** if the monomorphism m above is also an epimorphism and **exactly b-distributive** if it is b -distributive and e is also a monomorphism.

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and $\text{colim}_A Tr_1(\theta) =$

$$\{1, 2, 3, 6, 7, 8, 9, 6', 7', 8', 9', 10, 11, 12, 13, 14, 10', 11', 12', 13', 14'\}$$

and so $\text{colim}_A Tr_1(\theta) \rightarrow Tr_1(\tau)$ is epic but not monic.

An example of an exactly distributive 1-cone in $\text{Seg}(\Omega : 18)$ over the discrete diagram $A = \{\bullet \bullet \bullet\}$ is given by:

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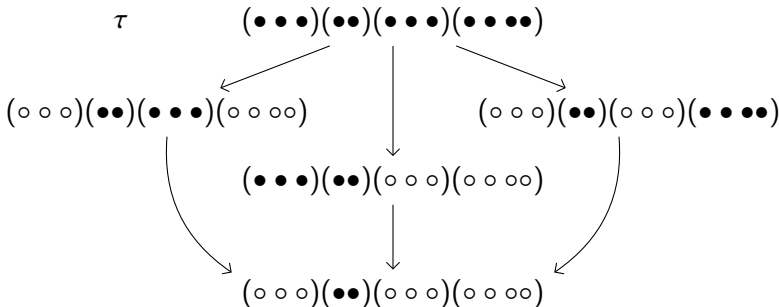
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Exactly distributive 1-cones cannot have any common black patches that are not related via the underlying diagram A.

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Here's an example of an exactly distributive 1-cone in which common black patches are identified via the diagram A:



What are some things that we can model using these cones within this framework?

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Duplication

What are some things that we can model using these cones within this framework?

Duplication

CRISPR

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Inversions

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Consider the following pair of morphisms in $\text{Seg}(\Omega)$:

$$f_1 : (\bullet_1 \bullet_2 \bullet_3) \rightarrow (\bullet_1 \bullet_2 \bullet_3)(\circ \circ \circ)$$

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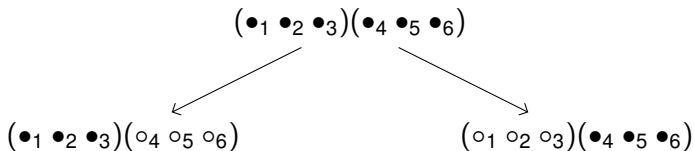
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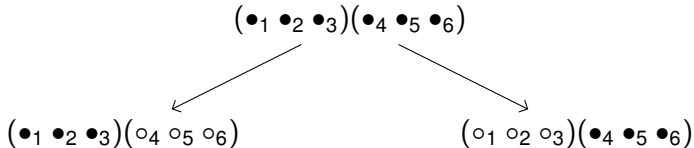
The functor E_1^ϵ applied to either f_1 or f_2 is an identity which sends any word of length 3 in (E, ϵ) to itself, e.g.

$$(A \ T \ G) \xrightarrow{E_1^\epsilon(f_1)} (A \ T \ G)$$

Consider the following exactly 1-distributive cone:

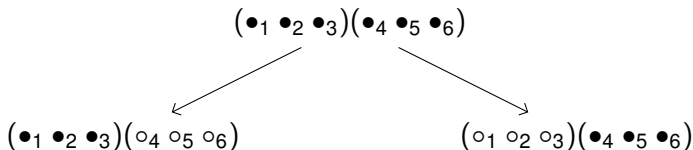


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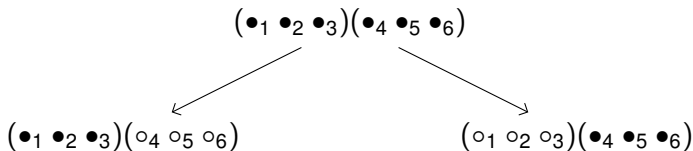


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$$\mu: E_1^\epsilon((\bullet_1 \bullet_2 \bullet_3)(\bullet_4 \bullet_5 \bullet_6)) \rightarrow E_1^\epsilon((\bullet_1 \bullet_2 \bullet_3)(\circ_4 \circ_5 \circ_6)) \times E_1^\epsilon((\circ_1 \circ_2 \circ_3)(\bullet_4 \bullet_5 \bullet_6))$$

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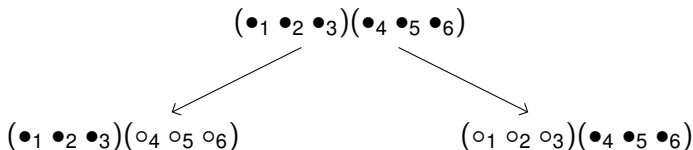
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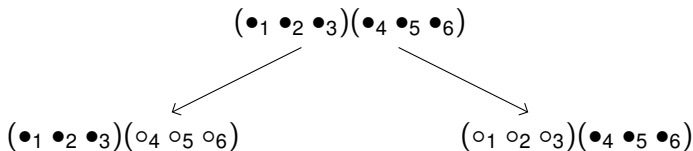
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$$(A T G, G A T) \rightarrow A T G G A T$$

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CRISPR

CRISPR - Clustered Regularly Interspaced Short Palindromic Repeats

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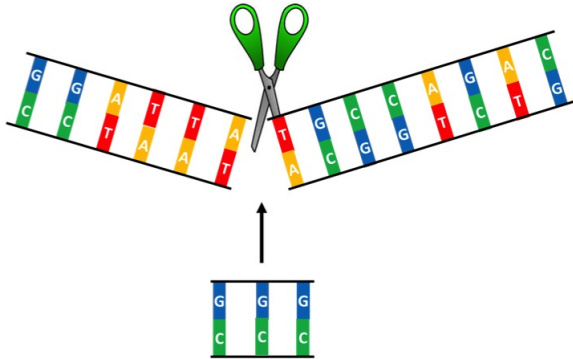
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mouse and rat models
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Mouse Models

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Conditional KO/KI
CRISPR KO/KI
Transgenic

Rat Models

CRISPR KO/KI
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In order to do this, we need to first select the subsegment C G T inside of the segment A T C G T C and then replace it with T T C.

The word A T C G T C is an element of the set

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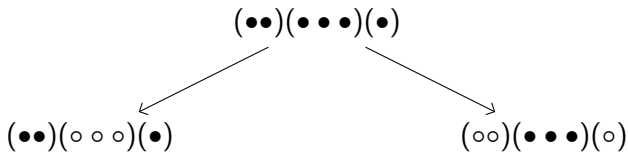
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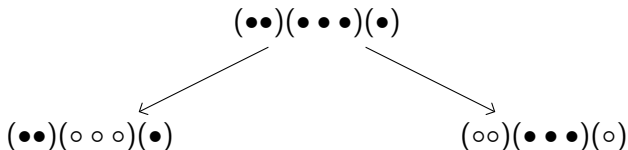
$$E_1^\epsilon((\bullet\bullet)(\bullet\bullet\bullet)(\bullet)) \times E_1^\epsilon((\circ\circ)(\bullet\bullet\bullet)(\circ)) \xrightarrow{(E_1^\epsilon(f), E_1^\epsilon(id))} E_1^\epsilon((\bullet\bullet)(\circ\circ\circ)(\bullet)) \times E_1^\epsilon((\circ\circ)(\bullet\bullet\bullet)(\circ))$$

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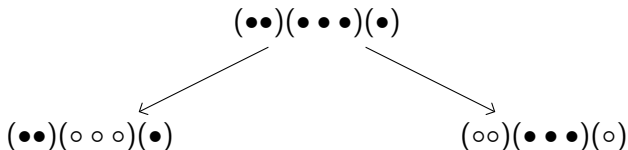


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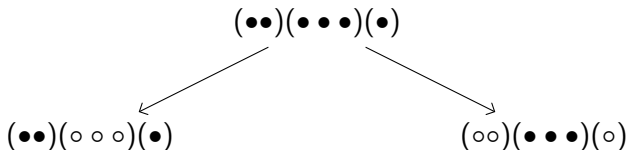
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we get the map $\mu^{-1}(E_1^\epsilon(f), E_1^\epsilon(id))$:

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The image of the pair (A T **C G T** C, **T T C**) is A T **T T C** C.

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$$A \mapsto U$$

$$T \mapsto A$$

$$G \mapsto C$$

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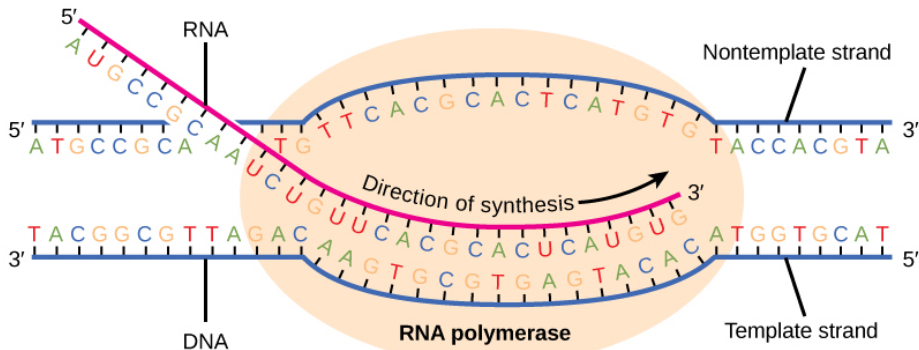
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$$p_b^*: (E \times E, (\epsilon, \epsilon)) \Rightarrow (E, \epsilon)$$

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Inversions

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E.g. for $rv_5: [5] \rightarrow [5]$, we have

$$1 \mapsto 5$$

$$2 \mapsto 4$$

$$3 \mapsto 3$$

$$4 \mapsto 2$$

$$5 \mapsto 1$$

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The map $(t, c) \mapsto (t, c)^\dagger$ induces an endofunctor $Inv: \text{Seg}(\Omega) \rightarrow \text{Seg}(\Omega)$.

If we take $E = \{A, C, G, T, \epsilon\}$ as our pointed set and $b \in \Omega = \{0 \leq 1\}$, then the functor

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induces a natural transformation

$$E_b^\epsilon \Rightarrow E_b^\epsilon \circ \text{Inv}$$

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which maps any word to its inversion.

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$$\text{CTTACA} \mapsto \text{ACATTC}$$

Inversion is useful for interpreting the 'lagging strand' (red) having to be read backwards.

