

# Statistical analysis of full-length antibody repertoire using immunosequencing data

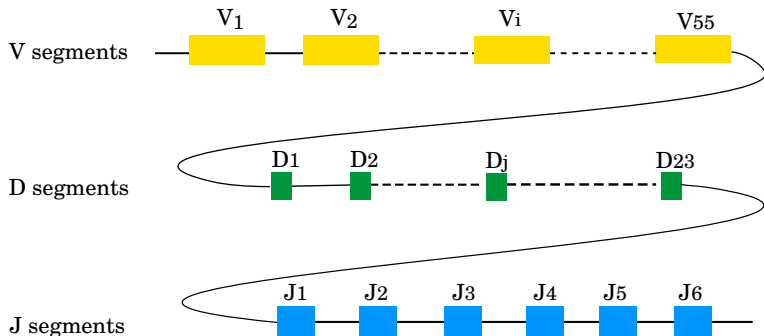
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September 13, 2015

- 1 Introduction and Motivation
- 2 Cleavage and specific gene segments
- 3 Two types of palindromes

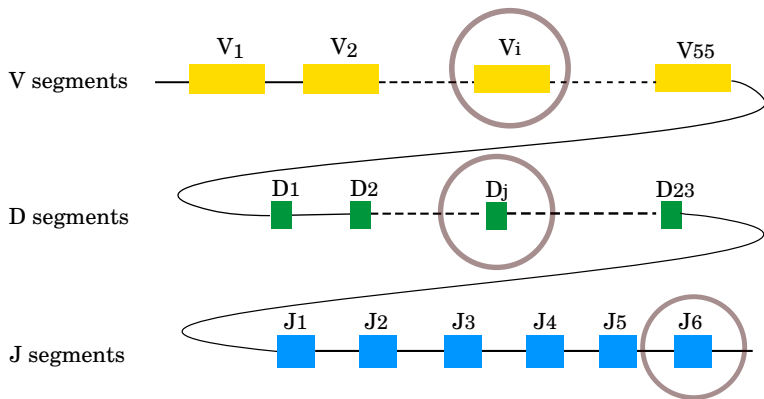
# Introduction: V(D)J-recombination

Immunoglobulin heavy chain locus:



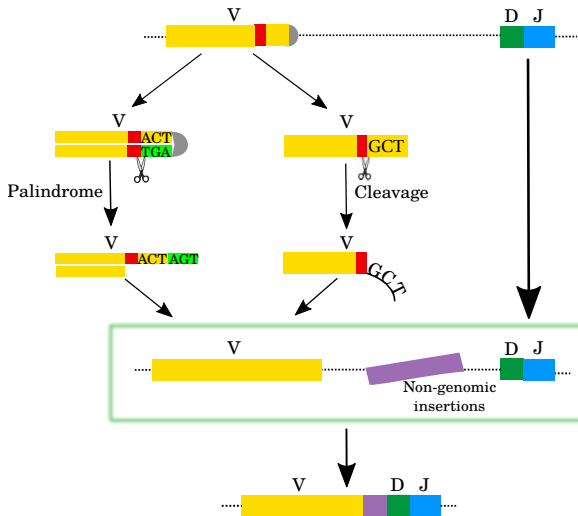
# Introduction: V(D)J-recombination

Segment of each type is selected:



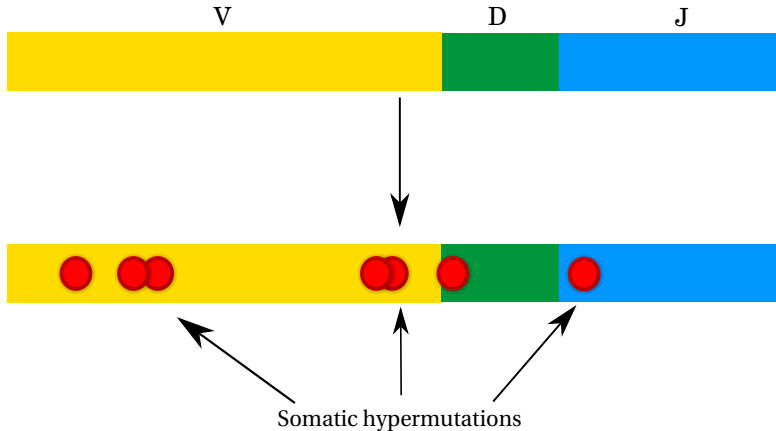
# Introduction: V(D)J-recombination

3 types of biochemical events: *palindrome*, *cleavage*, *non-genomic insertion*.



# Introduction: V(D)J-recombination

Further optimization of antibody affinity is achieved through extensive mutations referred as *somatic hypermutations*:



# Introduction: V(D)J-recombination

Because we do not know the deterministic nature of the V(D)J-recombination, it is reasonable to consider it as a **random** (stochastic) process.

Hence the analysis of somatic recombination can be done in statistical and simulation terms.

# Motivation: comparing different antibody repertoires

## B-cells:

- Comparison of Antibody Repertoires against *Staphylococcus aureus* in Healthy Individuals and in Acutely Infected Patients — Agnieszka Dryla *et al.*, CVI, 2005.
- Comparison of the antibody repertoire generated in healthy volunteers following immunization with a monomeric recombinant gp120 construct derived from a CCR5/CXCR4-using human immunodeficiency virus type 1 isolate with sera from naturally infected individuals — Beddows S. *et al.*, Journal of Virology, 1999.


## T-cells:

- Donor Unrestricted T Cells: A Shared Human T Cell Response — Van Rhijn I, Moody DB, Journal of Immunology, 2015.
- Exhaustive T-cell repertoire sequencing of human peripheral blood samples reveals signatures of antigen selection and a directly measured repertoire size of at least 1 million clonotypes — Warren RL *et al.*, Genome Research, 2011.



# Motivation: simulation of a repertoire

Appropriate statistical model of somatic recombinations potentially improves IgSimulator, making it more “realistic”.

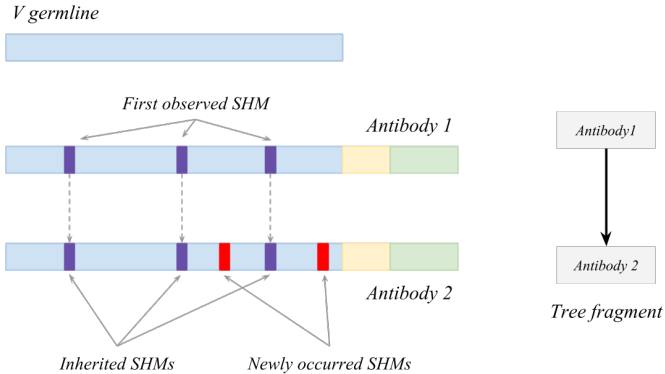


IgSimulator

Statistical  
Model

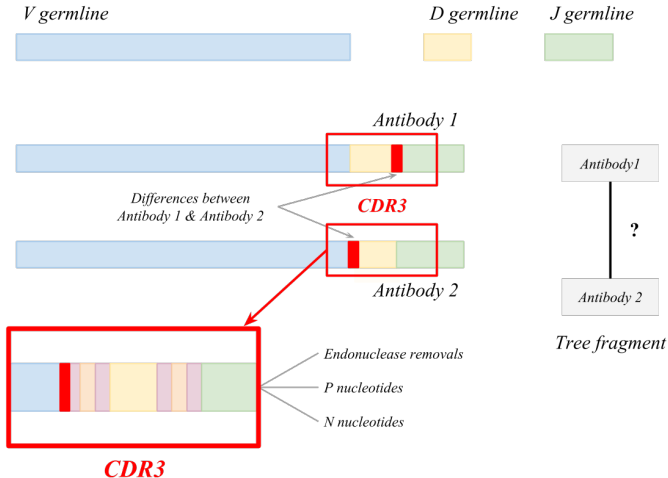
# Motivation: Clonal trees

Clear situation:

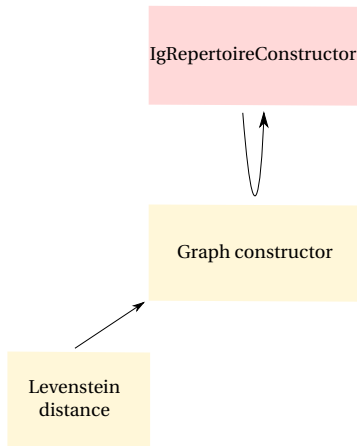


# Motivation: Clonal trees

Arguable situation:

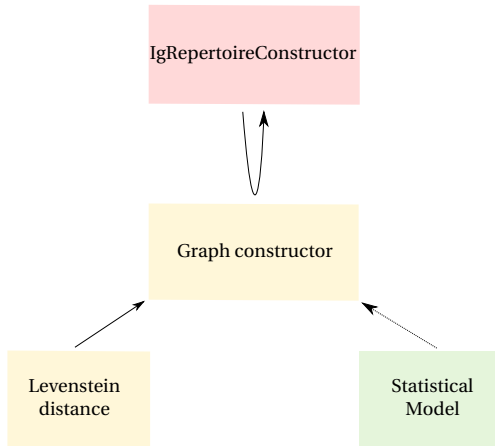


# Motivation: IgRepertoireConstructor



The current release of the IgRepertoireConstructor uses Levenstein distance to construct edges in the graph.

# Motivation: IgRepertoireConstructor



The statistical model could suggest a more delicate approach.

There are plenty of tasks. To name a few:

- What is the correlation between D-J and V-DJ joining?
- Is there any correlation between the *cleavage* / *palindromes* and specific gene segments?
- What are the properties of the *non-genomic insertion*?

An article about the distribution law of CDR3 generating recombinations for T-cells:

Anand Murugana, Thierry Morab, Aleksandra M. Walczakc and Curtis G. Callan — 2012:

- Analysis is focused on non-productive CDR3s.
- Suggested model sets joint distribution over the set of discrete variables: *identities* of V-, D-, J- genes, number of *deletions* from the end of a segment, *palindromic* nucleotides and *non-genomic insertion* at the end of a gene.

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- 2865(!) parameters to estimate.



## Questions about the paper:

- Is the suggested model really adequate (including the problem of potential overfitting)?
- Are the results statistically significant?
- Are similar results true for B-cells?

# Two types of events

The goals

- correlations between *palindromes* and specific gene segments,
- properties of the *non-genomic insertion*

include the task of distinguishing “biological” (meaningful) events from “accidental” (random) observations and hence require additional knowledge about repertoire structure.

Considering that first we decided to concentrate on a problem of computation of correlation between **cleavage and specific gene segments**.

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Unlike two problems above *cleavage* can always be detected precisely according to the alignment.

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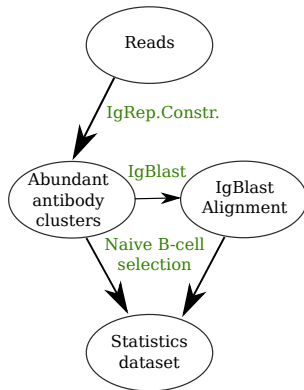
# Cleavage and specific gene segments

Antibody repertoire is a result of V(D)J recombination and secondary diversification. To analyze properties of V(D)J recombination only we perform the following steps:

# Cleavage and specific gene segments

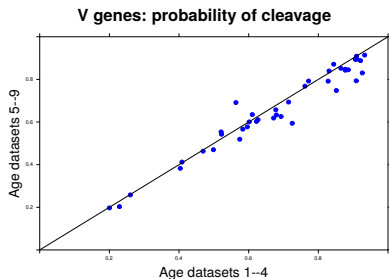
Antibody repertoire is a result of V(D)J recombination and secondary diversification. To analyze properties of V(D)J recombination only we perform the following steps:

- Construct a full-length antibody repertoire using `IgRepertoireConstructor`.
- Consider **highly abundant antibody clusters** of the constructed repertoire.
- Apply `IgBlast` to reads corresponding to selected clusters.
- To avoid effects of the secondary diversification filter out reads with *low* alignment score.

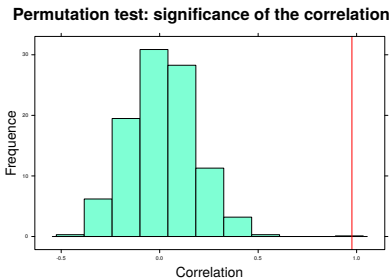


# Cleavage and specific gene segments: V-genes

Age datasets — 9 heavy chain datasets sequenced from human serum samples without cell sorting.



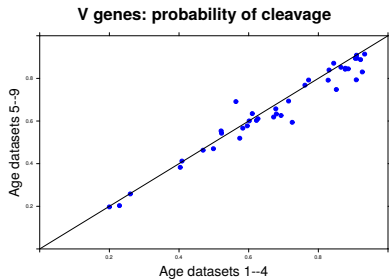
**Figure :** Age datasets. The point is the V gene segments. Pearson correlation is 0.98.



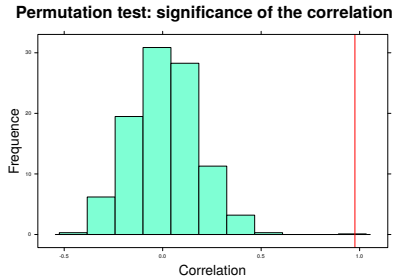
**Figure :** Histogram of statistics of permutation test that shows the significance of Pearson correlation.

# Cleavage and specific gene segments: V-genes

Age datasets — 9 heavy chain datasets sequenced from human serum samples without cell sorting.



**Figure :** Age datasets. The point is the V gene segments. Pearson correlation is 0.98.



**Figure :** Histogram of statistics of permutation test that shows the significance of Pearson correlation.

Hence reads in the dataset are dependent standard pooled Z-test for equal proportions is not applicable.



Find out factors to clusterize  $V$  segments.

Probability of *cleavage* is not appropriate. It is reasonable to seek a way to clusterize  $V$ -genes by

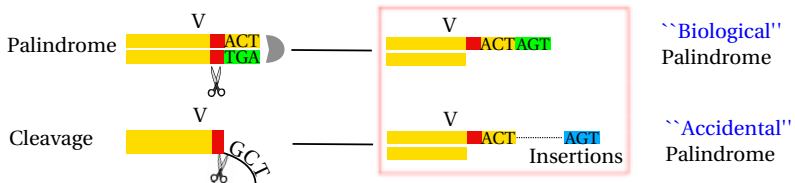
- *palindromes* length;
- GC-content;
- different type of genes ( $V$  vs  $J$  etc. . . ).

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# Two types of palindromes

If a *cleavage* took place, then no “biological” *palindrome* could happen.

An “accidental” *palindrome* can still happen due to the *non-genomic insertions*.



# Two types of palindromes

- The simplest model assumes that every nucleotide  $\xi$  in the sequence is distributed **uniformly**:

$$\mathbb{P}(\xi = x) = \frac{1}{4} \text{ where } x \in \{ 'A', 'C', 'G', 'T' \}.$$

- In that model the length  $\eta$  of an “accidental” palindrome has  $\text{Geom}(3/4)$  distribution, so

$$\mathbb{P}(\eta = n) = \frac{3}{4^{n+1}} \text{ for all } n \in \mathbb{N}_0.$$

# Two types of palindromes

Emperical (Age-datasets) and Geom(3/4) distributions in log scale:



Figure : The mean of length is 0.33.

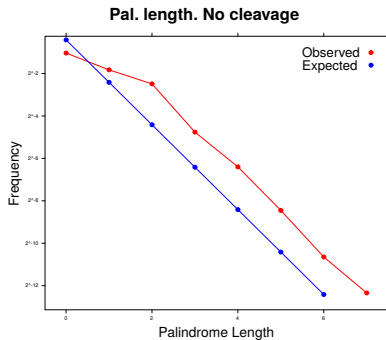


Figure : The mean of length is 0.82.

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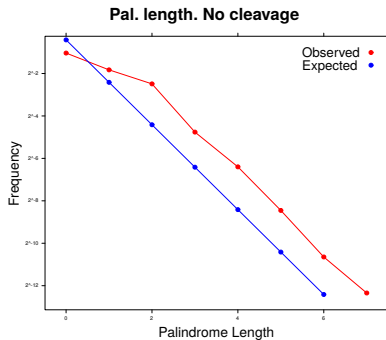


Figure : The mean of length is 0.33.      Figure : The mean of length is 0.82.

Hence reads in the dataset are dependent goodness-of-fit  $\chi^2$ -test is not applicable.

- To find out the distribution of “biological” palindrome length.
- To construct more adequate model for nucleotide distribution.

Statistical analysis of an antibody repertoire is very promising research with lots of applications. Some of them:

- Comparing antibodies repertoires.
- Simulation of a repertoire.
- Edges in clonal trees.
- Improvement of `IgRepertoireConstructor`.

Our goals:

- Construct an adequate statistical model of the V(D)J-recombination.
- Find out correlations between segments of genes.
- Find out correlations between various biological events, including *cleavage*, *palindromes* and *non-genomic-insertions*.