IMGT WP1 & WP8

Phylogenetic analysis of IG and TR genes
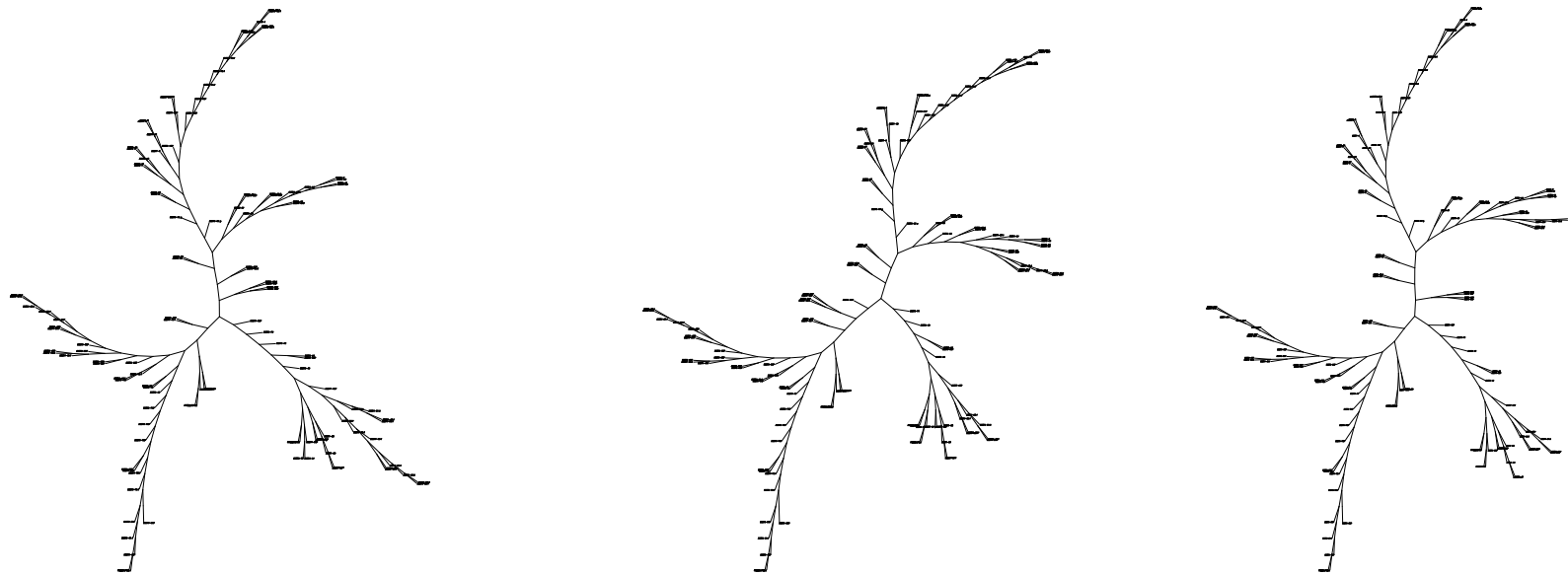
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- Traditional approach

- Example : the IGHV locus

- Online tools for phylogenetic analysis

- Educational page on phylogenetic analysis

- Novel approach

Traditional approach

–   provide one or several trees for every locus of repeated IG and TR genes

–   build trees using the PHYLIP package

–   make no assumptions about the duplication process

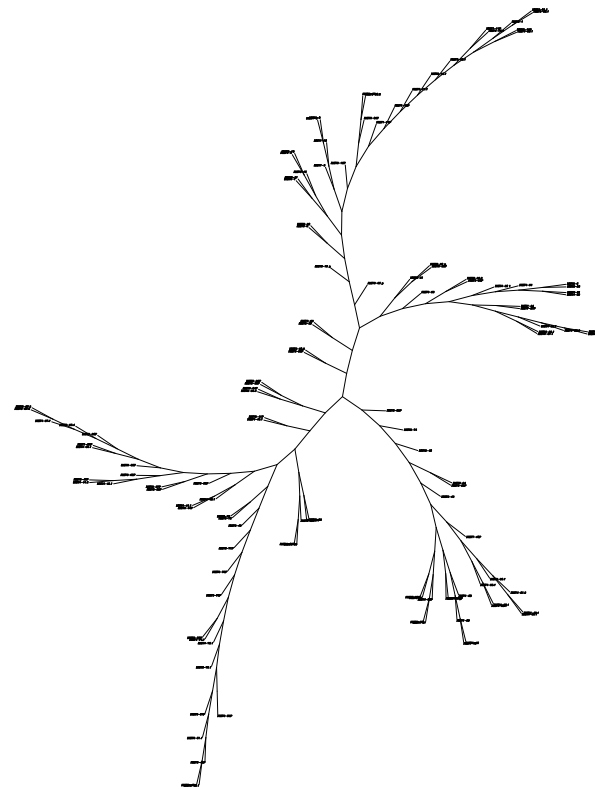–   use several methods, and provide every different tree

Example : the IGHV locus
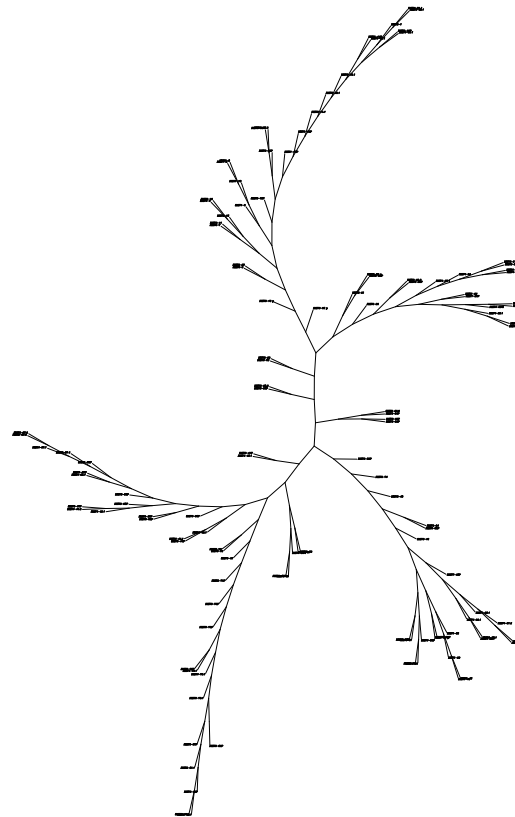
Maximum parcimony trees

Example : the IGHV locus

Neighbor joining (NJ) tree

Example : the IGHV locus

Maximum likelihood tree

Educational page on phylogenetic analysis

– explain the tree building process

– describe the main methods and their benefits/drawbacks

– describe ways to assess the quality of the reconstruction

Online tools for phylogenetic analysis

– build new trees using different parameters and models of evolution

– add new sequences to existing trees (engineered sequences for example)

– interface PHYLIP programs (EMBOSS/Embassy version)
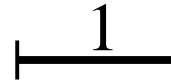
– output tree representations "on the fly"

Novel approach

– use a simple model of evolution by tandem duplication

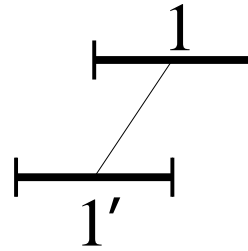# Novel approach

The duplication events

1-duplication

$\longmapsto$ 1 $\longmapsto$

Novel approach

The duplication events

1-duplication

The duplication events

1-duplication

Novel approach

The duplication events
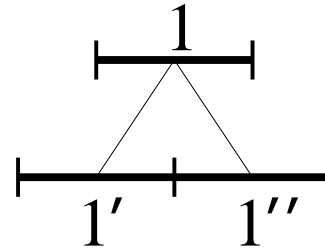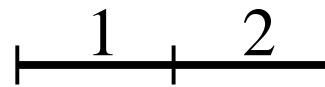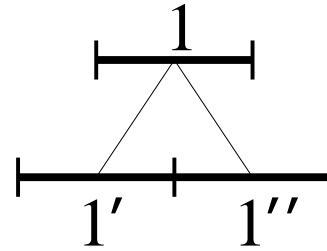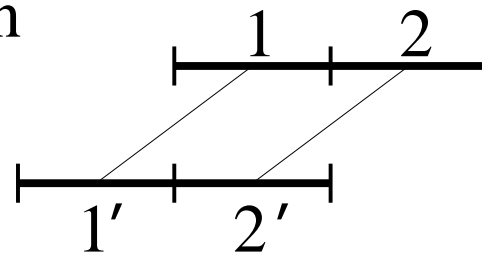
1-duplication

$$\begin{array}{c} \overline{\quad 1 \quad} \\ \diagup \diagdown \\ \overline{1' \quad 1''} \end{array}$$

2-duplication

$$\overline{1 \quad 2}$$
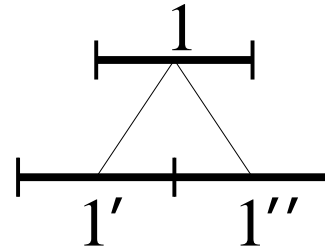
Novel approach
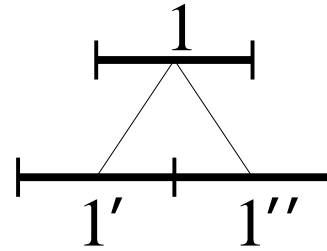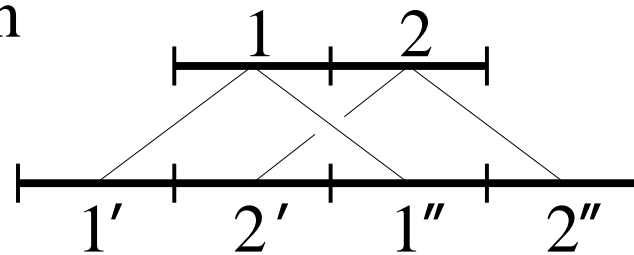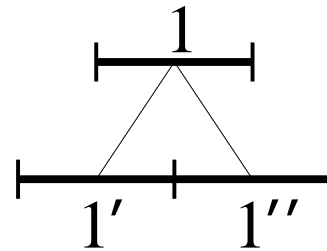
The duplication events

1-duplication

2-duplication

Novel approach

The duplication events

1-duplication

2-duplication

The duplication events

1-duplication

2-duplication

n-duplication

Novel approach

The duplication events

1-duplication

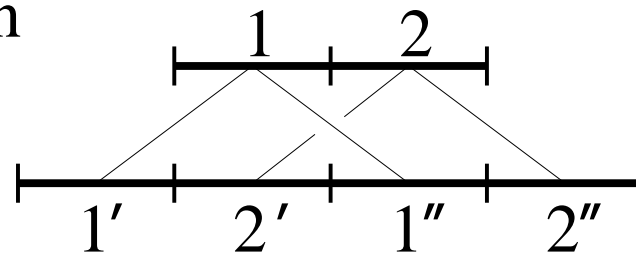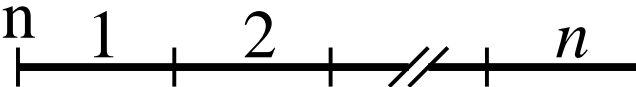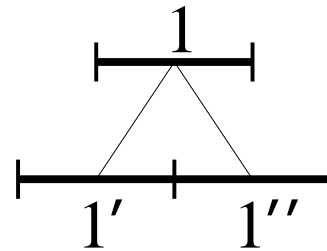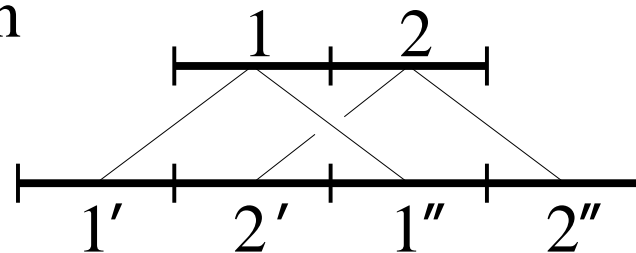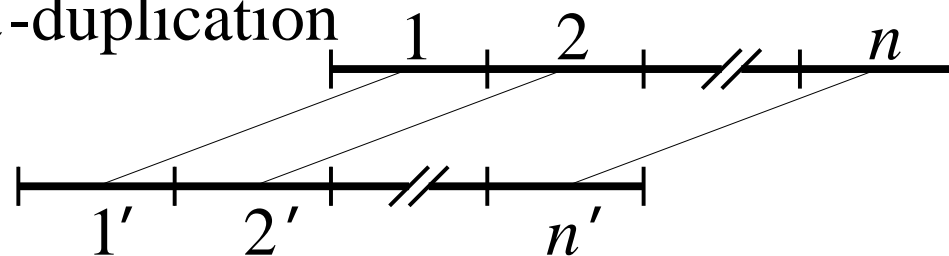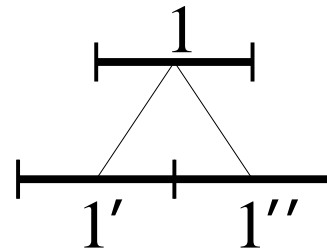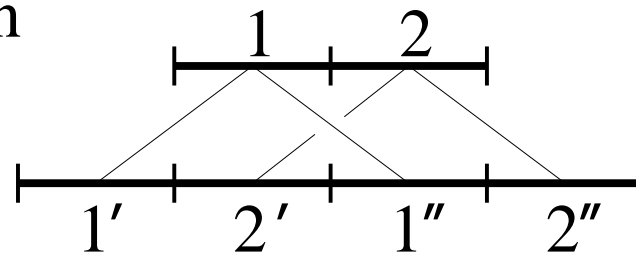2-duplication

n-duplication

Novel approach

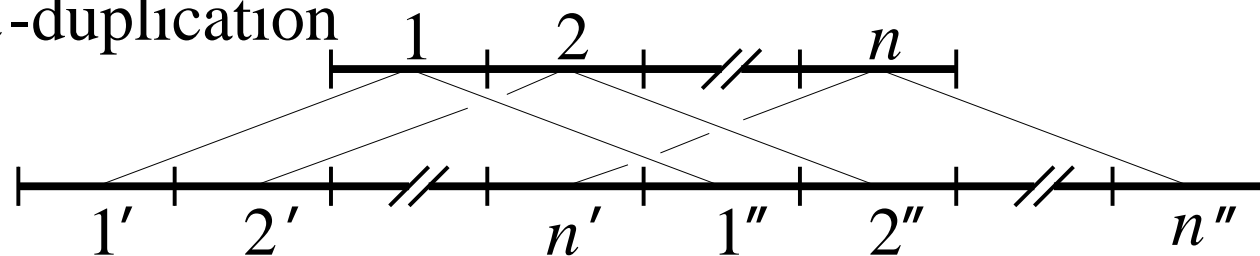## The duplication events

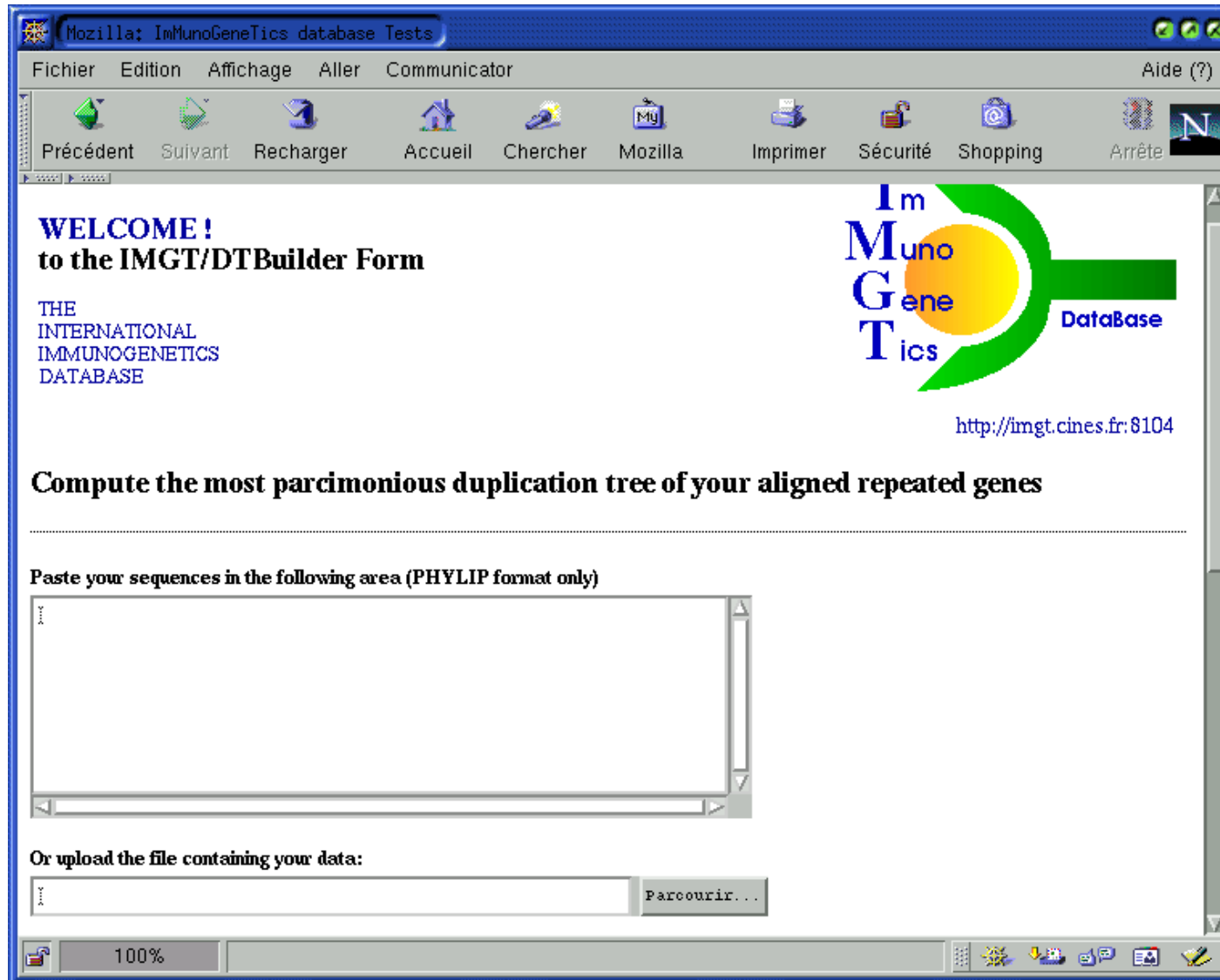1-duplication

2-duplication

n-duplication

Novel approach

– use a simple model of evolution by tandem
 duplication

– implement algorithms to derive the optimal
 duplication trees

– results on some IG and TR locus support the
 duplication model

Novel approach

Novel approach