

Analysis Phase	Research Question	Model ID	Statistical Method	Key Findings
Laboratory Development				
Discovery	Can immune genes predict infection costs?	DISC-1	Linear regression (PC1, PC2 → weight loss)	Significant prediction
Optimization	Can machine learning improve prediction?	DISC-2	Random forest (19 genes → weight loss)	Substantial improvement
Validation	Is the model reliable?	DISC-3	Train-test cross-validation	Strong performance
Field Translation				
Detection	Does the model work in wild populations?	FIELD-1	Predicted vs. observed infection status	Successful detection
Discrimination	Can it distinguish parasite species?	FIELD-2	Predicted loss by species identity	Species-specific
Scaling	Does it correlate with infection severity?	FIELD-3	Predicted loss vs. parasite load	Scales with intensity
Biological Validation				
Physiological relevance	Does it capture real health impacts?	PROOF-1	Predicted loss vs. body condition	Correlation with body weight
Specificity	Is the response Eimeria-specific?	PROOF-2	Predicted loss vs. parasite community	Specific to infective stages

¹ Significance levels: *p < 0.05, **p < 0.01, ***p < 0.001

² Progressive sample sizes reflect train→test validation approach

³ E.f: Eimeria falciformis; E.r: E. ferrisi

Framework progresses from basic linear prediction ($R^2 = 0.106$) through machine learning optimization ($R^2 = 0.45$) to biological relevance.