

Optimally choosing PWM motif databases and
sequence scanning approaches based on ChIP-seq data
– Supplementary materials

Michał Dąbrowski, Norbert Dojer, Izabella Krystkowiak, Bozena Kaminska, Bartek Wilczynski

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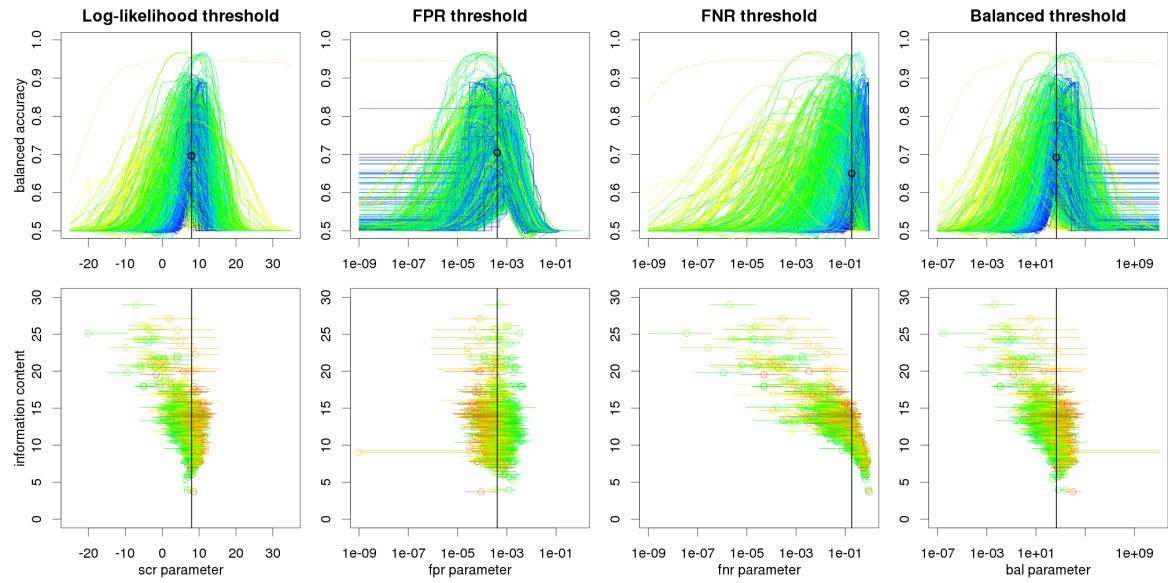


Figure 1: Balanced accuracies for various approaches to threshold selection (vs 3rd exons).

Top row: balanced accuracy vs threshold parameter. Colors represent motif information content: from blue (low), through green and yellow to beige (high). Vertical black lines indicate optimal thresholds, black circles indicate corresponding average balanced accuracies. Bottom row shows how (sub-)optimal parameter values of a motif (X-axis) depends on its information content. For each motif, a circle represents parameter value yielding maximal balanced accuracy and a horizontal line represents a parameter range, for which BA is at least 95% of the maximum. Colors represent motif AUC: from green (low), through yellow to red (high). Balanced accuracies are calculated with respect to negative sequences composed of 3rd exons.

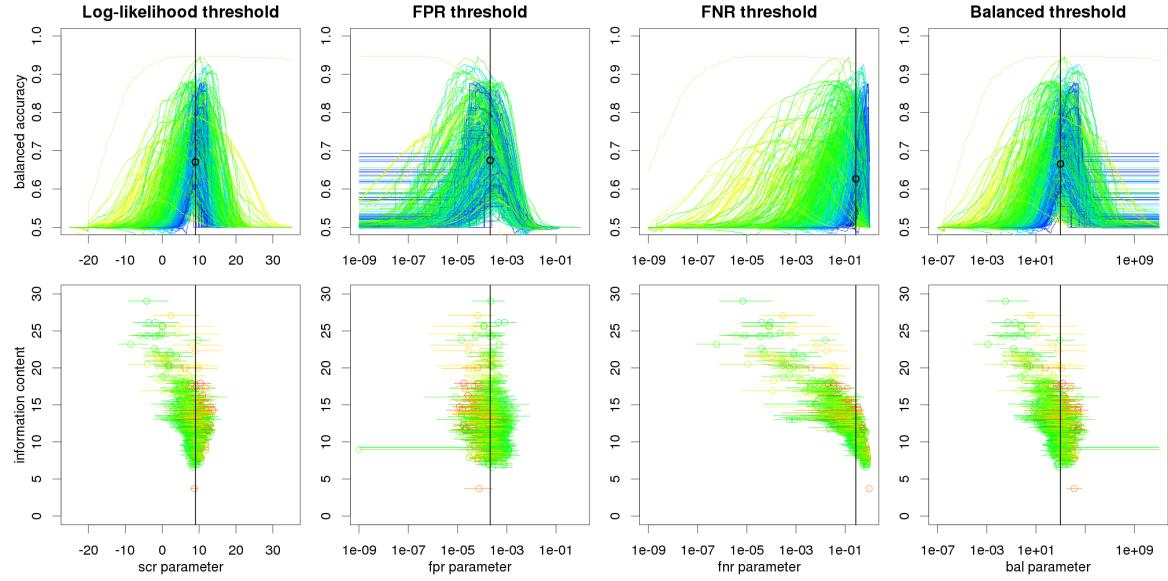


Figure 2: Balanced accuracies for various approaches to threshold selection (vs shuffled peaks).

Top row: balanced accuracy vs threshold parameter. Colors represent motif information content: from blue (low), through green and yellow to beige (high). Vertical black lines indicate optimal thresholds, black circles indicate corresponding average balanced accuracies. Bottom row shows how (sub-)optimal parameter values of a motif (X-axis) depends on its information content. For each motif, a circle represents parameter value yielding maximal balanced accuracy and a horizontal line represents a parameter range, for which BA is at least 95% of the maximum. Colors represent motif AUC: from green (low), through yellow to red (high). Balanced accuracies are calculated with respect to negative sequences composed of ChIP-seq peaks shuffled with BiasAway.

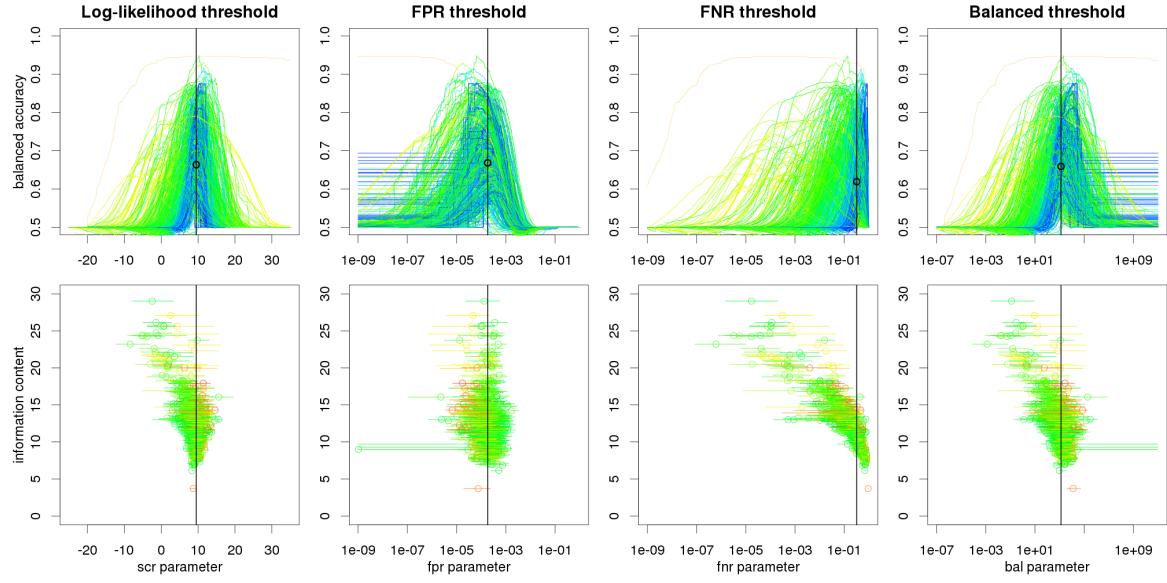


Figure 3: Balanced accuracies for various approaches to threshold selection (vs 2nd order Markov chain). Top row: balanced accuracy vs threshold parameter. Colors represent motif information content: from blue (low), through green and yellow to beige (high). Vertical black lines indicate optimal thresholds, black circles indicate corresponding average balanced accuracies. Bottom row shows how (sub-)optimal parameter values of a motif (X-axis) depends on its information content. For each motif, a circle represents parameter value yielding maximal balanced accuracy and a horizontal line represents a parameter range, for which BA is at least 95% of the maximum. Colors represent motif AUC: from green (low), through yellow to red (high). Balanced accuracies are calculated with respect to negative sequences generated by 2nd order Markov chain learned on ChIP-seq peaks.

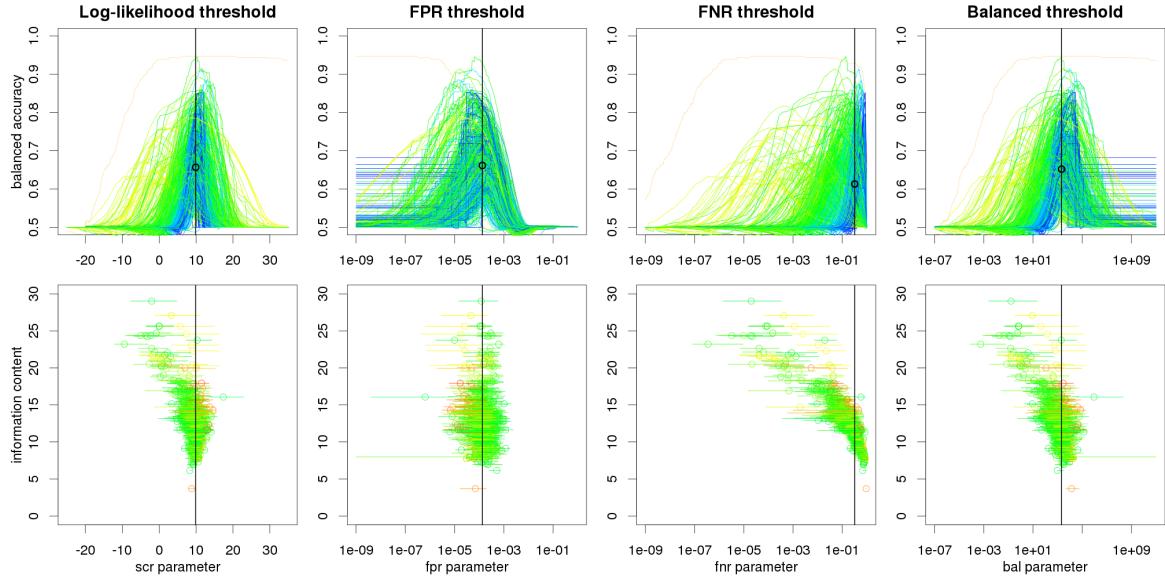


Figure 4: Balanced accuracies for various approaches to threshold selection (vs 3rd order Markov chain). Top row: balanced accuracy vs threshold parameter. Colors represent motif information content: from blue (low), through green and yellow to beige (high). Vertical black lines indicate optimal thresholds, black circles indicate corresponding average balanced accuracies. Bottom row shows how (sub-)optimal parameter values of a motif (X-axis) depends on its information content. For each motif, a circle represents parameter value yielding maximal balanced accuracy and a horizontal line represents a parameter range, for which BA is at least 95% of the maximum. Colors represent motif AUC: from green (low), through yellow to red (high). Balanced accuracies are calculated with respect to negative sequences generated by 3rd order Markov chain learned on ChIP-seq peaks.

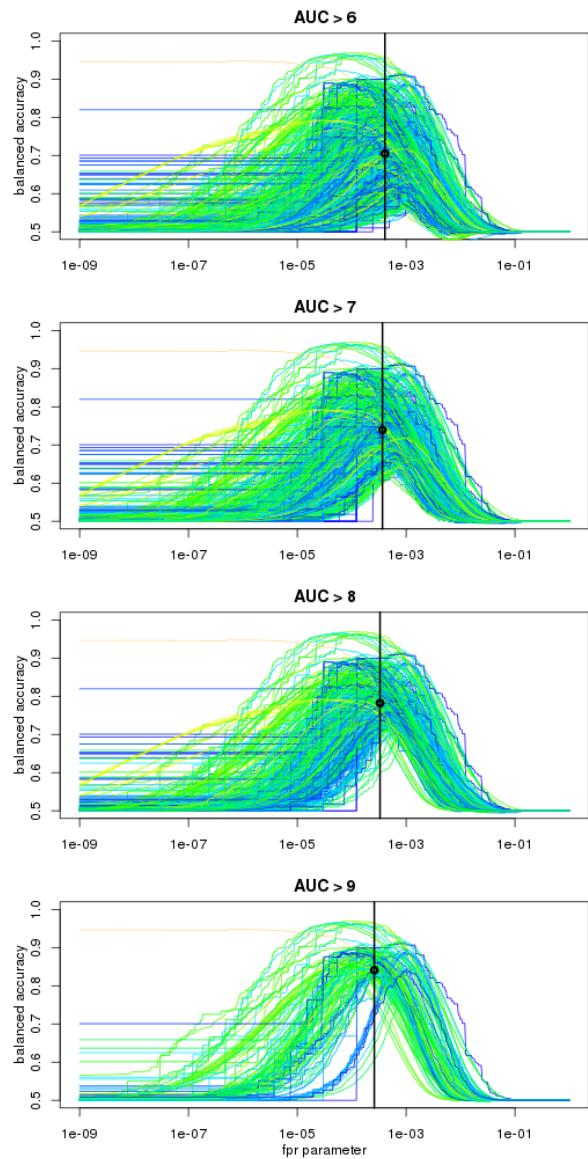


Figure 5: Balanced accuracy versus the FPR threshold for various AUC cutoffs (vs 3rd exons). Colors etc. as on Figures 1 and 2, top row. Balanced accuracies are calculated with respect to negative sequences composed of 3rd exons.

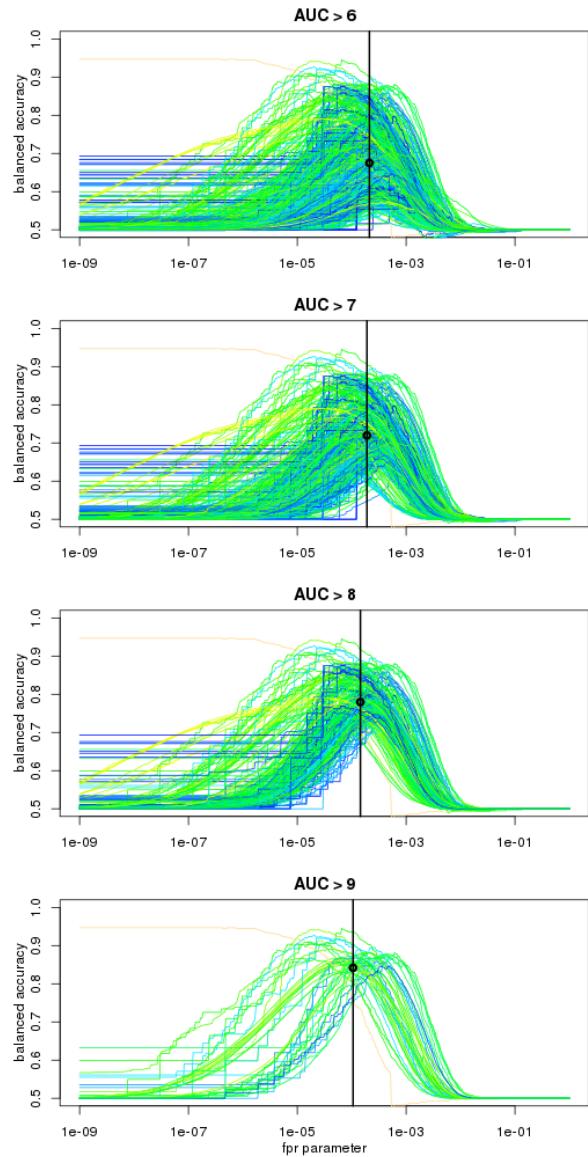


Figure 6: Balanced accuracy versus the FPR threshold for various AUC cutoffs (vs shuffled peaks). Colors etc. as on Figures 1 and 2, top row. Balanced accuracies are calculated with respect to negative sequences composed of ChIP-seq peaks shuffled with BiasAway.

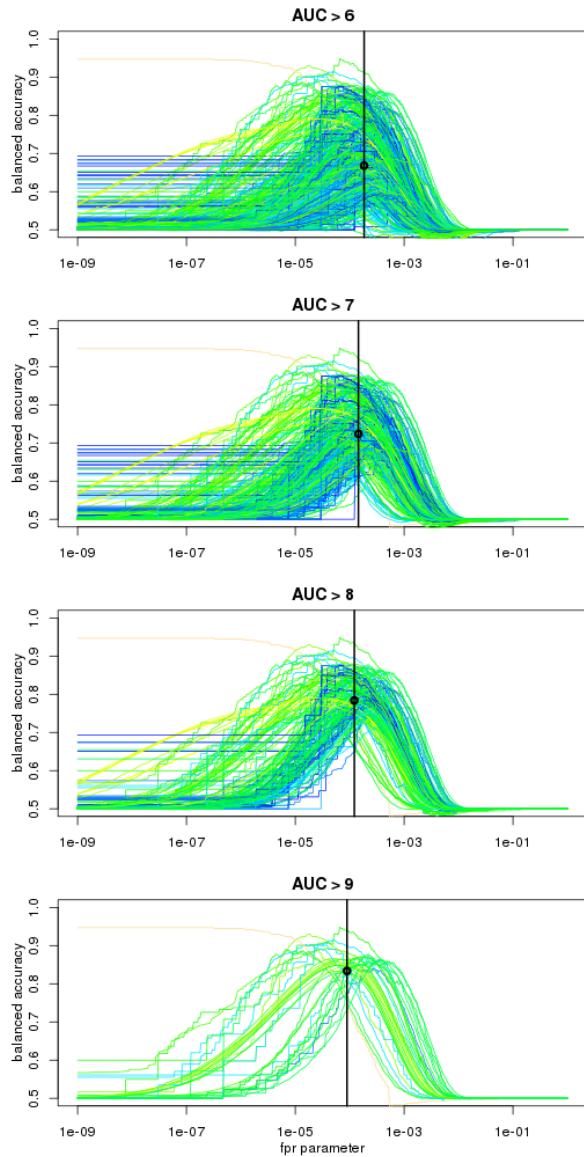


Figure 7: Balanced accuracy versus the FPR threshold for various AUC cutoffs (vs 2nd order Markov chain). Colors etc. as on Figures 1 and 2, top row. Balanced accuracies are calculated with respect to negative sequences generated by 2nd order Markov chain learned on ChIP-seq peaks.

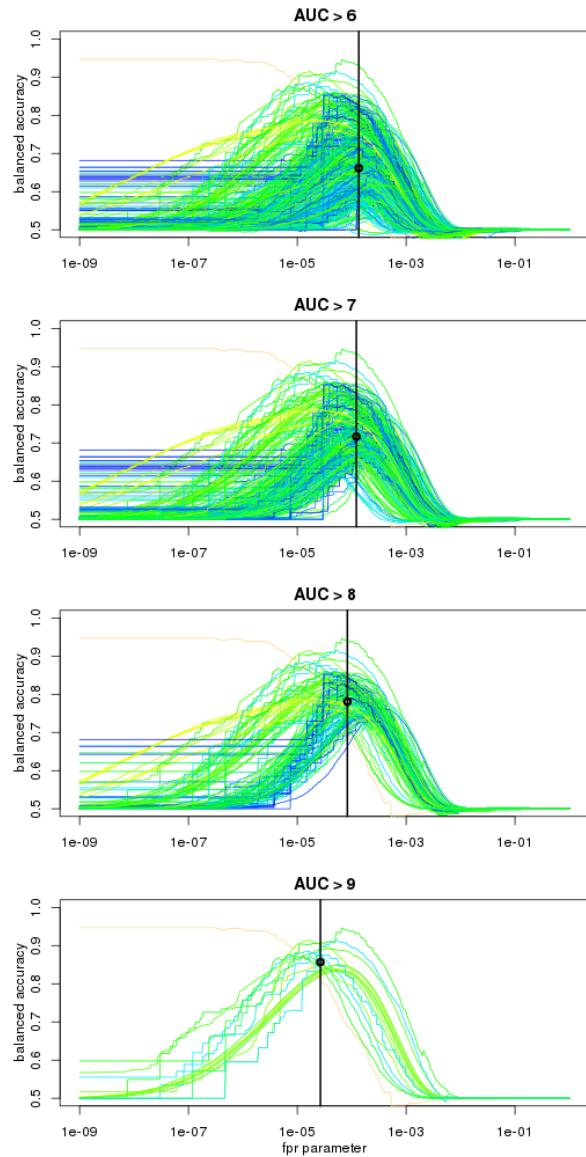


Figure 8: Balanced accuracy versus the FPR threshold for various AUC cutoffs (vs 3rd order Markov chain). Colors etc. as on Figures 1 and 2, top row. Balanced accuracies are calculated with respect to negative sequences generated by 3rd order Markov chain learned on ChIP-seq peaks.

