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Classification of Genome Wide Association data by Belief Propagation Neural network

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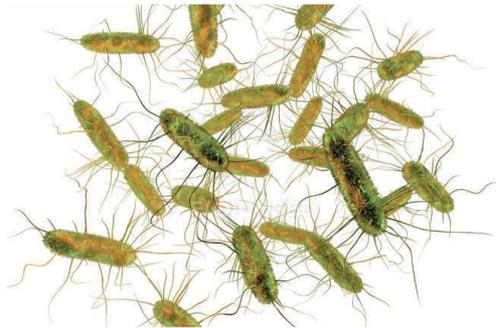
Presented by:
Daniele Dall'Olio

Trento, Italy
July 1-3, 2019

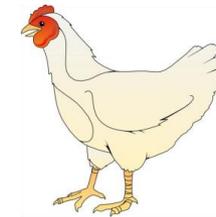
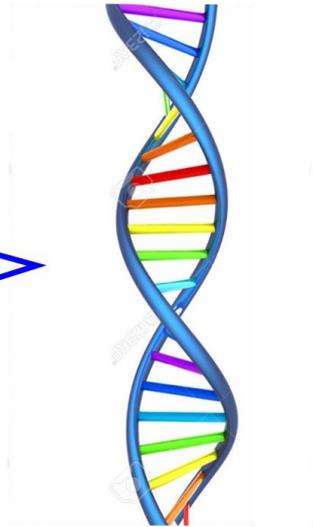
Objective: Identification, containment and mitigation of emerging infectious diseases and foodborne outbreaks.

Source Attribution

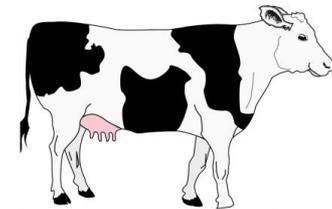
Bacteria



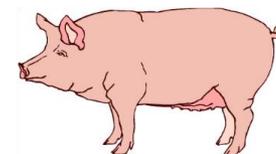
Genome Wide Association



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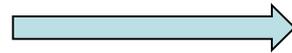
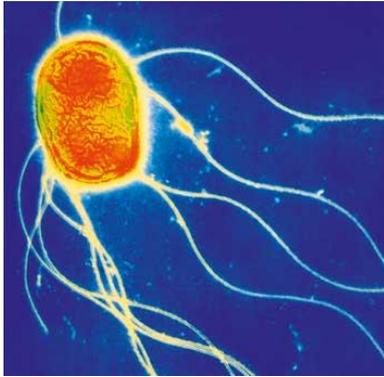


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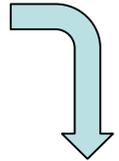
Salmonella Enterica



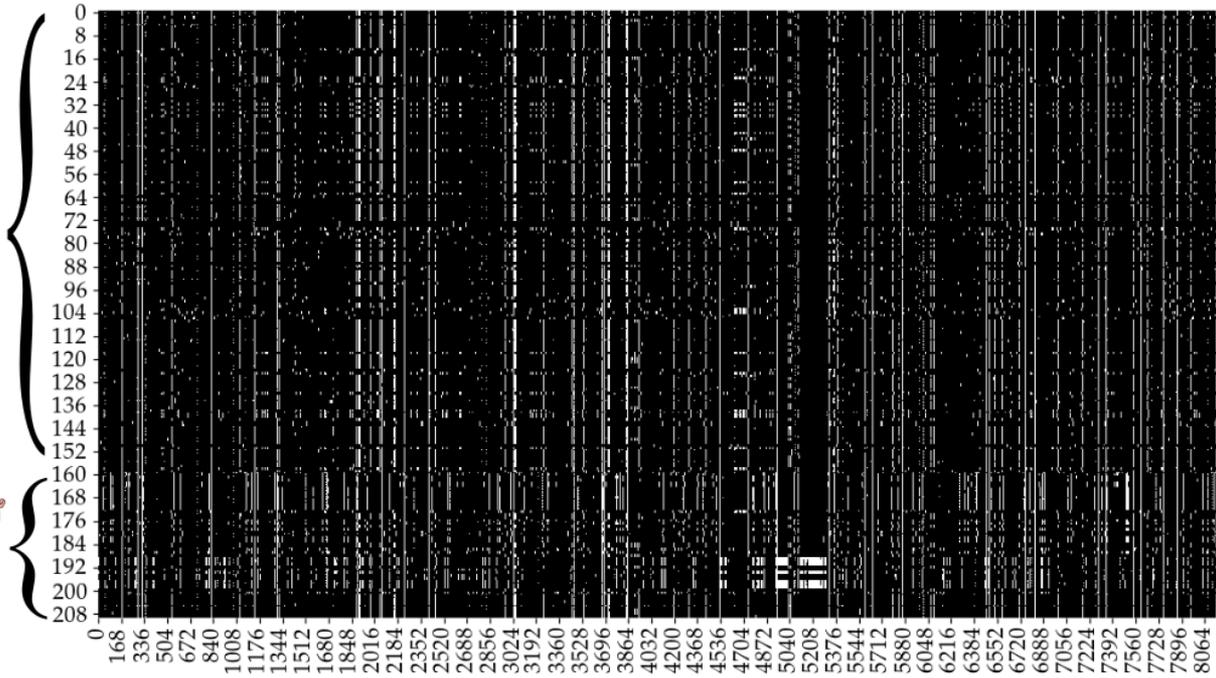
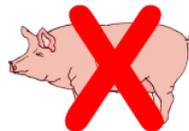
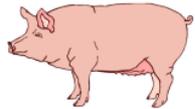
Reference : CCGTTAGAGTTACAATTCGA

Sample : CGGTTAGAGTAACTATTCCA

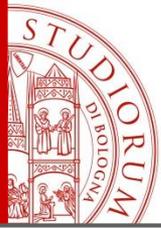
Binary SNPs : 01000000001001000010



Samples	210
Pigs	159
no-Pigs	51
Filtered Bases	8189



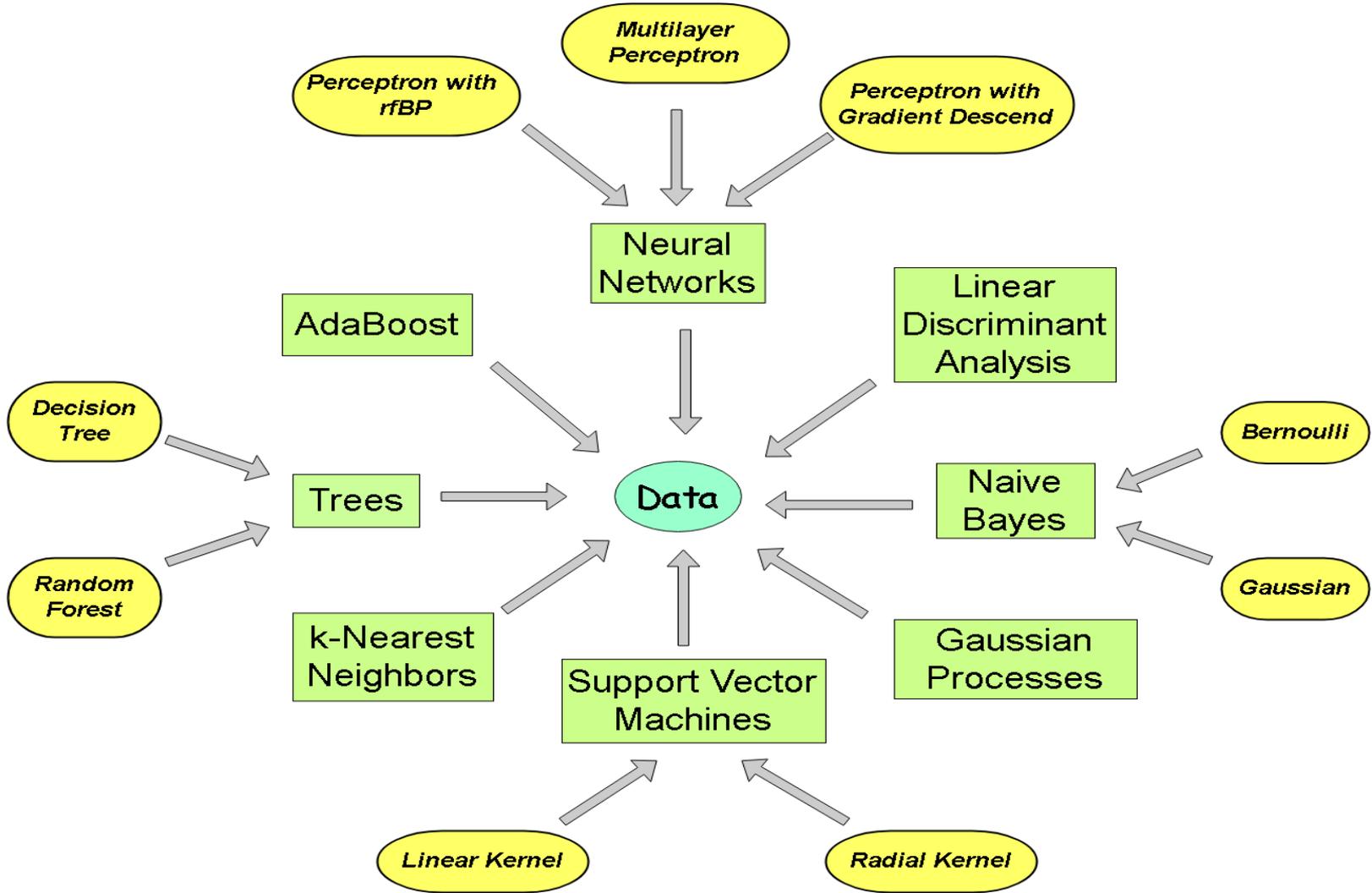
Filtered Bases



Classifiers



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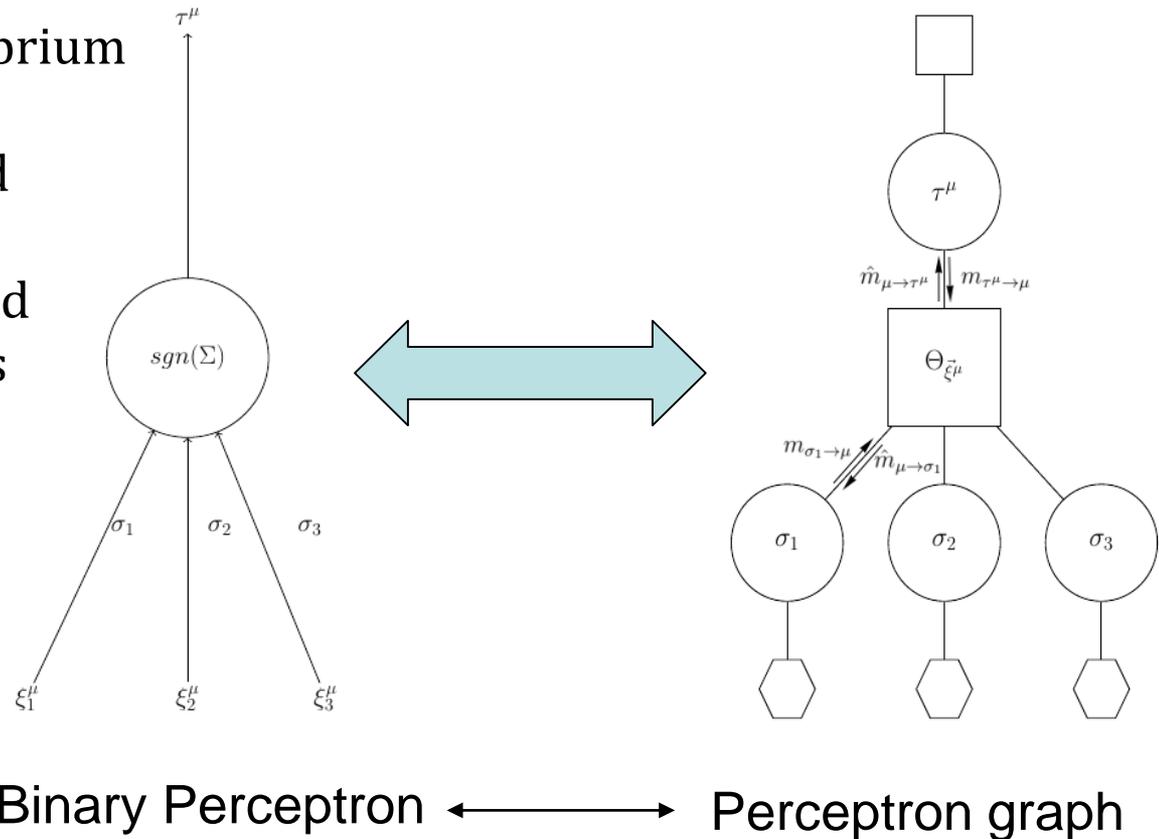
replicated focusing Belief Propagation¹

- Derived from a out-of-equilibrium distribution
- Entropy-maximization based learning rule
- Parameterized and reinforced Belief Propagation equations

New implementation:

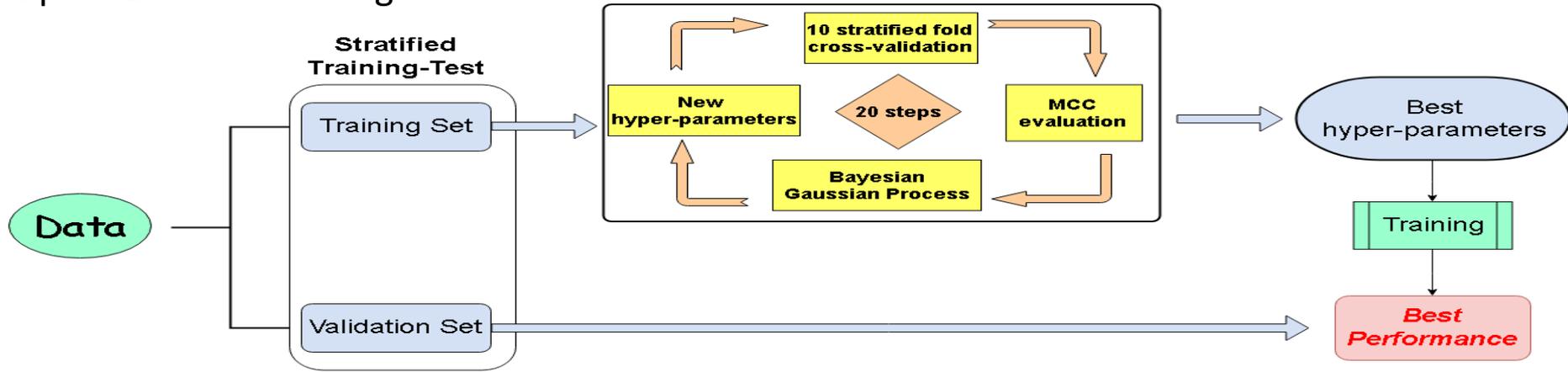
- C++ library
- Python wrapper
- Optimized for parallel computing
- Integrated with *scorer* library

- Link: <https://github.com/Nico-Curti/rFBP>

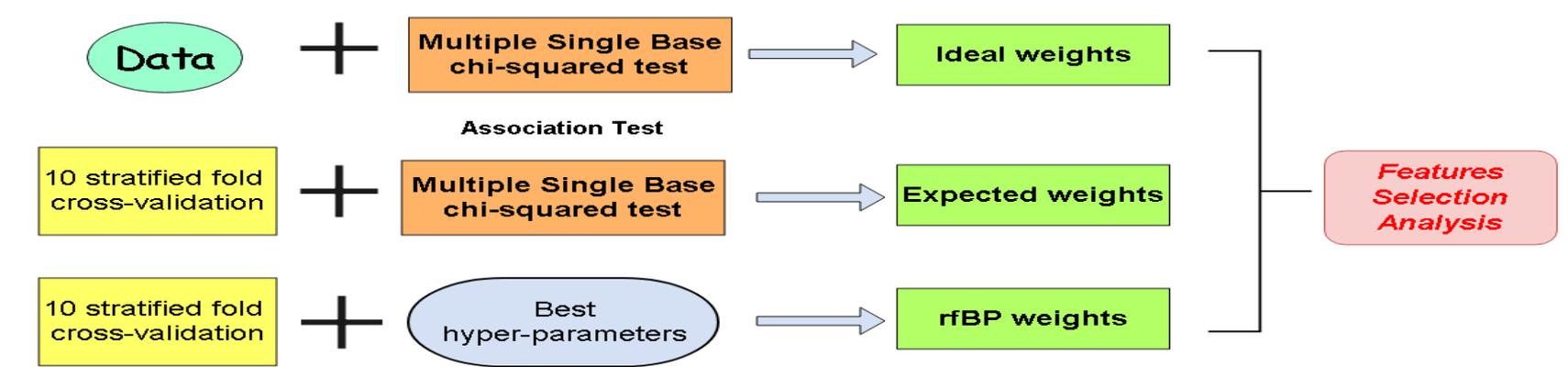


¹C. Baldassi et al. *Unreasonable Effectiveness of Learning Neural Networks: From Accessible States and Robust Ensembles to Basic Algorithmic Schemes*, 2016.

Optimization + Training



rfBP vs Statistics



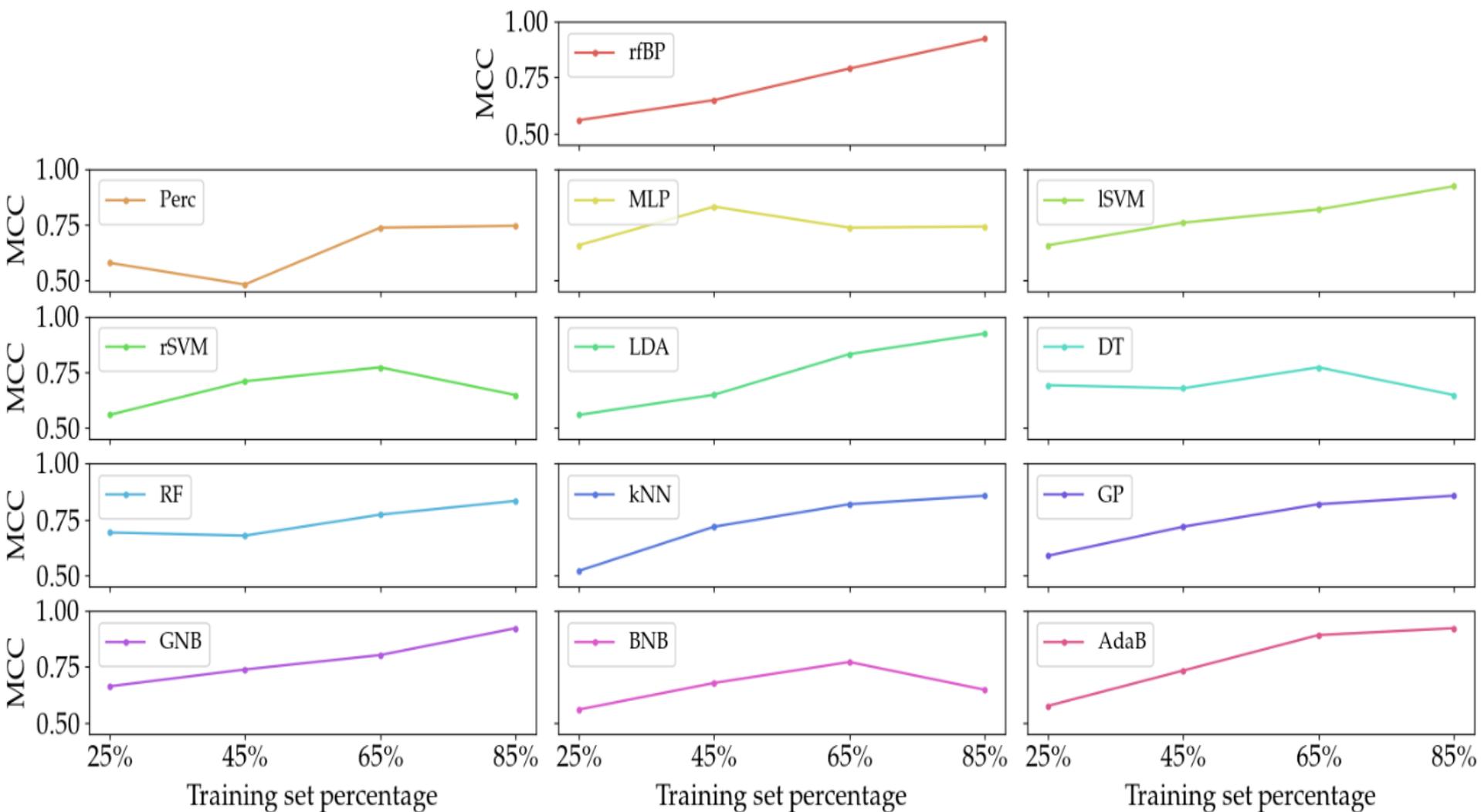


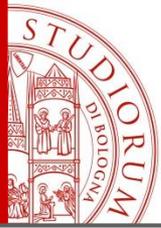
Performances



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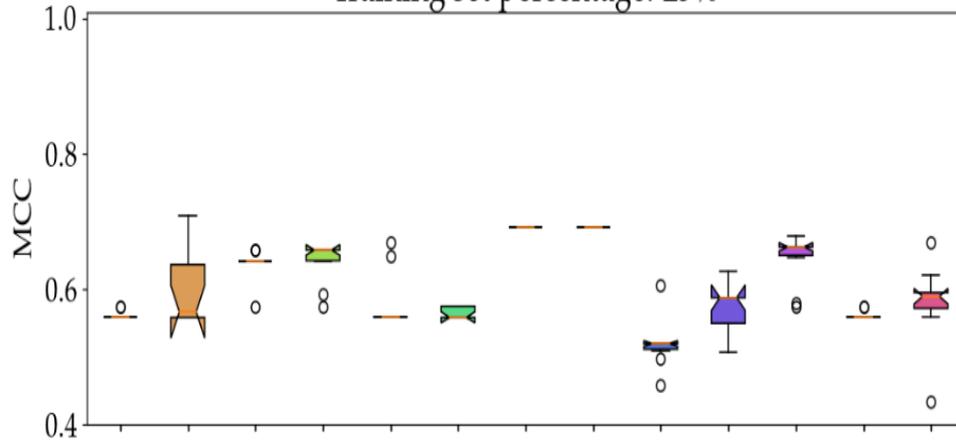
Performances



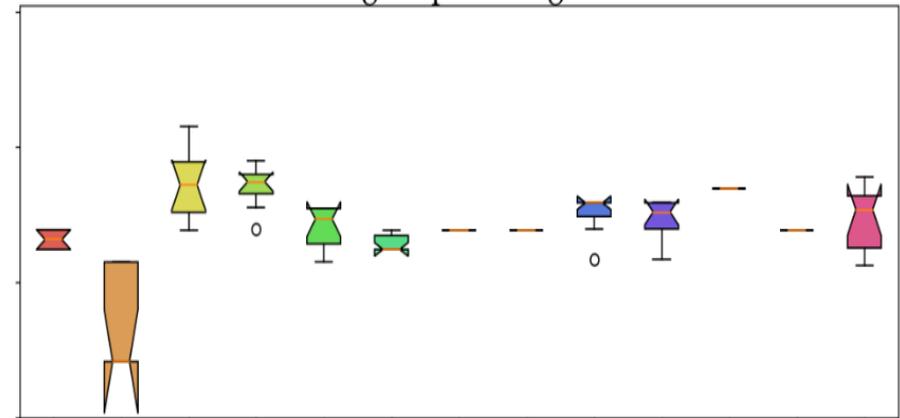
European Commission

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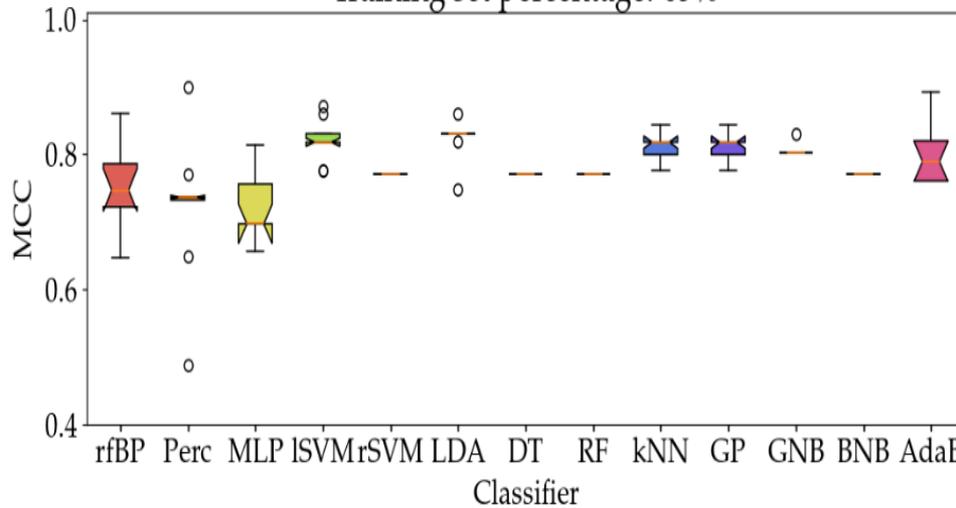
Training set percentage: 25%



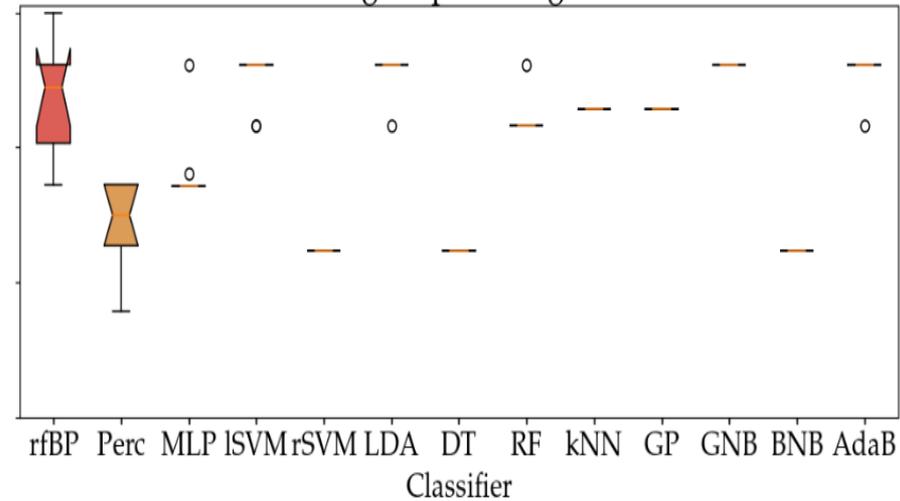
Training set percentage: 45%



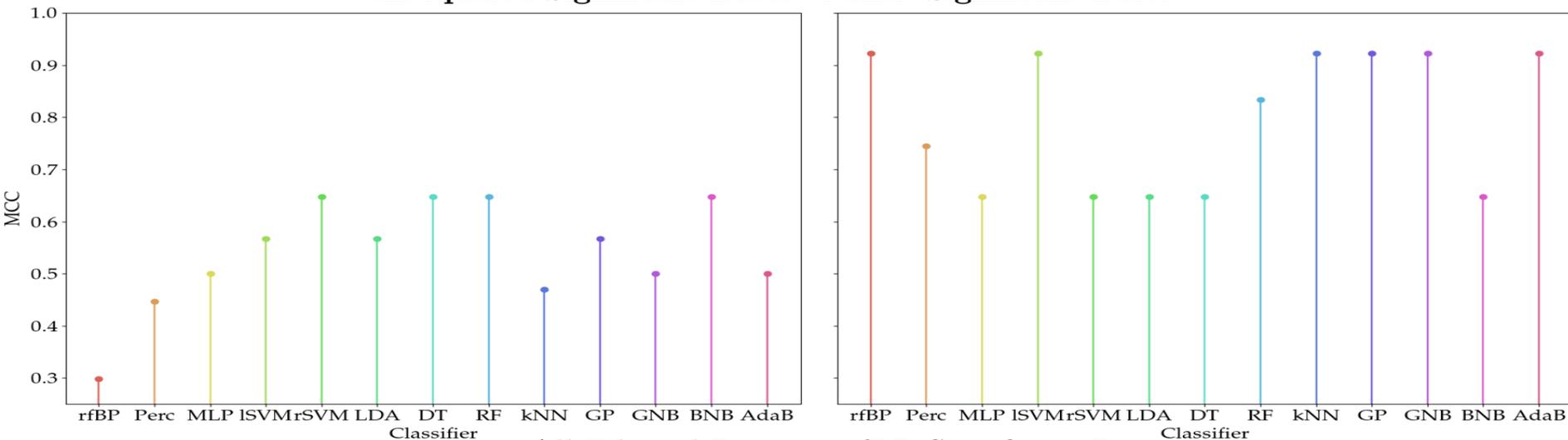
Training set percentage: 65%



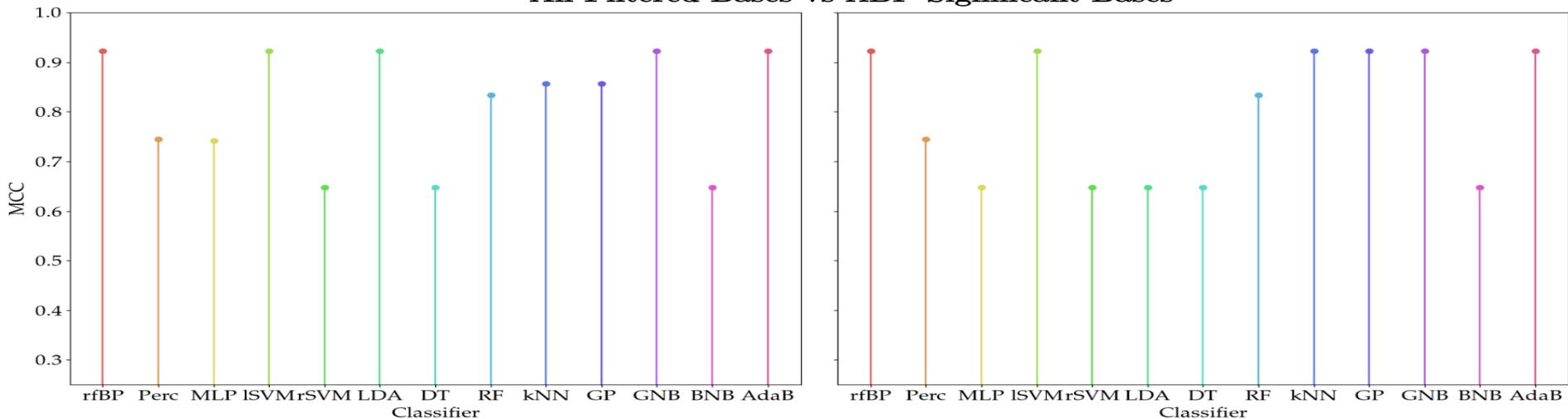
Training set percentage: 85%

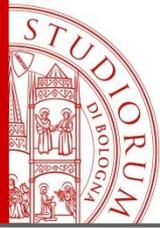


chi-squared Significant Bases vs rfBP Significant Bases



All Filtered Bases vs rfBP Significant Bases





Conclusion



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- **Classification of binary SNPs for Source Attribution is optimally performed by Entropy-maximization based algorithm called rfBP**
- **SNPs binary nature seems to favour rfBP binary properties**
- **rfBP significant bases are much better to classify than test association significant bases → can be actively used for Features Selection**
- **New C++ and Python (scikit-learn format) implementations are user-friendly and can be efficiently run on real data**

Link: <https://github.com/Nico-Curti/rFBP>



Acknowledgement



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