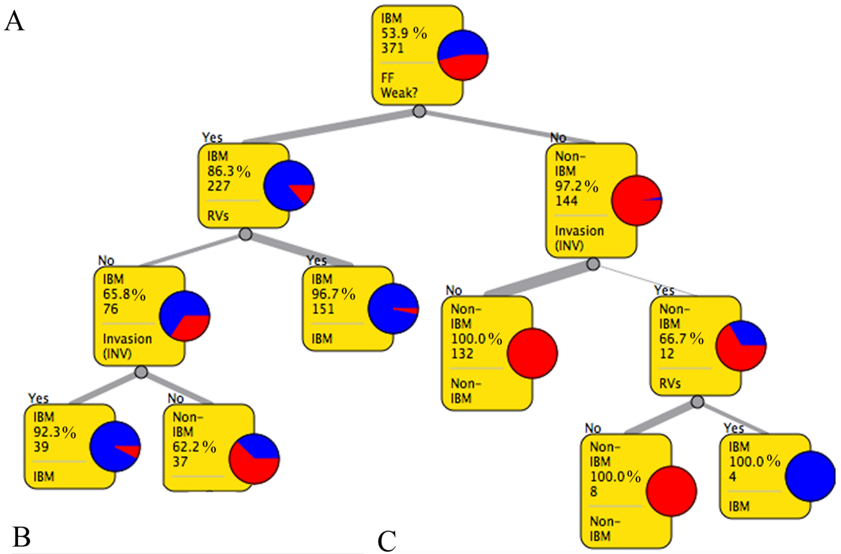
Appendix e-1. Diagnoses of non-IBM patients

Category	**# of patients (% total)**
Inflammatory Myopathy	87 (51%)
Dermatomyositis	36
Polymyositis	22
Necrotizing myopathy	22
Other inflammatory myopathy	7
Statin myopathy	11 (6%)
Muscular Dystrophy	27 (16%)
Limb Girdle Muscular Dystrophy	10
Myotonic Dystrophy	4
Fascioscapulohumeral Muscular Dystrophy	2
Oculopharyngeal Muscular Dystrophy	1
Myofibrillar Myopathy	1
Other/undefined muscular dystrophy	9
Hereditary Inclusion Body Myopathy (hIBM)	6 (4%)
Valosin Containing Protein mutation	3
GNE mutation (hIBM2)	1
Undefined mutation	2
Metabolic myopathy	11 (6%)
Other myopathy	29 (17%)
Total:	**171**

Appendix e-2. Machine learning applied to IBM features in 371 patients.



B

Method	Sens	Spec	Acc
Classification Tree	98%	91%	95%
Naïve Bayes	94%	91%	93%
Logistic Regression	98%	93%	95%
kNearestNeighbors	98%	92%	95%
SVM	98%	92%	95%

C

Data Derived Criteria (DDC)
All 3 of the following features:
1. Unilateral or bilateral finger flexion OR unilateral or bilateral knee extension weakness
2. Endomysial inflammation
3. Invasion of non-necrotic muscle fibers OR rimmed vacuoles

Machine learning algorithms were implemented using the software package Orange[1], using training/testing sets of 66%/33% of the data respectively and random sampling applied 10 times. That a small number of features could be used was suggested by the use of principal components analysis, indicating that most variance was accounted for by several features alone (e.g., 3 components account for > 80% of variance). (A) Example of a classification tree, suggesting the highest performance features are finger flexion weakness, rimmed vacuoles, and invasion of non-necrotic muscle fibers. Each node indicates majority class, % of patients in that class, and number of patients in that class. For example, the top node has majority IBM, with 53.9% of 371 patients having IBM. The feature “FF weak” (finger flexion weakness) divides that class into “Yes” (227 patients, 86.3% of which have IBM) and “No” (144 patients, 97.2% of which do not have IBM). (B) High sensitivities (Sens), specificities (Spec), and classification accuracy (Acc) of multiple machine learning methods using classification trees, Naïve Bayes, logistic regression, k-nearest neighbors (kNN), and support vector machines (SVM). (C) Data derived criteria from machine learning (DDC).

1. Curk T, Demsar J, Xu Q, Leban G, Petrovic U, Bratko I, Shaulsky G, Zupan B. Microarray data mining with visual programming. Bioinformatics. 2005;21:396-398