ON THE TRANSCRIPTION-BASED SOLENOIDAL MODEL OF CHROMOSOMES

Epigenomics of molecular networks

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Macromolecular encoding

Level of expression

DNA structure

...

Translational control

**DNA transcriptional organization**
**Data**

**List of targets of the dedicated Transcription Factor Rap1p**
(based on bench experiments, either classical or CHromatin Immuno-Precipitation):

<table>
<thead>
<tr>
<th>Gene</th>
<th>Position on chromosome IX, left arm</th>
</tr>
</thead>
<tbody>
<tr>
<td>YIL012W</td>
<td>409 325 bp</td>
</tr>
<tr>
<td>YIL044C</td>
<td>150 230 bp</td>
</tr>
<tr>
<td></td>
<td>...</td>
</tr>
<tr>
<td>YIL087C</td>
<td>025 839 bp</td>
</tr>
</tbody>
</table>
Measuring distances between co-regulated genes
1 period $\leftrightarrow n$ base pairs
Yeast transcriptional scheme

One Transcription Factor

Chromosome IX

Frequency

Distances between co-regulated genes kbp
Yeast transcriptional scheme

One Transcription Factor

Randomized chromosome IX

Frequency

Distances between co-regulated genes kbp
Yeast transcriptional scheme

All Transcription Factors

![Graph showing distances between co-regulated genes in kbp]
Yeast transcriptional scheme

All Transcription Factors

Randomized chromosome IX

Frequency

Distances between co-regulated genes kbp
Conclusion 1:

• Same period for all Transcription Factors

⇒ Solenoidal configuration of DNA
Linear DNA
Radial DNA
Solenoidal DNA
Solenoidal DNA
Solenoidal DNA

Face view
Conclusion 2:

• Different periods for different chromosome arms

$$\Rightarrow$$ A consequence of transcription dynamics
Solenoidal DNA

Side view

Left arm
Left telomere
Centromere

Right arm
Right telomere
Reverse interpretation
Reverse interpretation

Right arm of chromosome XII

Relative frequency

Distances between co-regulated genes kbp
Underlying mechanism: the case of the lactose repressor

A DNA loop induced by

- bivalency of the repressor and
- the presence of 2 binding sites b.s.

B. Müller-Hill
Underlying mechanism: local concentration effect

Underlying mechanism: from intra-genic to inter-genic
Underlying mechanism: from intra-chromosomal to inter-chromosomal
Underlying mechanism: from intra-chromosomal to inter-chromosomal
Transcription foci: the case of the nucleolus

E. coli transcriptional scheme

- Frequency
- Distances between regulator and target (kbp)

Graph showing frequency distribution of distances between regulatory and target genes.
*E. coli* transcriptional scheme
E. coli transcriptional scheme

![Graph showing frequency vs. distances between coregulated genes in kbp.](image)
E. coli transcriptional scheme
Solenoidal DNA

Types of clustering between coregulated targets, or between the gene encoding a transcription factor (TF) and its targets:

<table>
<thead>
<tr>
<th>Distance</th>
<th>target/target</th>
<th>TF / target</th>
</tr>
</thead>
<tbody>
<tr>
<td>Clustering</td>
<td>1-D</td>
<td>3-D</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Organism</th>
<th>Bacteria</th>
<th>Yeast</th>
<th>Animal</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td></td>
<td>++</td>
<td></td>
<td>ND</td>
</tr>
</tbody>
</table>
Genetic and Evolutionary Computation

Before evolution: random gene positions

1-D

3-D

Evolution

After evolution: regular gene positions

1-D

3-D

Morphogenesis

Morphogenesis
3 sets of 10 genes each