

Testing four approaches for climate-sensitive models of individual-tree mortality

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Northeastern Mensurationists Organization -- Southern
Mensurationists Joint Conference November 2, 2014

Background

- Climate change is likely to have significant effects on tree mortality.
- The development of climate-sensitive mortality is challenging due to the binary nature of mortality and its relative infrequency.
- Dependency of mortality on site, species, and stand conditions

Objective

- Compare relative model performance on the prediction of individual tree survival-mortality probabilities over time for 20 common eastern U.S. species
- Predict individual tree mortality under influence of changing climate, eventually implement into Climate-FVS.

Data

- Vegetation
 - Forest Inventory and Analysis (FIA) field plot data
- Soils
 - Soil Survey Geographic (SSURGO) online database linked to FIA by plot geographic coordinates.
- Climate
 - Forest Service Moscow, ID Forestry Sciences Laboratory (FSL) online database linked to FIA by plot geographic coordinates.
 - Contemporary climate records for 1961–1990

Predictors

- Response variable: tree status at time two
- 7 Tree & stand related variables at time one
 - N, number of trees per hectare (trees ha⁻¹);
 - BA, stand basal area (m² ha⁻¹);
 - Tree DBH (cm) and its inversed and squared forms DBH⁻¹ and DBH²;
 - QMD, quadratic mean diameter (cm);
 - RDBH, ratio of individual tree DBH to plot QMD;
 - SCsp, percentage of stand basal area by species component.
 - The length of the measurement interval (L, years)
- 21 Climate variables
 - Annual temperature & precipitation
 - Seasonal temperature & precipitation
 - Various indices of dryness & seasonality
- 13 soils variables
 - Water holding capacity, texture and depth
 - Slope gradients
 - Chemistry (pH) and erodibility

Table 1 Summary statistics and mortality status by species

Species code	Scientific name	Common name	n	Mortality	L		QMD (cm)	
				%	Mean	sd	Mean	sd
1	loblolly pine	<i>Pinus taeda</i>	147,134	5.0	6.6	3.7	20.6	4.9
2	red maple	<i>Acer rubrum</i>	92,139	2.3	5.2	1.6	24.5	4.6
3	sugar maple	<i>Acer saccharum</i>	51,635	0.4	5.0	0.8	25.6	4.5
4	white oak	<i>Quercus alba</i>	42,026	2.2	5.2	2.1	25.9	4.7
5	sweetgum	<i>Liquidambar styraciflua</i>	40,508	5.3	6.3	3.4	24.8	5.4
6	yellow-poplar	<i>Liriodendron tulipifera</i>	25,640	4.4	5.3	2.3	26.1	5.7
7	northern red oak	<i>Quercus rubra</i>	25,174	1.9	5.0	1.4	26.0	5.0
8	eastern white pine	<i>Pinus strobus</i>	19,504	0.9	4.9	0.9	25.1	5.2
9	shortleaf pine	<i>Pinus echinata</i>	19,289	6.9	6.0	3.6	23.5	4.3
10	post oak	<i>Quercus stellata</i>	19,064	3.8	6.7	4.4	23.8	4.3
11	chestnut oak	<i>Quercus prinus</i>	18,470	2.4	5.0	1.4	26.2	4.6
12	black cherry	<i>Prunus serotina</i>	18,115	2.5	5.3	1.8	24.2	5.1
13	black oak	<i>Quercus velutina</i>	17,671	3.8	5.4	2.4	25.5	4.9
14	eastern hemlock	<i>Tsuga canadensis</i>	17,084	0.7	5.0	0.8	25.9	4.6
15	eastern redcedar	<i>Juniperus virginiana</i>	15,407	3.6	5.4	2.5	22.2	4.0
16	water oak	<i>Quercus nigra</i>	15,379	7.0	6.8	3.6	24.9	5.7
17	green ash	<i>Fraxinus pennsylvanica</i>	14,719	3.7	5.9	2.8	25.2	5.6
18	white ash	<i>Fraxinus americana</i>	14,279	1.4	5.2	1.4	24.9	5.0
19	American beech	<i>Fagus grandifolia</i>	13,811	0.8	5.2	1.5	26.3	5.1
20	white willow	<i>Salix alba</i>	11,604	2.9	5.5	2.3	25.4	5.7

Method

- Predict individual tree survival-mortality probabilities over time using four classification methods:

- Logistic regression ignoring measurement interval length (LR1)

$$P = \frac{1}{1 + e^{-(\beta_0 + \beta_1 + \dots + \beta_k x_k)}}$$

- Generalized logistic regression modeling with a variable measurement interval (LR2)

$$P = \left(\frac{1}{1 + e^{-(\beta_0 + \beta_1 + \dots + \beta_k x_k)}} \right)^L$$

- Artificial neural networks (ANN)
- Random forests (RF)

Model Comparison

- Mean absolute deviation (MAD) (Burkhardt, 2012)

$$MAD = \frac{\sum_{i=1}^{i=n_{OOB}} |p_i - \hat{p}_i|}{n_{OOB}}$$

- where n_{OOB} is the number of OOB or validation observations for each bootstrap replicate
- p_i the i^{th} OOB observed value, and \hat{p}_i the prediction of p_i .
- ROC plots and Areas Under the Curve (AUC) (Fawcett, 2006)
 - sensitivity or true positive rate
 - specificity or true negative rate

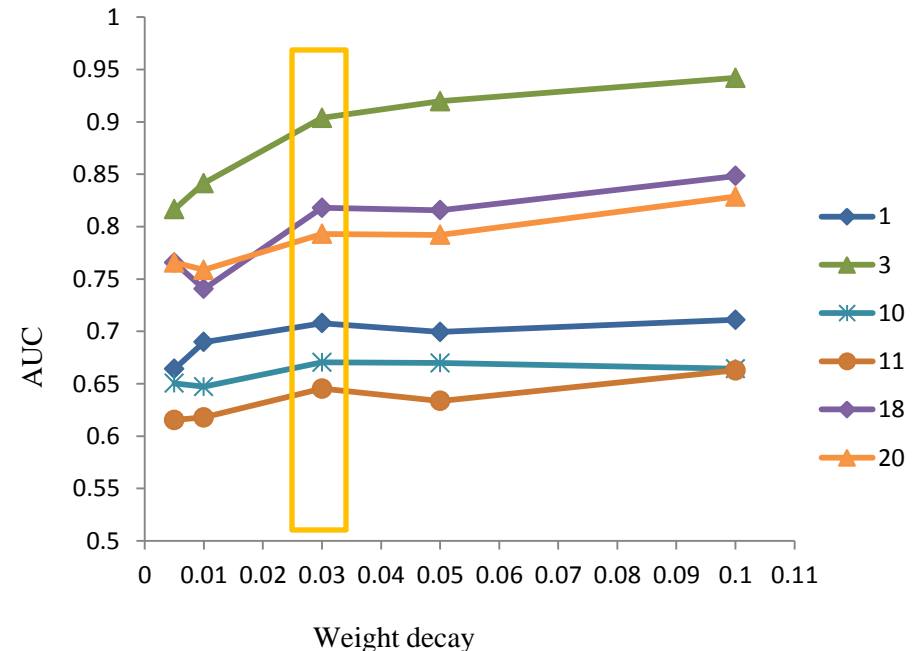
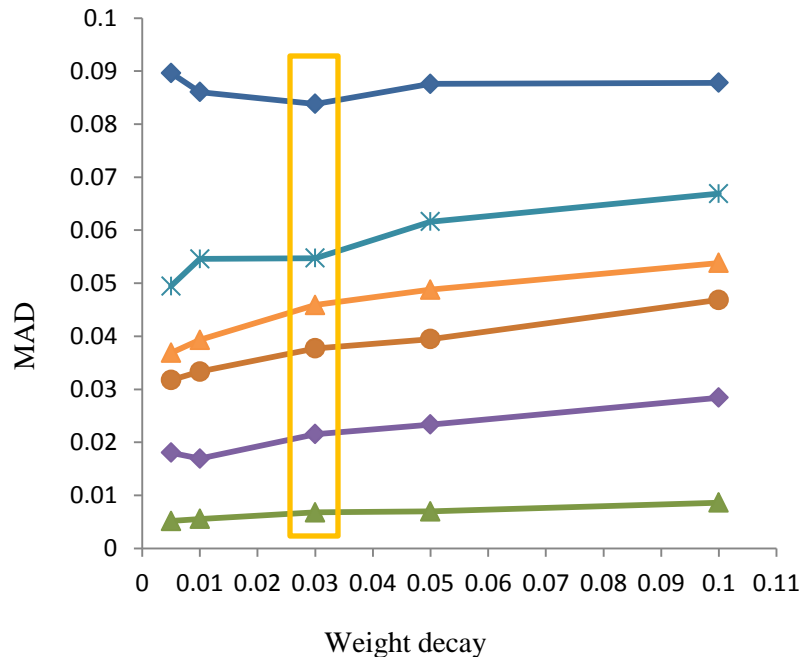
Data Preparation

- Project soils and climate variables into components via PCA.
 - First five components were retained to explain > 80% of variance.
- Variable selection

Species	Selected Variables (VIF <10)
Shortleaf pine and Black cherry	N, SCsp, DBH ⁻¹ , DBH ² , QMD, L, PCAcom1, PCAcom2, PCAcom3, PCAcom4, PCAcom5
Other species	BA, N, SCsp, DBH ⁻¹ , DBH ² , QMD, L, PCAcom1, PCAcom2, PCAcom3, PCAcom4, PCAcom5

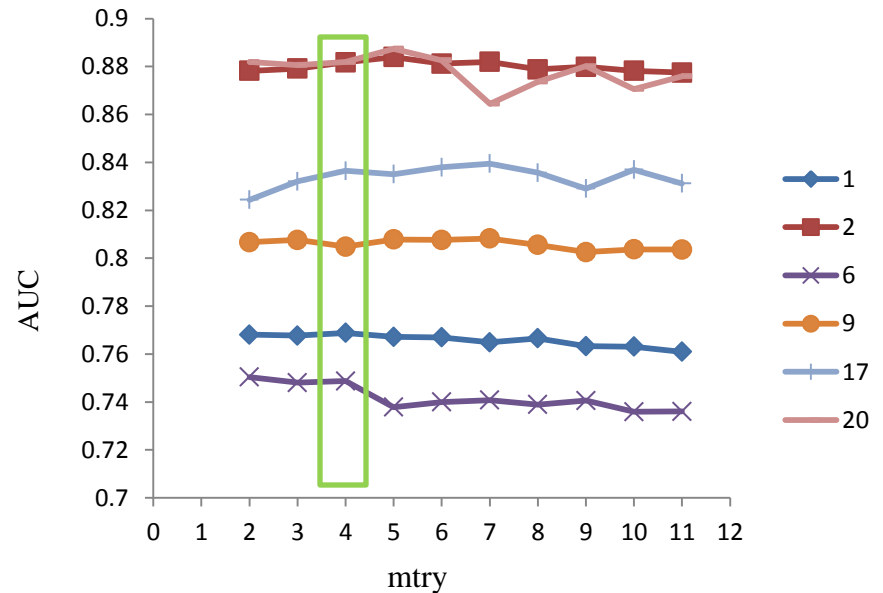
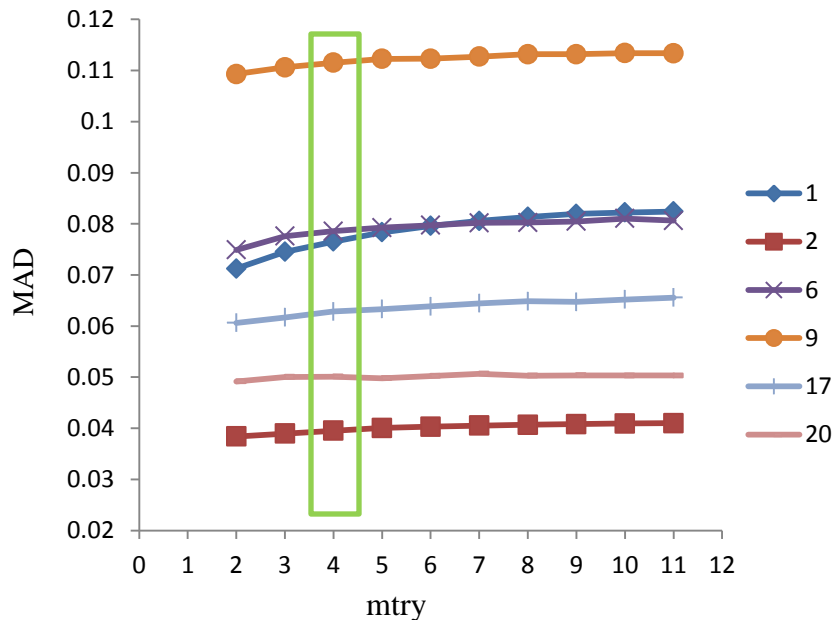
Parameter tuning

- ANN models close to optimum
 - Single hidden layer with 20 neurons was set. Inspecting the validation error versus weight decay (0.005, 0.01, 0.03, 0.05 and 0.1, MAD and AUC in the test data were increasing with rising value of weights and compromised at 0.03 for most species.



Parameter tuning

- RF models close to optimum
 - `ntree = 500` was selected. Inspecting the validation error versus “`mtry`” from 2 to 11 to find an random forest structure close to optimum. Setting `mtry` equals to 3 generally gave near optimum results for most species based on the trade-off benefits of MAD and AUC.



Model comparison

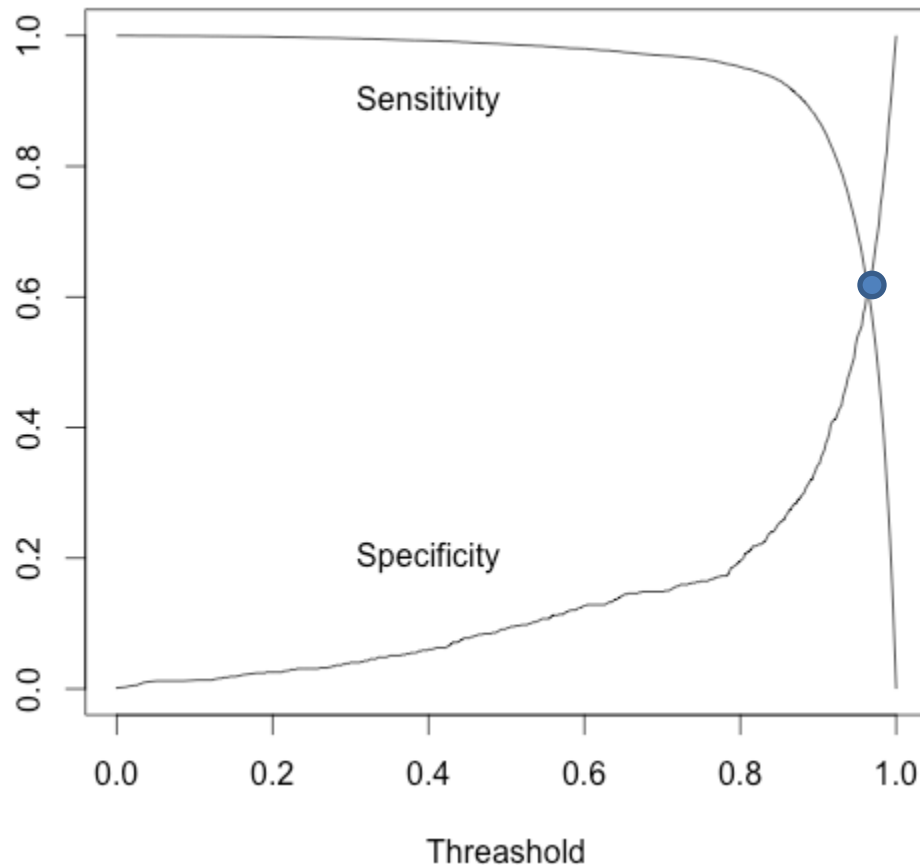
- Ranking model performances for an individual species
 - Bootstrap from the original dataset, splitting into in-bag training data and out-of-bag validation data.
 - Build/fit LR1,LR2,RF, and ANN models based on training data
 - Test models using MAD and AUC with validation data.
 - Compute pairwise differences
$$\begin{aligned} \text{MADD}_{ij} &= \text{MAD}_i - \text{MAD}_j \\ \text{AUCD}_{ij} &= \text{AUC}_i - \text{AUC}_j \end{aligned} \quad i \neq j \in \{\text{LR1, LR2, RF, ANN}\}$$
 - Repeat the bootstrap procedure 40 times.
 - Conduct Student's paired t test $H_0: \overline{\text{MADD}_{ij}} = 0$ from 40 bootstrap values of MADD_{ij} and $H_0: \overline{\text{AUCD}_{ij}} = 0$ from 40 bootstrap values of AUCD_{ij} separately.
 - Rank LR1,LR2,RF, and ANN and repeat for other species.

Model comparison

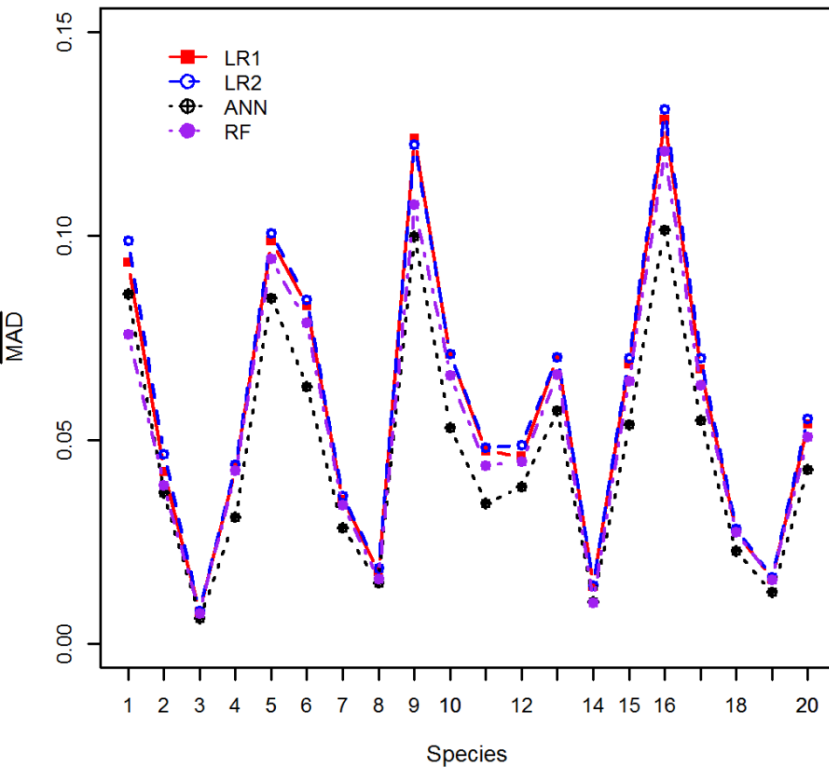
- Ranking model performances regardless of species
 - Compute bootstrap averages \overline{MAD} and \overline{AUC} for each species
 - Compute pairwise differences
$$\overline{MADD}_{ij} = \overline{MAD}_i - \overline{MAD}_j$$
$$\overline{AUCD}_{ij} = \overline{MAD}_i - \overline{MAD}_j \quad i \neq j \in \{\text{LR1, LR2, RF, ANN}\}$$
 - Repeat for all 20 species
 - Conduct Wilcoxon signed-rank test $H_0: \widetilde{\overline{MADD}}_{ij} = 0$ from 20 species values of \overline{MADD}_{ij} and $H_0: \widetilde{\overline{AUCD}}_{ij} = 0$ from 20 species values of \overline{AUCD}_{ij}
 - Rank LR1,LR2,RF, and ANN

Threshold selection

- Choose the optimal threshold by balancing the sensitivity and specificity of model prediction on validation data.

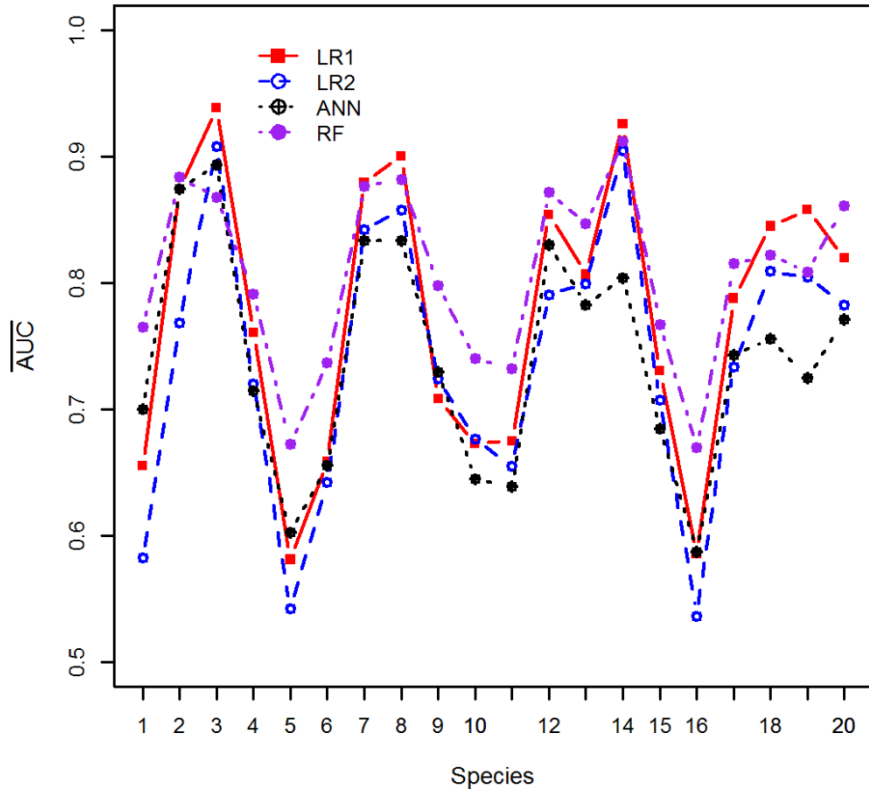


Student's paired t test on MADs over 40 bootstraps



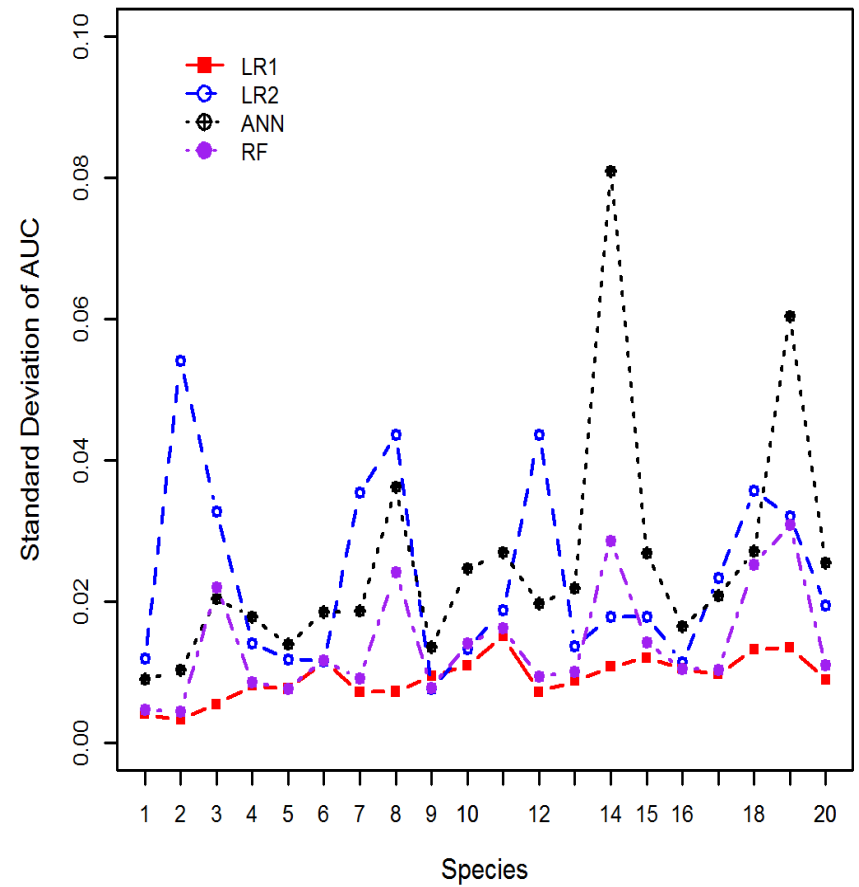
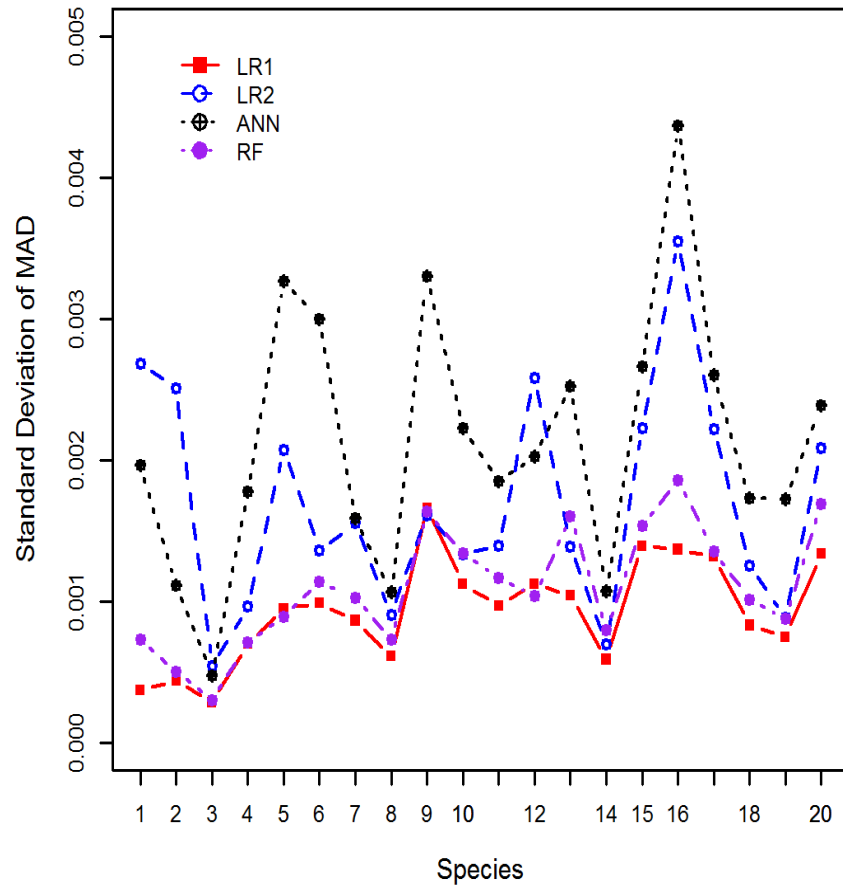
Species	\overline{MAD}							
	LR1	R	LR2	R	ANN	R	RF	R
1	0.0936	3	0.0988	4	0.0858	2	0.0759	1
2	0.0422	3	0.0464	4	0.037	1	0.0389	2
3	0.0077	3	0.008	4	0.0062	1	0.0074	2
4	0.0431	3	0.0438	4	0.031	1	0.0424	2
5	0.0989	3	0.1007	4	0.0847	1	0.0945	2
6	0.0829	3	0.0843	4	0.0631	1	0.0787	2
7	0.0352	3	0.0362	4	0.0284	1	0.0339	2
8	0.0176	3	0.0185	4	0.0149	1	0.0158	2
9	0.1239	4	0.1224	3	0.0999	1	0.1077	2
10	0.071	3	0.0711	3	0.053	1	0.0658	2
11	0.0473	3	0.0482	4	0.0344	1	0.0437	2
12	0.0459	3	0.0487	4	0.0385	1	0.0447	2
13	0.0702	3	0.0703	3	0.0571	1	0.0661	2
14	0.014	3	0.0143	4	0.0103	1	0.01	1
15	0.0686	3	0.07	4	0.0537	1	0.0644	2
16	0.1285	3	0.1311	4	0.1014	1	0.1209	2
17	0.0673	3	0.07	4	0.0548	1	0.0635	2
18	0.0274	2	0.0282	4	0.0227	1	0.0273	2
19	0.0158	2	0.0163	4	0.0126	1	0.0157	2
20	0.0538	3	0.0552	4	0.0427	1	0.0507	2

Student's paired t test on AUCs over 40 bootstraps



Species	\overline{AUC}							
	LR1	R	LR2	R	ANN	R	RF	R
1	0.6552	3	0.5821	4	0.7002	2	0.7648	1
2	0.8741	2	0.7688	4	0.8743	2	0.8837	1
3	0.9389	1	0.9079	2	0.8937	3	0.8676	4
4	0.7607	2	0.72	3	0.7145	3	0.7912	1
5	0.5811	3	0.5422	4	0.6024	2	0.6725	1
6	0.6586	2	0.6419	3	0.6553	2	0.7369	1
7	0.8797	1	0.8425	2	0.8338	2	0.8768	1
8	0.9004	1	0.858	3	0.8333	4	0.8823	2
9	0.7084	4	0.7239	3	0.7296	2	0.7982	1
10	0.673	2	0.6762	2	0.6448	4	0.7402	1
11	0.675	2	0.6551	3	0.6388	4	0.7322	1
12	0.8542	2	0.7907	4	0.8302	3	0.8718	1
13	0.8068	2	0.7997	3	0.7828	4	0.8473	1
14	0.9261	1	0.9045	3	0.8038	4	0.912	2
15	0.7303	2	0.7074	3	0.6846	4	0.7672	1
16	0.5854	2	0.5359	4	0.5872	2	0.6699	1
17	0.788	2	0.7333	3	0.7429	3	0.8153	1
18	0.8451	1	0.8092	2	0.756	4	0.8224	2
19	0.8582	1	0.8047	2	0.7248	4	0.8086	2
20	0.8196	2	0.7828	3	0.7712	4	0.861	1

Model performance on SD of MADs and AUCs over 40 bootstraps



Model performance comparison over 20 species

Wilcoxon signed rank test on model comparison over 20 species: The median, $\overline{\widetilde{MADD}}$, of 20 paired differences ($\overline{\widetilde{MADD}} = \overline{MAD}_{\text{row}} - \overline{MAD}_{\text{column}}$), The median, $\overline{\widetilde{AUCD}}$, of 20 paired differences ($\overline{\widetilde{AUCD}} = \overline{AUC}_{\text{row}} - \overline{AUC}_{\text{column}}$)

	LR2	ANN	RF
LR1	$\overline{\widetilde{MADD}} = -0.001^*$	$\overline{\widetilde{MADD}} = 0.011^*$	$\overline{\widetilde{MADD}} = 0.004^*$
	$\overline{\widetilde{AUCD}} = 0.036^*$	$\overline{\widetilde{AUCD}} = 0.035^*$	$\overline{\widetilde{AUCD}} = -0.032^*$
LR2		$\overline{\widetilde{MADD}} = 0.013^*$	$\overline{\widetilde{MADD}} = 0.005^*$
		$\overline{\widetilde{AUCD}} = 0.044$	$\overline{\widetilde{AUCD}} = -0.07^*$
ANN			$\overline{\widetilde{MADD}} = -0.007^*$
			$\overline{\widetilde{AUCD}} = -0.071^*$

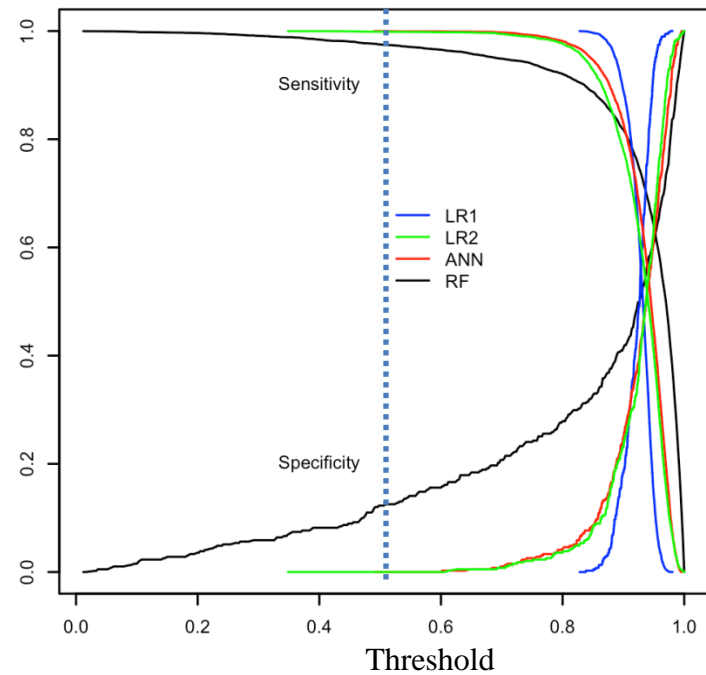
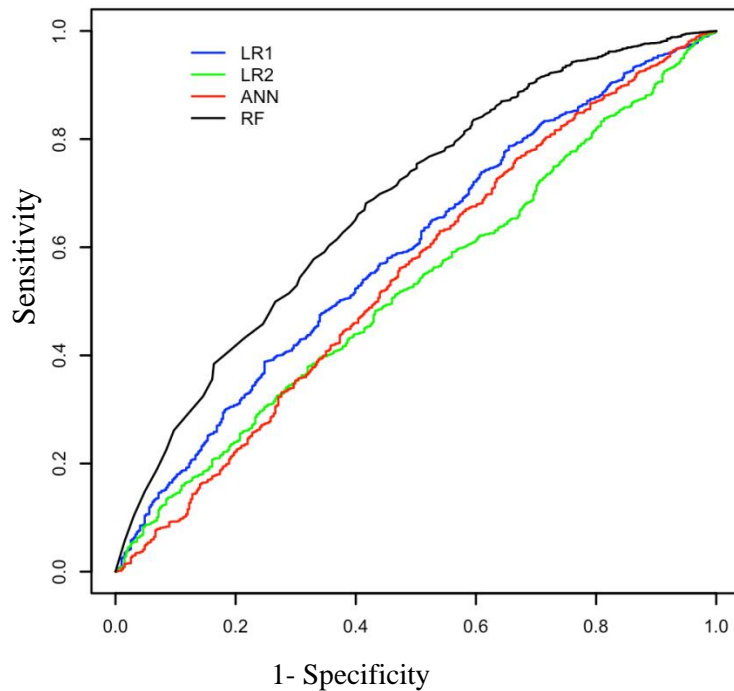
Note: * indicates significant difference between paired methods $\alpha = 0.05$

\overline{MAD} Performance : ANN < RF < LR1 < LR2

\overline{AUC} Performance : RF > LR1 > LR2 = ANN

Threshold selection

The threshold was chosen where the sensitivity equals specificity
(ex. Water oak: $n = 15,379$ 7% mort)



Threshold decision

	Species	Sensitivity				Threshold			
		LR1	LR2	ANN	RF	LR1	LR2	ANN	RF
1	loblolly pine	0.618	0.584	0.579	0.704	0.952	0.954	0.971	0.980
2	red maple	0.794	0.803	0.776	0.803	0.969	0.972	0.968	0.984
3	sugar maple	0.887	0.894	0.698	0.843	0.991	0.990	1.000	0.998
4	white oak	0.707	0.729	0.676	0.718	0.975	0.976	0.979	0.984
5	sweetgum	0.557	0.543	0.551	0.610	0.947	0.954	0.952	0.964
6	yellow-poplar	0.611	0.626	0.635	0.667	0.958	0.959	0.963	0.968
7	northern red oak	0.801	0.720	0.790	0.773	0.978	0.981	0.978	0.990
8	eastern white pine	0.828	0.837	0.995	0.794	0.988	0.988	1.000	0.998
9	shortleaf pine	0.643	0.658	0.545	0.740	0.932	0.932	0.957	0.944
10	post oak	0.608	0.637	0.586	0.700	0.962	0.968	0.978	0.978
11	chestnut oak	0.612	0.601	0.639	0.676	0.975	0.977	0.980	0.990
12	black cherry	0.772	0.700	0.755	0.795	0.970	0.978	0.985	0.972
13	black oak	0.719	0.723	0.689	0.765	0.961	0.969	0.966	0.968
14	eastern hemlock	0.844	0.844	0.703	0.891	0.990	0.990	1.000	0.996
15	eastern redcedar	0.671	0.622	0.649	0.719	0.964	0.968	0.969	0.974
16	water oak	0.563	0.520	0.540	0.627	0.929	0.939	0.942	0.952
17	green ash	0.689	0.675	0.689	0.760	0.959	0.972	0.962	0.970
18	white ash	0.753	0.696	0.737	0.771	0.983	0.987	0.987	0.990
19	American beech	0.767	0.724	0.847	0.745	0.991	0.993	1.000	0.996
20	white willow	0.724	0.723	0.606	0.756	0.967	0.970	0.996	0.978

The highest value is colored as orange.

Conclusions

- ANN models generally produced the lowest validation MAD for most species, followed by RF models.
- RF models generally gave highest validation AUC.
- Std. Dev. of bootstrap MAD and AUC showed that RF and LR1 models were more stable for mortality predictions.
- Wilcoxon signed rank test on 20 species showed that
 \overline{MAD} Performance : ANN < RF < LR1 < LR2
 \overline{AUC} Performance : RF > LR1 > LR2 > ANN
- Among four approaches, RF tended to have the highest specificity across all levels of threshold. When threshold was chosen so that sensitivity = specificity, RF models generally performed best.

Acknowledgements

- Army Corps of Engineers CERL
- USDA Forest Service
 - Forest Management Service Center
 - Moscow Forestry Sciences Lab
 - Northern Research Station & FIA
 - Southern Research Station & FIA