# Evaluating Contaminations in Genome Sequences

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# Introduction

- What is genome contamination?
- Possible contaminations are from
  - Vectors
  - Adapters
  - Linkers
- Sequencing errors
- How sequences can be contaminated?

# A scenario

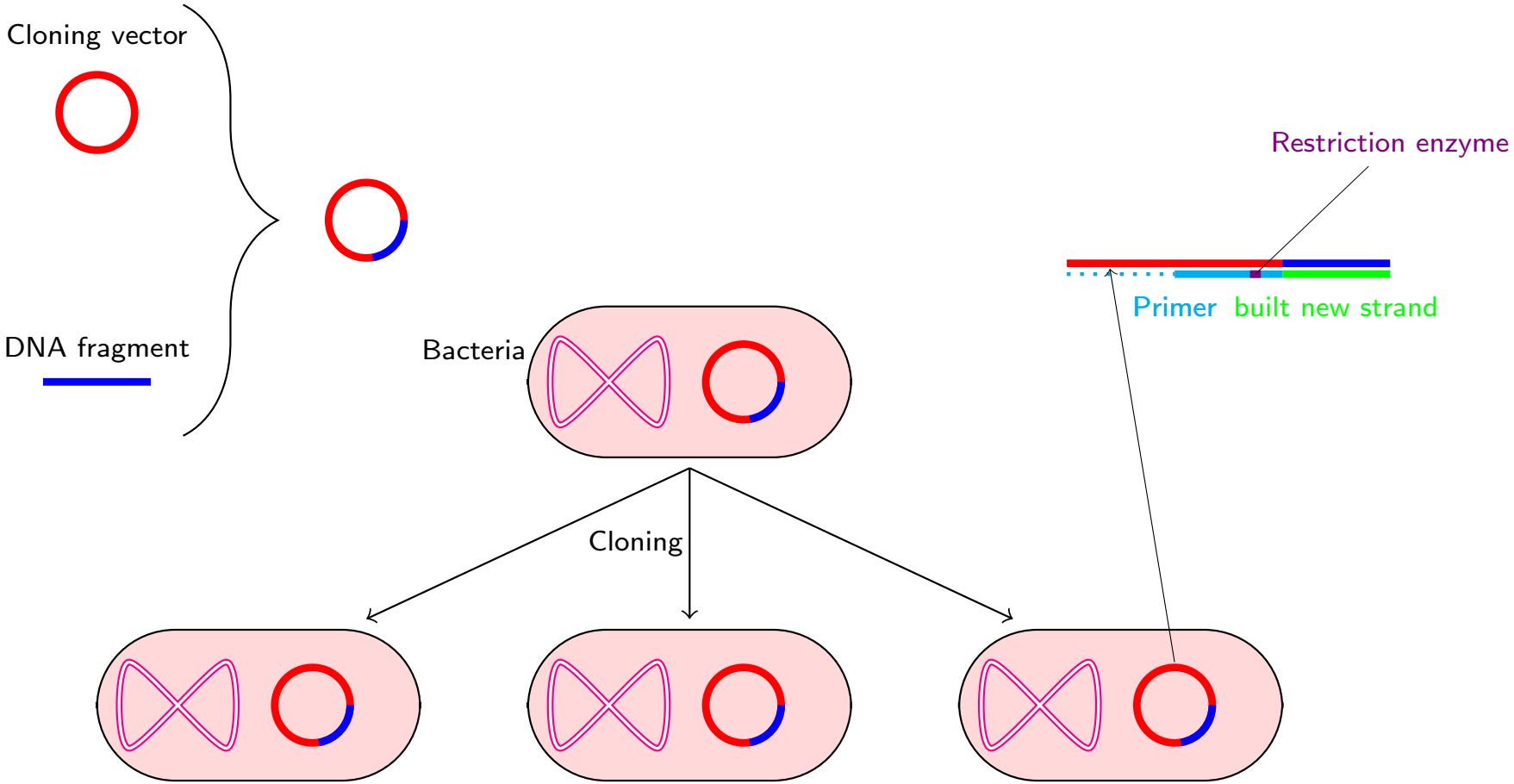



Figure: A scenario showing source of contamination

# Consequences of contaminations

- Pollution of public databases
- Meaningless analysis

# Our Strategy

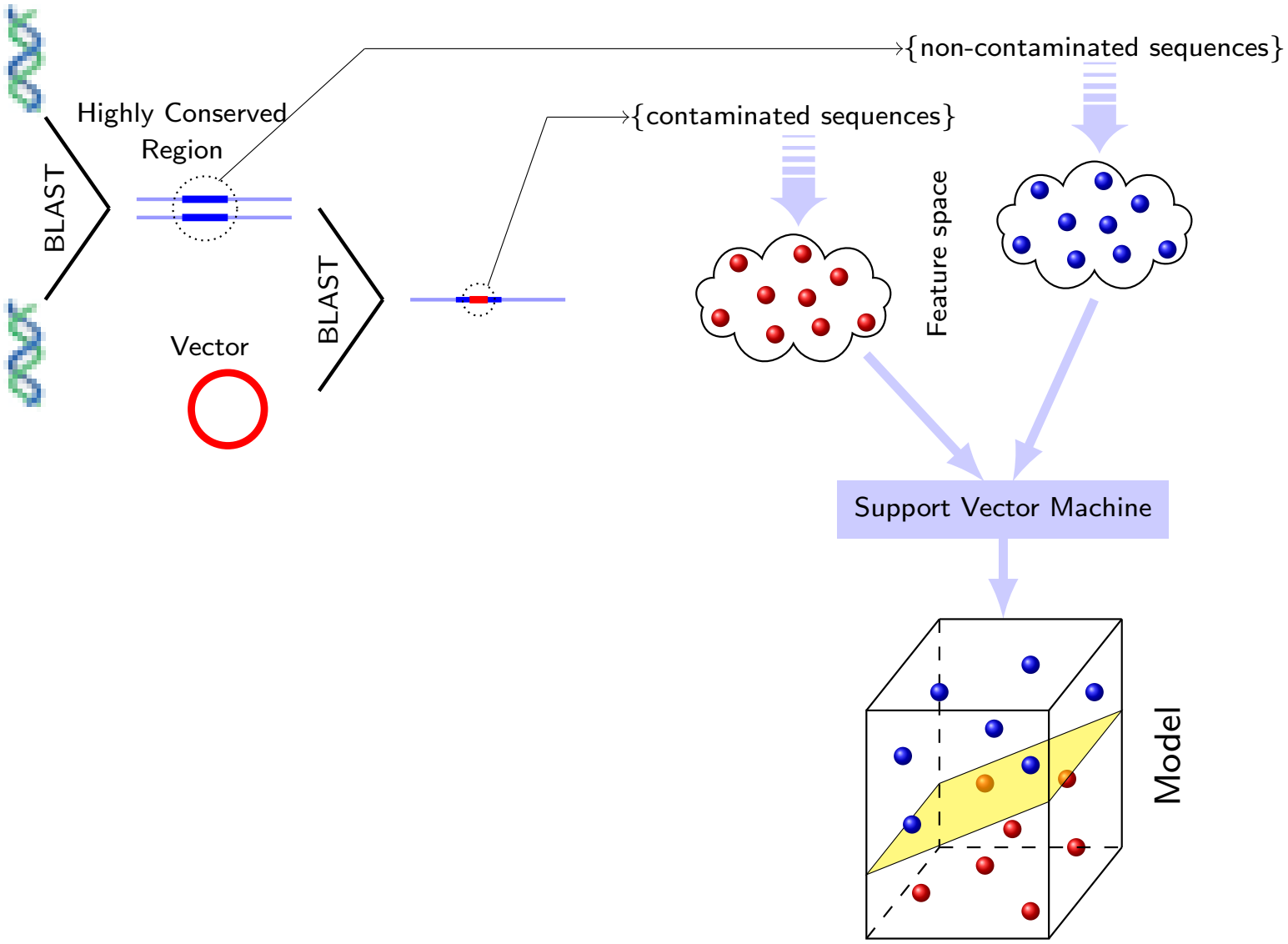



Figure: Model generation - classifies contaminated and non-contaminated sequences

# Fisrt of all, acquiring data

- Genomes
  - UCSC genome browser[1]
  - 58 different metazoans
- Vector sequences
  - UniVec database from NCBI[2]
  - VectorDB from Stanford[3]
  - Total of 4696 unique sequences

[1] http://hgdownload.cse.ucsc.edu/downloads.html
[2] ftp://ftp.ncbi.nih.gov/pub/UniVec/
[3] http://genome-www.stanford.edu/vectordb/

# Before choosing genomes

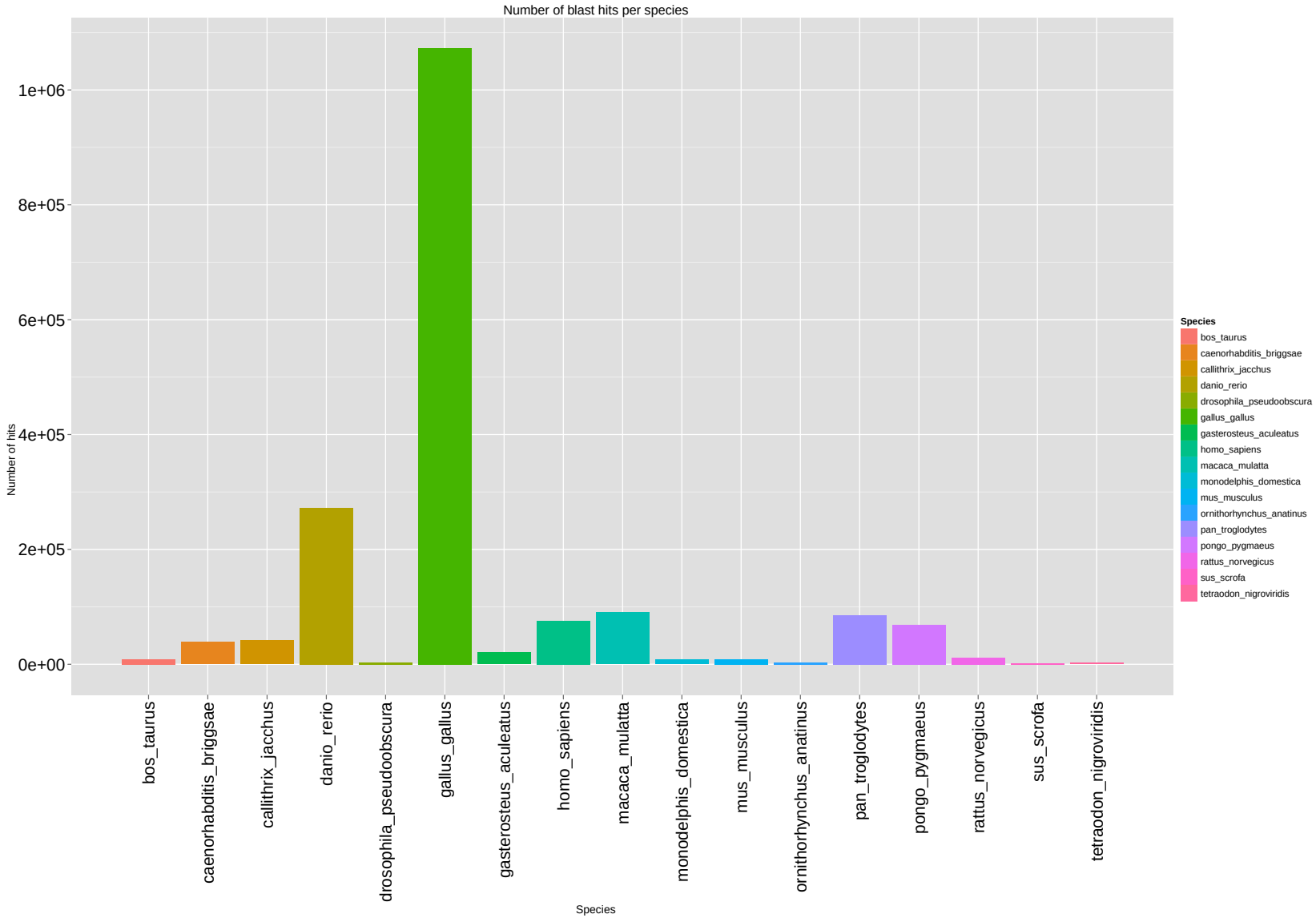



Figure: BLAST hits vectors against genomes

# Hunt for Highly Conserved Regions

- Megablast with E-value '1e-5' and identity greater than or equal to 90%.

- Callithrix jacchus
- Caenorhabditis briggsae
- Gasterosteus aculeatus
- Macaca mulatta
- Mus musculus
- Pan troglodytes

vs

Danio rerio

and

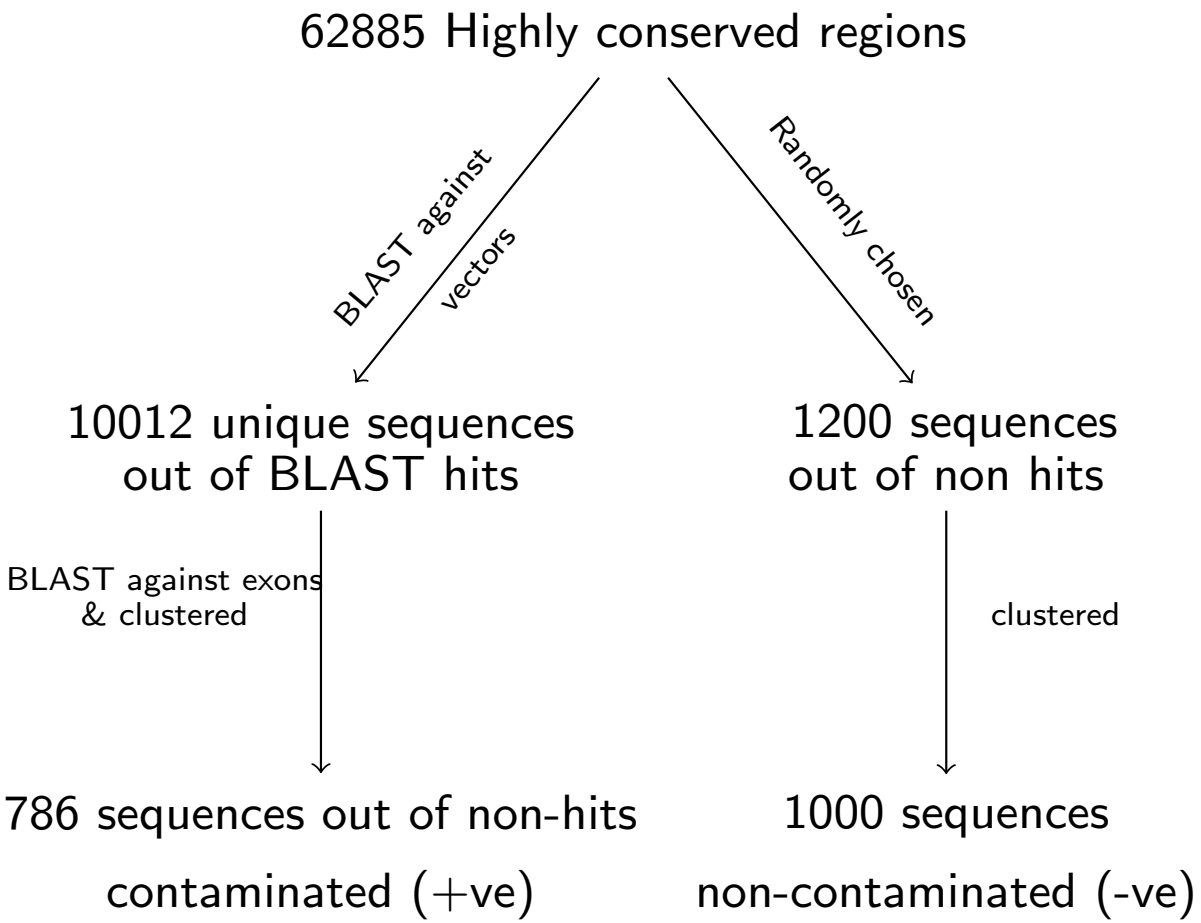
Gallus gallus

2852087 unique BLAST hits

↓

642885 Highly Conserved Regions

# Data sets extraction



# Glance at the data sets

- Contaminated sequences
  - Min length: 33
  - Max length: 528
  - Average length: 91.01
  - Median: 69.0000
  - SD: 55.0659
- Non-contaminated sequences
  - Min length: 33
  - Max length: 683
  - Average length: 105.11
  - Median: 77.00
  - SD: 86.0659

# Features and Support Vector Machine

- Features Used:
  - K-mer count
  - K-mer distances
  - K-mer existence as binary class
  - K-mer mismatch scores
  - GC content
  - Stop codons(ATG, CTG, GTG, TTG)
  - Start codons(TAA, TAG, TGA)
- Support Vector Machines:
  - Libsvm 3.0
    - Radial basis kernel
    - Polynomial kernel with degree 3
  - Weka 3.7.3
    - Sequential Minimal Optimization scheme, ploynomial kernel of degree 4
    - All other default parameters

# Results

| Test set | Total Number of Instances | Correctly Classified Instances | Incorrectly Classified Instances |
|---|---|---|---|
| Test set from existing data | 357(P:153,N:204) | 348(97.48%)<br>TP:146, TN:202 | 9(2.52%)<br>FP:7, FN:2 |
| Danio rerio ncRNA | 4431 | 4163<br>(93.96%) | 268<br>(6.04%) |
| Felis catus ncRNA | 738 | 677<br>(91.73%) | 61<br>(8.27%) |
| Gallus gallus ncRNA | 1102 | 1028<br>(93.29%) | 74<br>(6.71%) |
| Homo sapiens ncRNA | 2647 | 2580<br>(97.47%) | 67<br>(2.53%) |
| Homo sapiens mRNA | 1000 | 978<br>(97.80%) | 22<br>(2.20%) |
| Mus musculus ncRNA | 752 | 708<br>(94.15%) | 44<br>(5.85%) |
| Rattus norvegicus ncRNA | 757 | 704<br>(92.99%) | 53<br>(7.01%) |
| Rfam sequences | 786 | 718<br>(91.34%) | 68<br>(8.66%) |
| Human UCRs Watson strand | 2081 | 2008<br>(96.49%) | 73<br>(3.51%) |

Table: Results for different test sets

All ncRNAs from Ensembl ftp – http://www.ensembl.org/info/data/ftp/index.html

Human mRNA extracted from UCSC table browser – http://genome.ucsc.edu/cgi-bin/hgTables

Human Watson strand UCRs by Bejerano G – http://users.soe.ucsc.edu/~jill/ultra.html

# Results

- AUC of 0.972 for best model
- Observation: Most of incorrectly classified instances are from predicted sequences or DNA clones.

# Future Works

- Incorrect predictions - evidence for protein coding
- A standalone tool

# Conclusion

- Contaminations are sometimes hazardous
- Care should be taken while analysis
- More care should be taken while sequencing genomes

# Acknowledgements

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# Bibliography


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# Thank You

Thank you for your attention !!