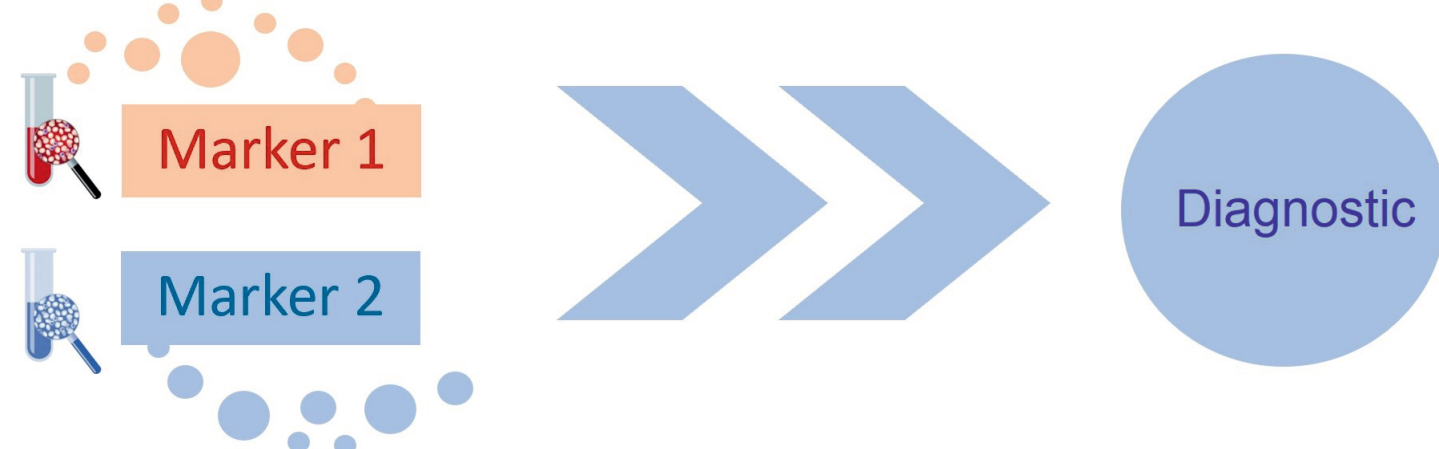


Introduction

- Accurate diagnosis often requires the integration of multiple biomarkers rather than reliance on a single diagnostic test.
- Combining markers may improve diagnostic discrimination, robustness, and clinical decision-making.
- This is especially important when individual biomarkers provide only partial or overlapping information about disease status.



The Gap

- Existing tools for diagnostic test combination are often limited to a small number of mainly linear methods.
- These tools may not adequately capture non-linear or complex relationships between biomarkers.
- In addition, many available workflows require programming knowledge, which reduces accessibility for clinicians and applied researchers.
- There is therefore a need for an accessible, code-free, and comprehensive platform for diagnostic test combination.



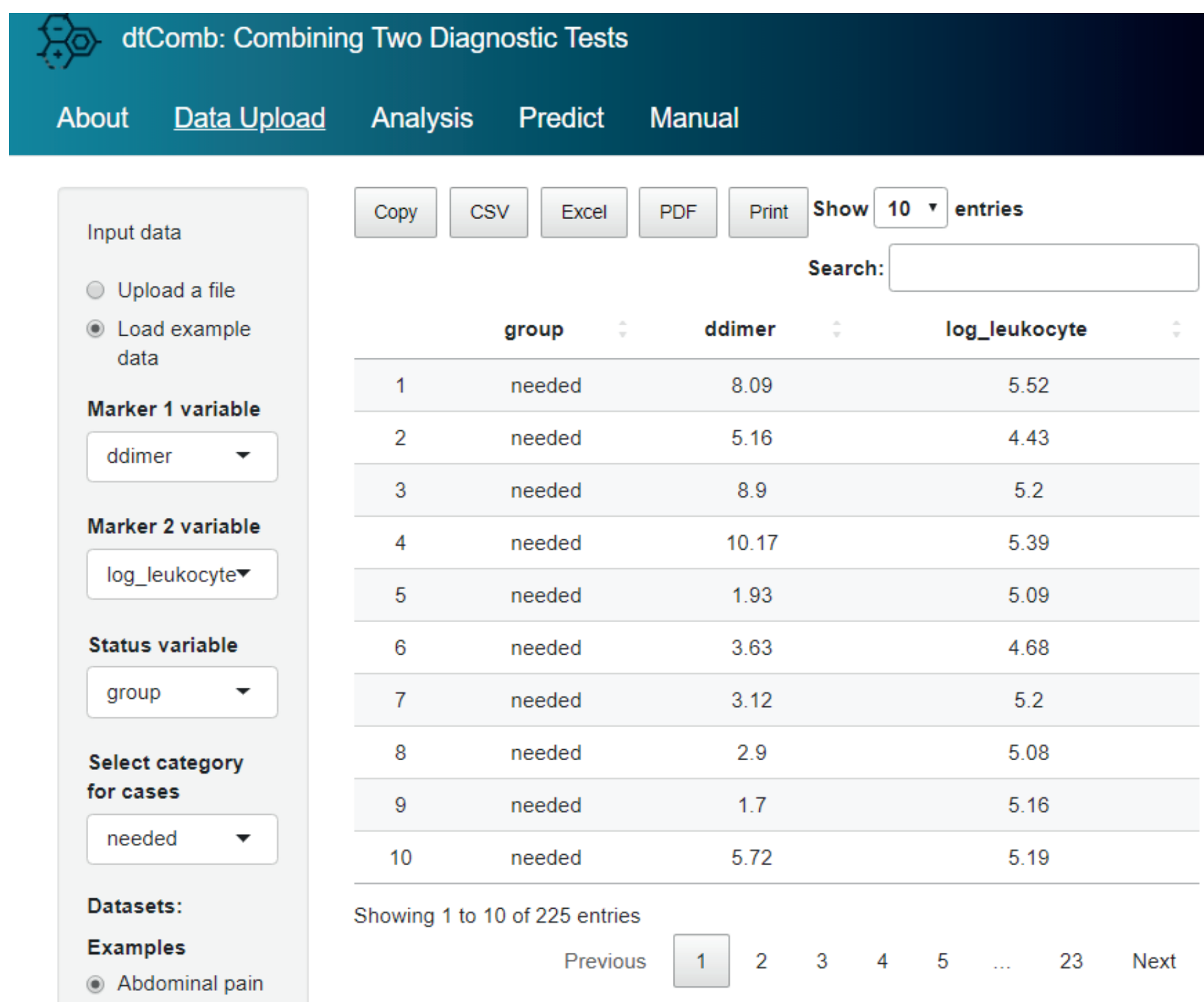
Drag-and-Drop Interface



R Package Backbone (dtComb)



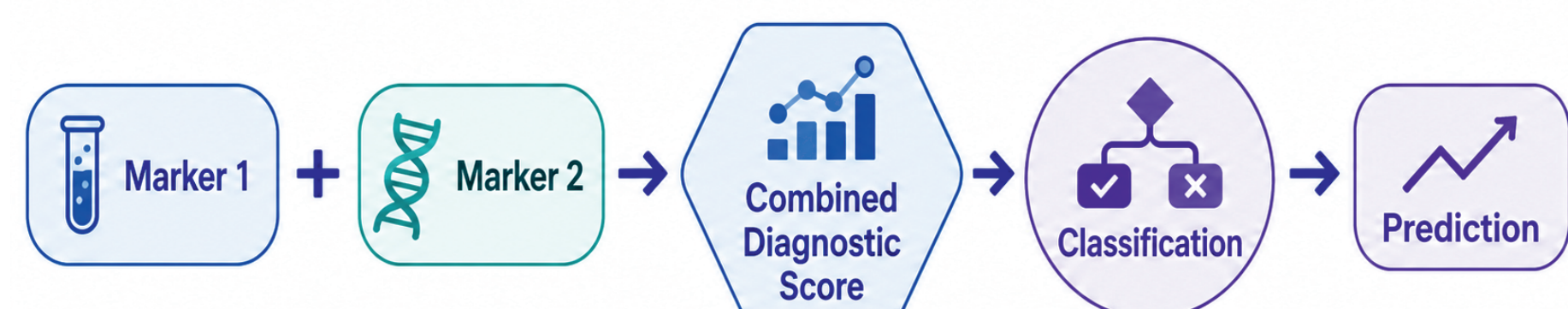
No Programming Required



Key Features of dtComb-Shiny

- Interactive web interface built on the dtComb R package
- Enables users to upload data and select diagnostic markers
- Allows definition of the gold standard variable and event class
- Supports linear, non-linear, mathematical operator-based, and machine learning-based combination methods
- Provides ROC analysis, optimal cut-off selection, diagnostic performance metrics, and visual outputs
- Enables prediction on new data using trained models

dtComb Workflow



The application was developed using key R packages and validated through 271 unit tests.



CONCLUSION

dtComb-Shiny offers an accessible, code-free platform for combining diagnostic markers, evaluating diagnostic performance, selecting optimal cut-off points, and generating predictions for new observations through 142 diagnostic test combination methods.

Combination Approaches

dtComb-Shiny provides a comprehensive methodological framework for combining two diagnostic markers through the dtComb R package.

142 Diagnostic Test Combination Methods

8 Linear Methods

Logistic regression, scoring-based methods, ROC-based linear combinations, and more.

7 Non-linear Methods

Polynomial models, ridge, lasso, elastic-net, splines, generalized additive models, and more.

14 Mathematical Operator-Based Methods

Arithmetic operators and distance-based combinations for generating new diagnostic scores.

113 Machine Learning Algorithms

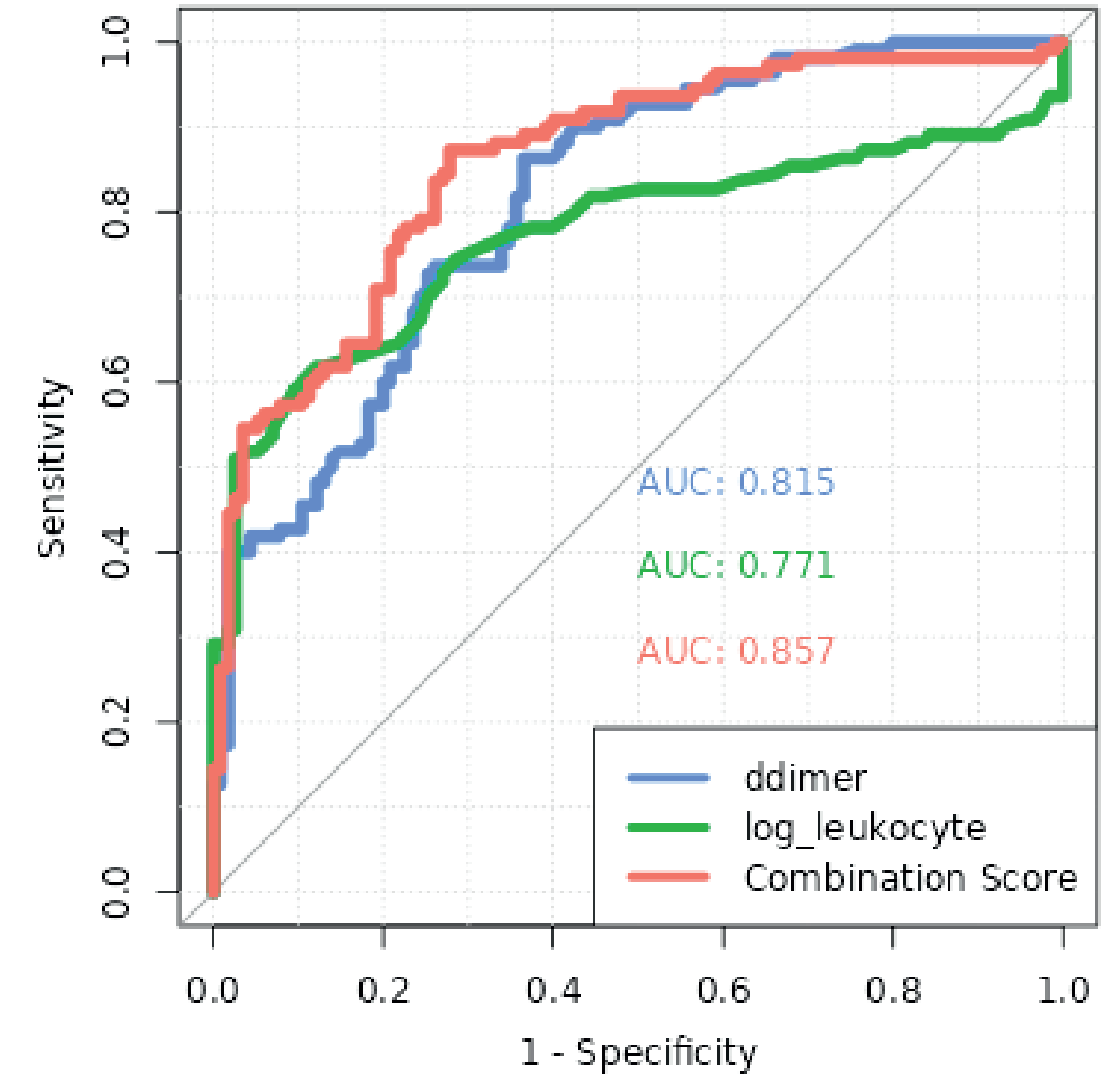
A wide range of machine learning algorithms for diagnostic test combination.

dtComb-Shiny Outputs

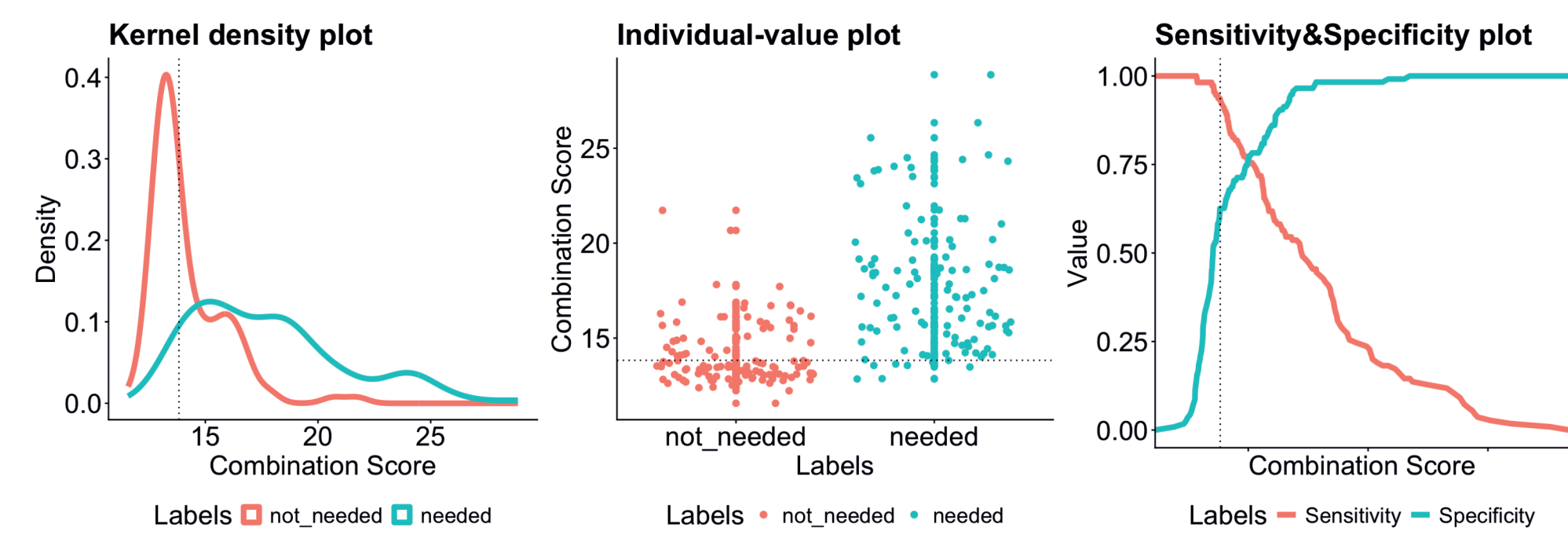
The output panel is designed to guide users from model evaluation to clinical interpretation. It enables side-by-side assessment of individual biomarkers and combined diagnostic scores, supporting the identification of the best-performing combination method and the most appropriate decision threshold for future classification.

ROC Curves

ROC Curves for Combination Diagnostic Test



Kernel density plots, individual-value plots, and sensitivity&specificity curves



AUC Table

	AUC	SE.AUC	LowerLimit	UpperLimit	z	p.value
dimer	0.815	0.028	0.761	0.889	11.452	2.30785884173231e-30
log_leukocyte	0.771	0.034	0.705	0.837	8.017	1.08162114140215e-15
Combination	0.857	0.025	0.809	0.906	14.423	3.7188562825958e-47

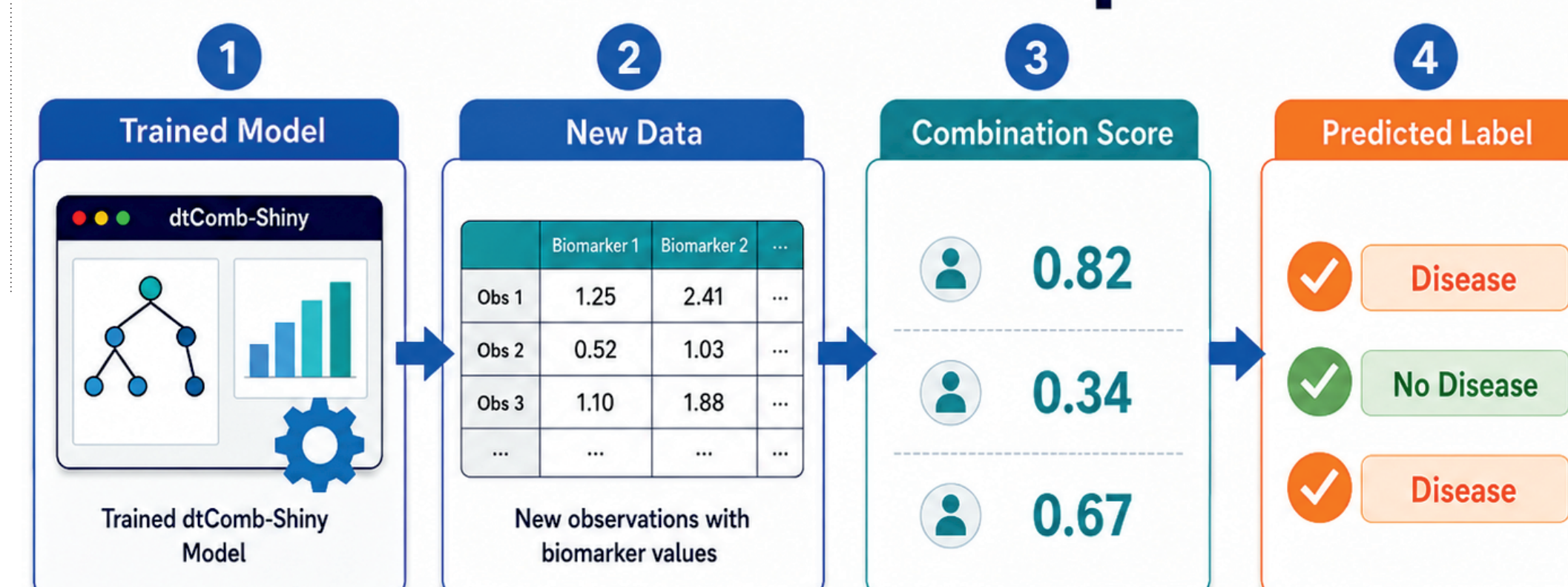
Multiple Comparison Table

Marker1 (A)	Marker2 (B)	AUC (A)	AUC (B)	(A-B)	SE(A-B)	z	p-value
Combination	dimer	0.857	0.815	0.042	0.02	2.089	0.03670801531790572
Combination	log_leukocyte	0.857	0.771	0.087	0.028	3.081	0.002565748667676247
dimer	log_leukocyte	0.815	0.771	0.044	0.042	1.055	0.291537598477965

Performance Measures

Statistic	est	lower	upper
1 Apparent prevalence	0.589	0.501	0.635
2 True prevalence	0.489	0.422	0.558
3 Sensitivity	0.873	0.796	0.929
4 Specificity	0.722	0.63	0.801
5 Correctly classified proportion	0.796	0.737	0.846
6 Positive predictive value	0.75	0.666	0.822
7 Negative predictive value	0.866	0.77	0.919
8 Positive likelihood ratio	3.138	2.317	4.246
9 Negative likelihood ratio	0.176	0.107	0.291
10 False T+ proportion for true D-	0.278	0.199	0.37
11 False T- proportion for true D+	0.127	0.071	0.204
12 False T+ proportion for T+	0.25	0.178	0.334
13 False T- proportion for T-	0.144	0.081	0.23

Prediction Output



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dtComb-Shiny

CORRESPONDENCE
Gökmen ZARARSIZ

