

Evaluation Metrics for sjSDM (JSDM)

Threshold-independent metrics	AUC, RMSE, Spearman rank correlation coefficient
Community dissimilarity indices	Bray-Curtis dissimilarity, Jaccard distance
Species richness metrics	Species richness difference
Likelihood metrics	Independent log-likelihood (Nagelkerke's R^2), joint log-likelihood (some sort of integral over community assemblage)



Spearman rank correlation coefficient	$\frac{\text{cov}(r_{obs}, r_{pred})}{\sigma_{r_{obs}} \sigma_{r_{pred}}}$ <p>works better for QP data</p>	<p>-1-1</p> <p>>0 more correct predictions</p> <p><0 more incorrect predictions</p>
Bray-Curtis dissimilarity	$\frac{A+B-2J}{A+B}$ <p>A: # obs presences, B: # pred, J: # correctly pred</p>	<p>0-1</p> <p>0 = same composition</p> <p>1 = opposite composition</p> <p>Lower = more correct assemblage prediction</p>
Jaccard distance	$\frac{2D}{1+D}$ <p>D: Bray-Curtis</p>	
Species richness difference	<p>pred richness – obs richness</p> <p>p = predicted value, y = observed value i = species or samples, and then average across species</p>	<p>$-\infty - \infty$</p> <p>>0 overpredicts species richness</p> <p><0 underpredicts species richness</p>
Nagelkerke's R ²	$L_p = \prod_i (p_i y_i + (1 - p_i)(1 - y_i))$ $\frac{1 - (L_0 / L_p)^{2/N}}{1 - L_0^{2/N}}$ <p>N = number of samples or species</p>	$R^2 = \frac{\log L_p - \log L_0}{1 - \log L_0}$