Phenofit calibration comparison

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This document provides some insights to compare different CMA-ES calibrations with different presence/absence subsets (*F. sylvatica* with 1000 random presence points and 1000 random absence points).

1. Species parameters

1.1. Leaf unfolding model

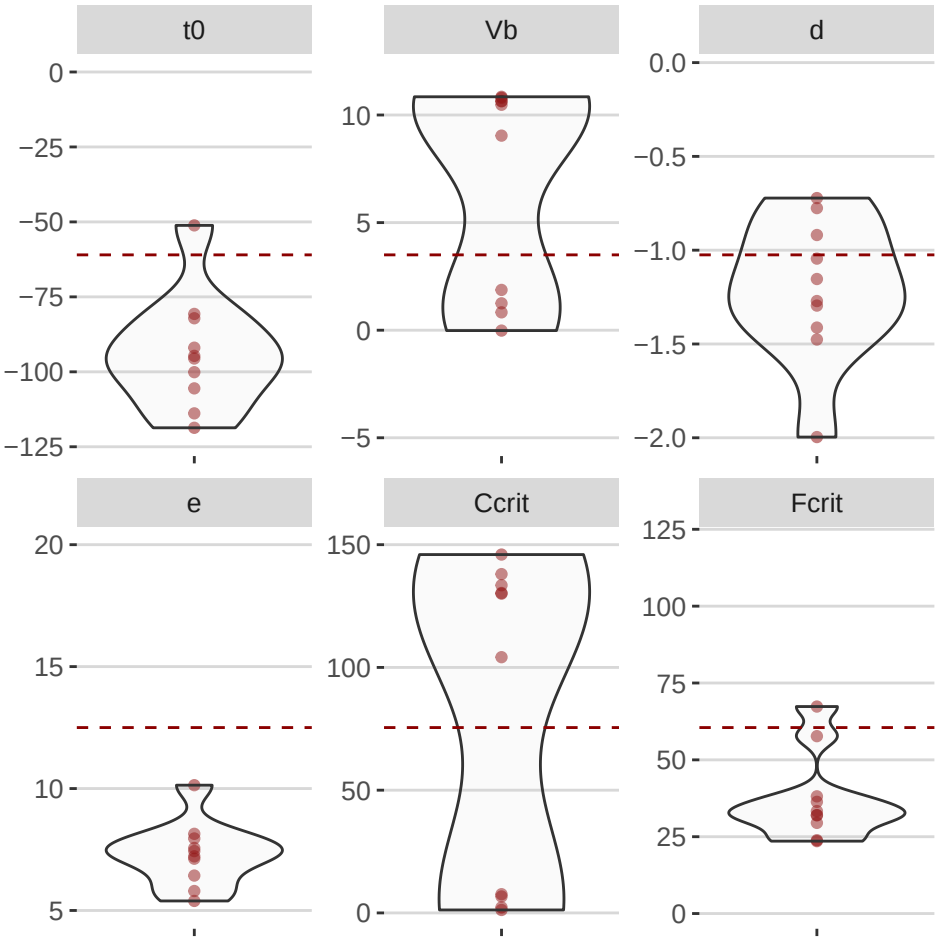

Figure 1: *Leaf unfolding model parameter values. Y-axis limits are lower and upper bounds used during calibration. Dashed line is initial parameter value.*

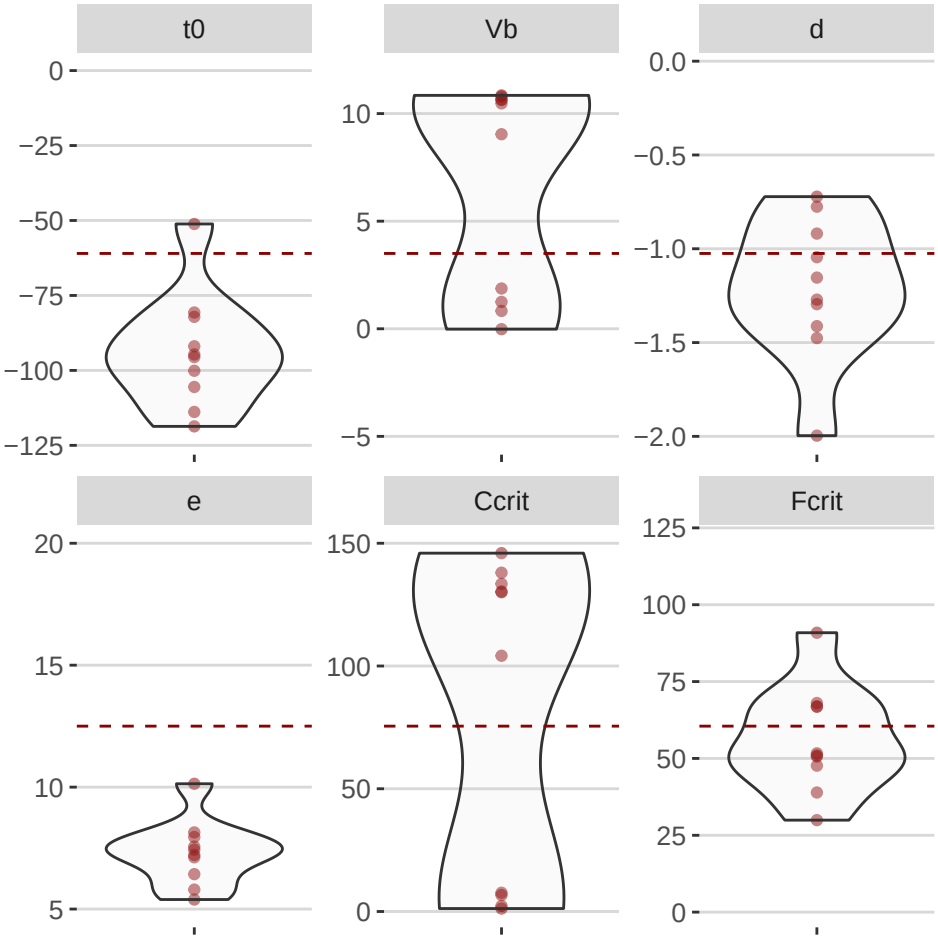

Figure 2: *Flowering model parameter values. Y-axis limits are lower and upper bounds used during calibration. Dashed line is initial parameter value.*

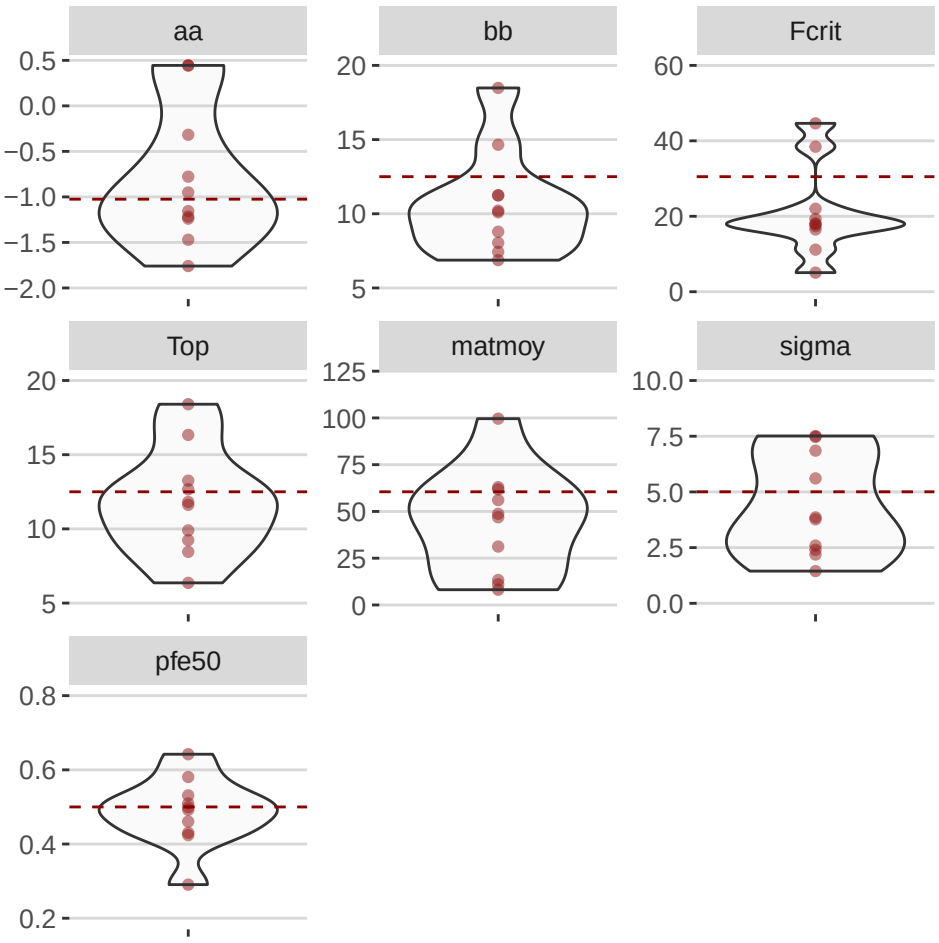

Figure 3: *Fruit maturation model parameter values. Y-axis limits are lower and upper bounds used during calibration. Dashed line is initial parameter value.*

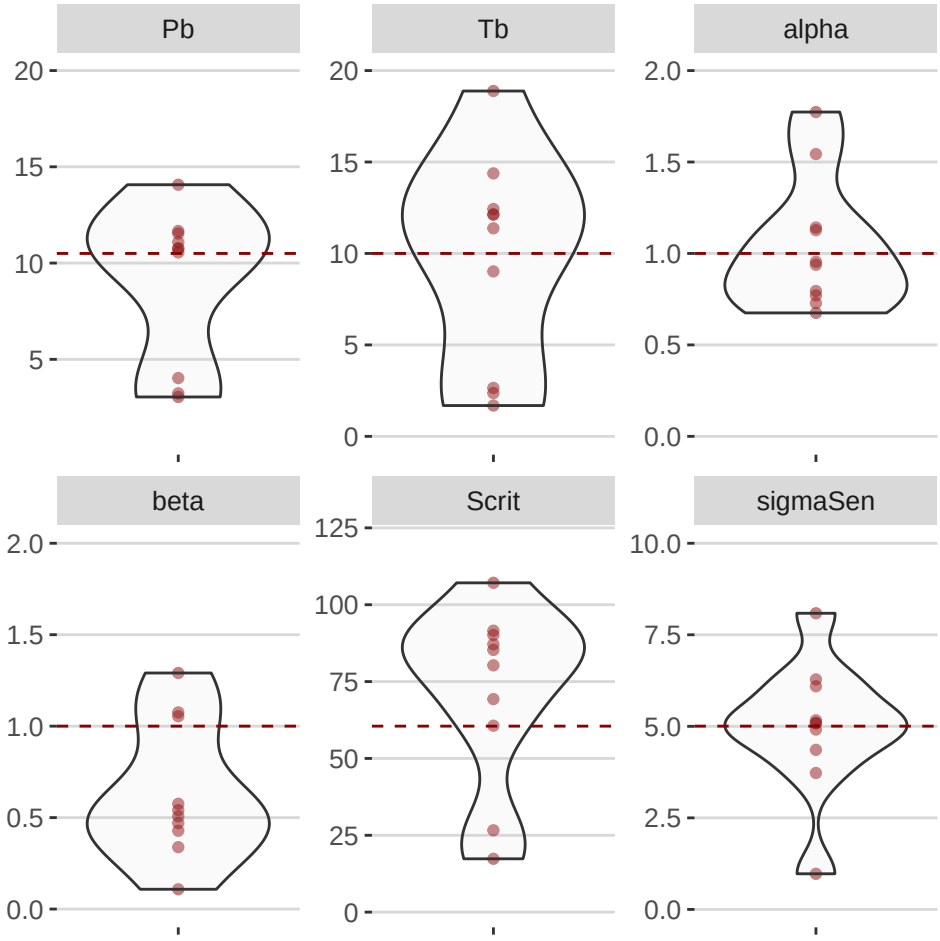

Figure 4: *Leaf senescence model parameter values. Y-axis limits are lower and upper bounds used during calibration. Dashed line is initial parameter value.*

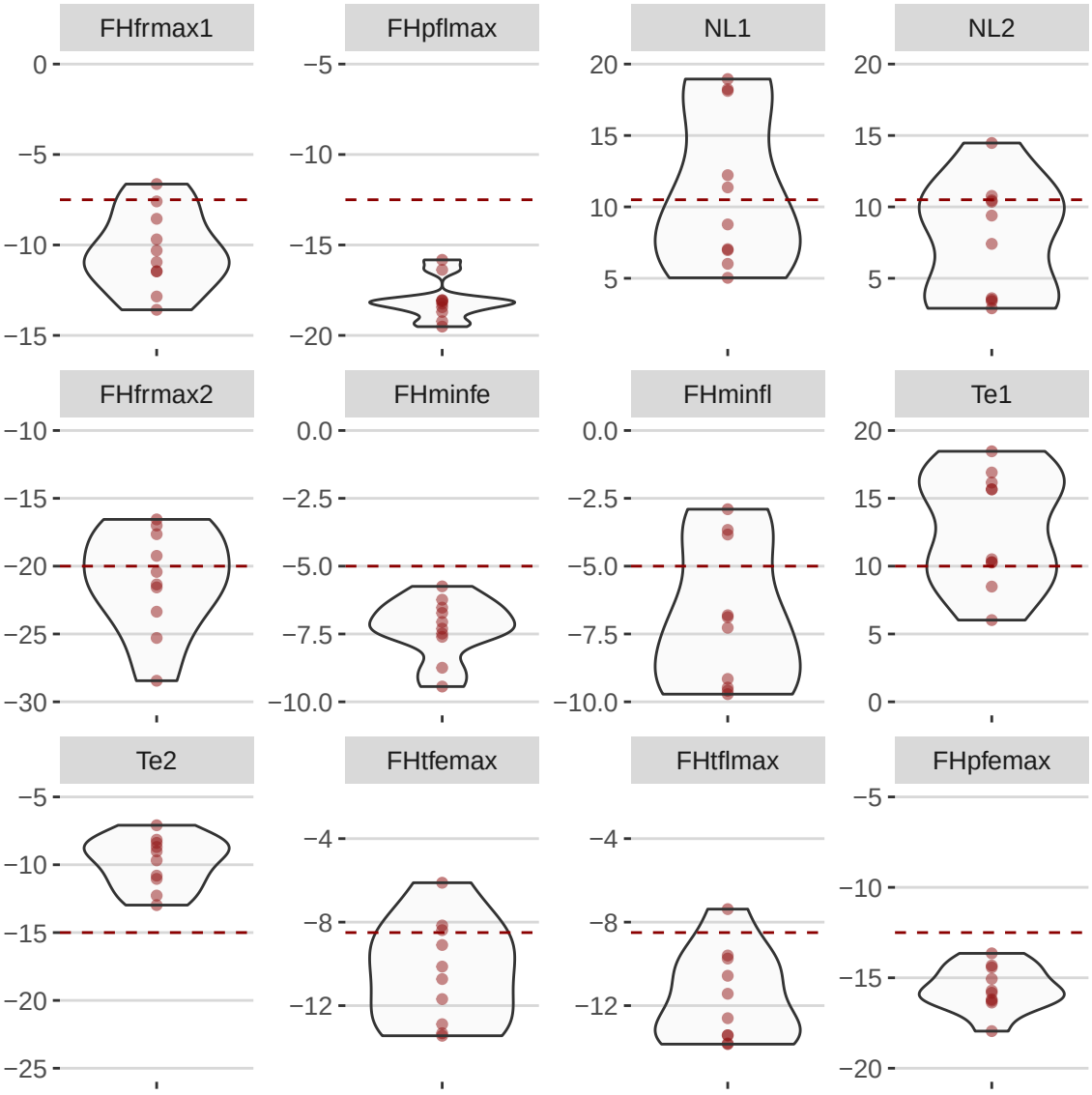

Figure 5: *Frost damage model parameter values. Y-axis limits are lower and upper bounds used during calibration. Dashed line is initial parameter value.*

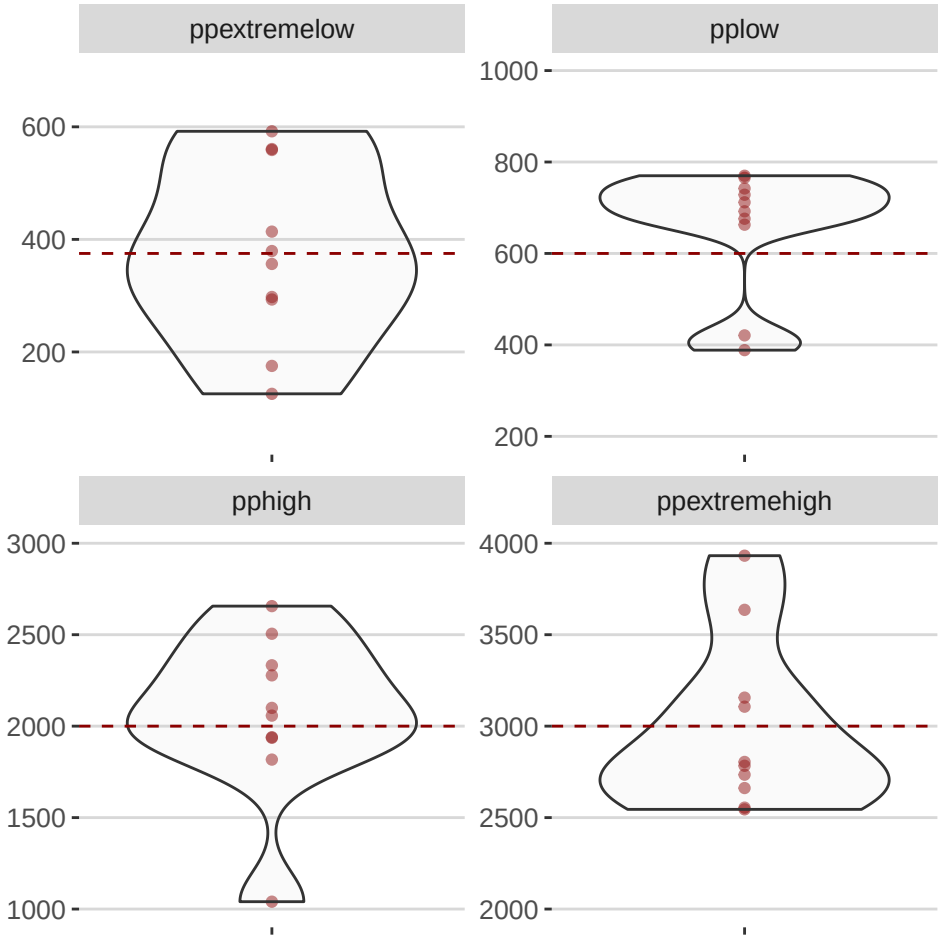

Figure 6: *Drought damage model parameter values. Y-axis limits are lower and upper bounds used during calibration. Dashed line is initial parameter value.*

2. Model outputs

2.1. Discrimination metrics

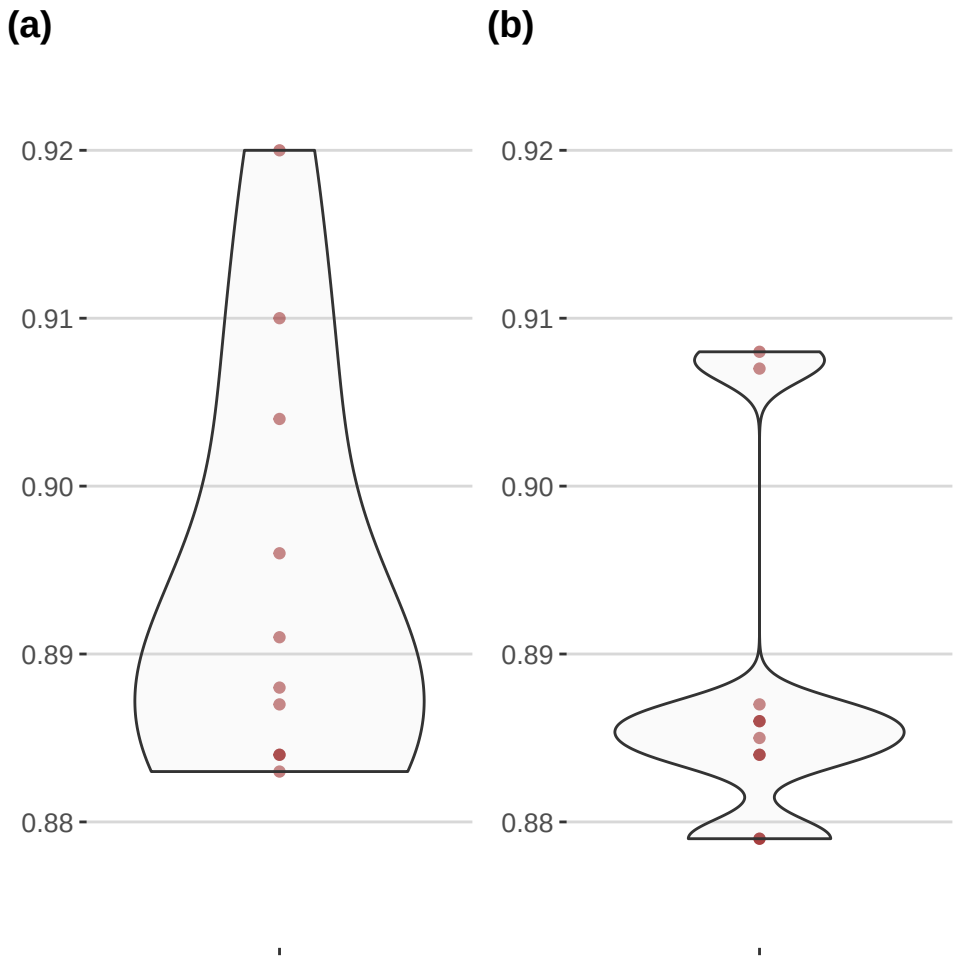

Figure 7: *AUC on (a) calibration points and (b) every presence/absence points.*

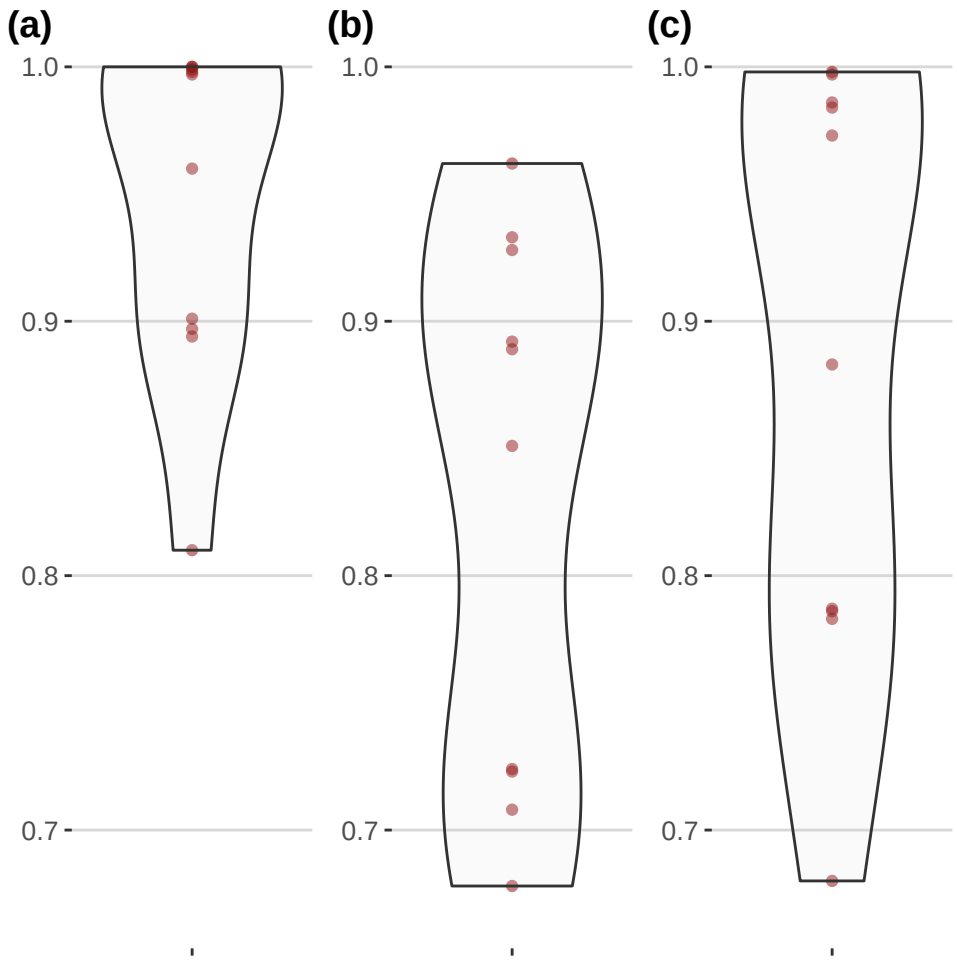

Figure 8: *Boyce index on every presence points, with (a) Spearman correlation, (b) Pearson correlation and (c) Kendall correlation.*

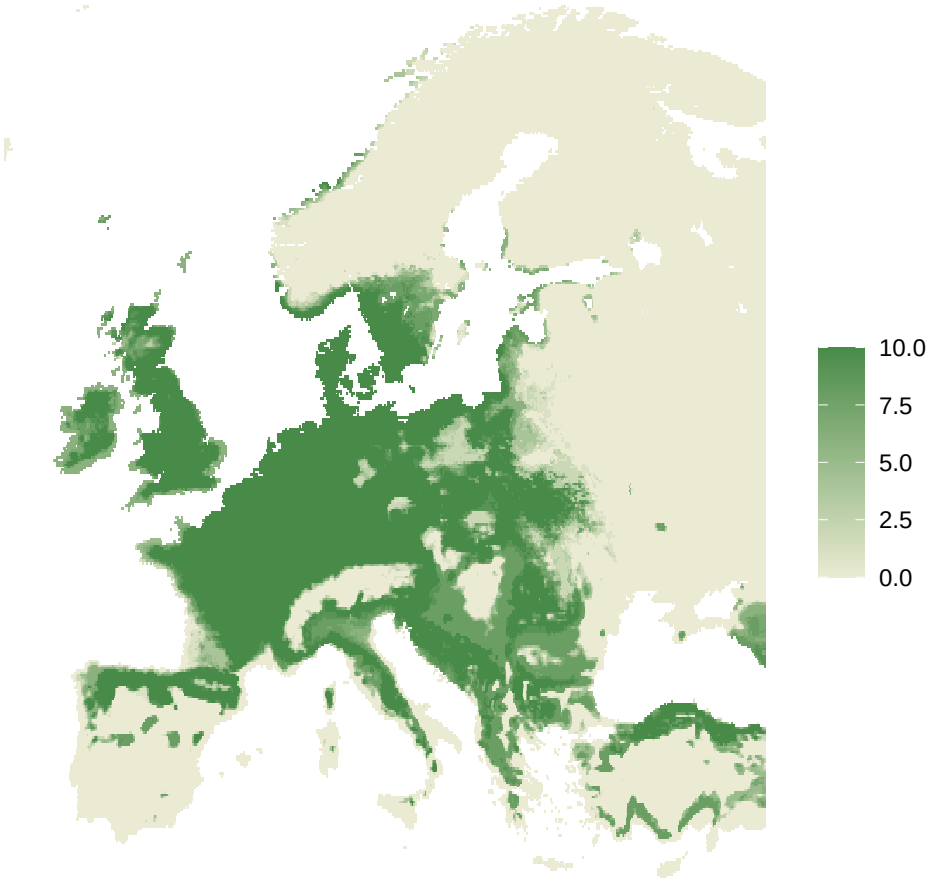

Figure 9: *Number of consensual presence predicted by models.*