



Development and internal validation of a VetCompass™ diagnostic prediction tool for Cushing's syndrome in dogs



“Can the clinical features at first suspicion of disease be predictive of gaining a diagnosis of Cushing's?”

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Background

Novel methods to aid the identification of dogs with Cushing's syndrome (CS) are warranted to optimise certainty in diagnostic blood test interpretation, reduce unnecessary testing and to aid decision-making for primary-care practitioners

Methods

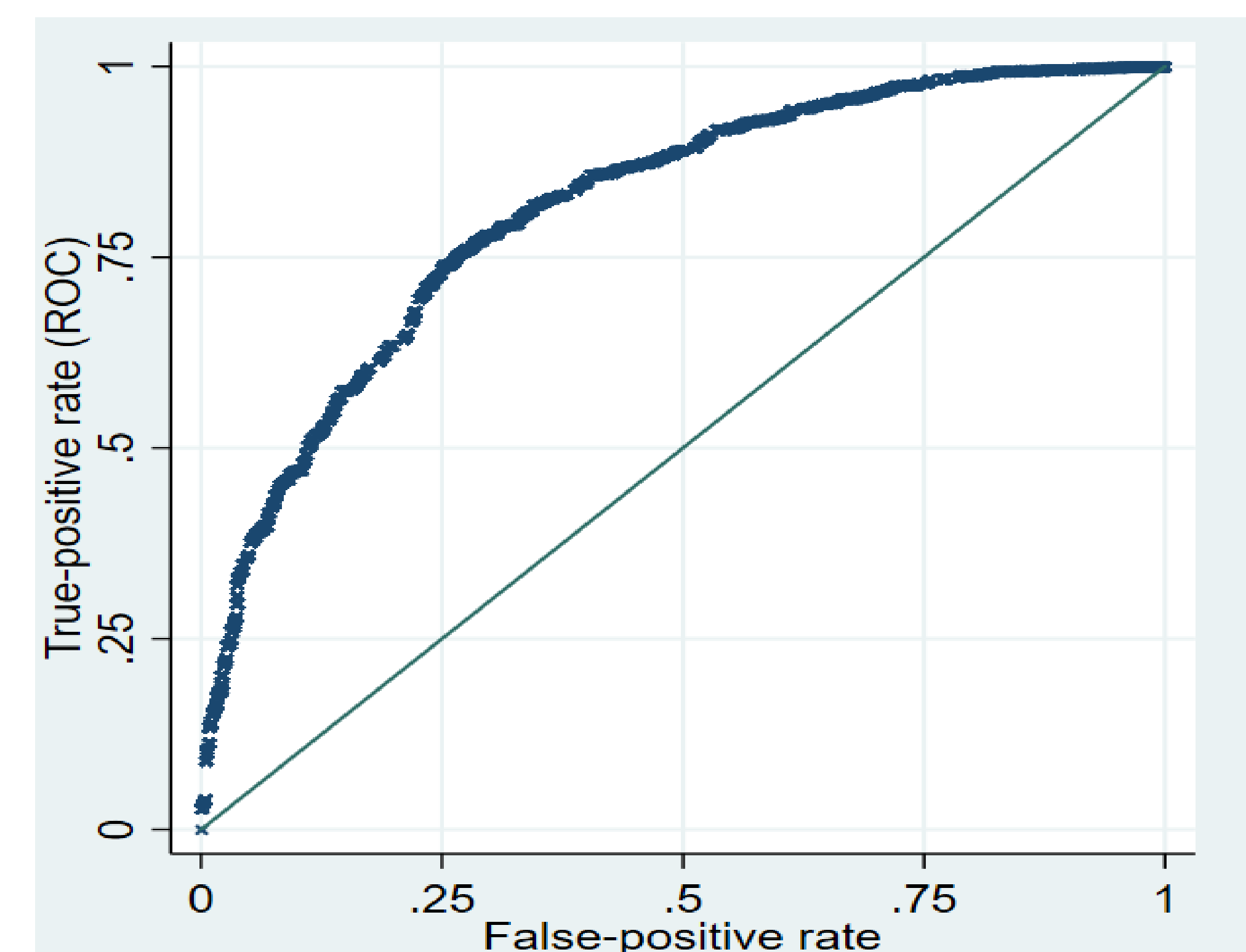
1. Prediction model was developed using **multivariable binary logistic regression** with backward stepwise selection
2. The model's predictive performance, measured by calibration and discrimination, was assessed and **internally validated through bootstrap re-sampling**
3. A clinical **prediction tool** that estimates the probability of CS was developed based on the function of the regression model coefficients

Multivariable results

Predictor	Category	Beta coefficient	Adjusted beta	Points	Rounded points
Sex	Female-entire	Baseline	-	-	0
	Female-neutered	-0.66	-0.57	-1.78	-2
	Male-entire	-0.35	-0.30	-0.94	-1
	Male-neutered	-0.60	-0.52	-1.62	-2
Age (years)	<7	Baseline	-	-	0
	≥7	0.70	0.61	1.91	2
Polydipsia	Yes	0.92	0.80	2.50	3
	No	Baseline	-	-	0
Thin/dry skin	Yes	0.37	0.32	1.00	1
	No	Baseline	-	-	0
Vomiting	Yes	-0.75	-0.65	-2.03	-2
	No	Baseline	-	-	0
Potbelly	Yes	1.05	0.91	2.85	3
	No	Baseline	-	-	0
Alopecia	Yes	0.85	0.74	2.31	2
	No	Baseline	-	-	0
Pruritus	Yes	-1.14	-0.98	-3.08	-3
	No	Baseline	-	-	0
Breed	Crossbreed	Baseline	-	-	0
	Bichon frise	0.66	0.57	1.80	2
	Border terrier	0.93	0.80	2.53	3
	Labrador	-1.07	-0.93	-2.91	-3
	Other purebred	-0.10	-0.09	-0.28	0
	Schnauzer	-0.76	-0.66	-2.07	-2
	WHWT	-1.11	-0.96	-3.02	-3
USG	Yorshire terrier	0.04	0.03	0.11	0
	Dilute	Baseline	-	-	0
	Not dilute	-0.88	-0.76	-2.39	-2
ALKP	Unknown	-0.42	-0.36	-1.13	-1
	Elevated	Baseline	-	-	0
	Not elevated	-1.58	-1.37	-4.29	-4
Constant	Unknown	-0.18	-0.15	-0.48	0
		-0.49	-0.42		

Revised coefficients to account for model overfitting was estimated through bootstrapping

A common denominator was applied to the coefficients to develop the tool's point system



Good model performance

- The developed model demonstrated good discrimination (AUROC = 0.79; 95% CI 0.76 – 0.81) and calibration (C-slope = 0.86)

Interpretable and practical prediction tool

- A points system was developed from the coefficients of the final model to create a tool for interpretation at the individual dog level.
- The tool has a scoring system of -16 to 12: **An individual dog scoring 12 reflects a 97% likelihood of having CS and -16 reflects a 0% likelihood**

Conclusion

The developed prediction tool can be used in clinical practice to support decision-making and increase confidence in diagnosis of CS

1. Collins, G. S., Reitsma, J. B., Altman, D. G. and Moons, K. G. M. (2015) 'Transparent reporting of a multivariable prediction model for individual prognosis or diagnosis (TRIPOD): the TRIPOD Statement', *BMC Medicine*, 13(1), 1

2. Goldstein, B. A., Navar, A. M., Pencina, M. J. and Ioannidis, J. (2017) 'Opportunities and challenges in developing risk prediction models with electronic health records data: a systematic review', *Journal of the American Medical Informatics Association*, 24(1), 198-208.

3. Steyerberg, E. W. and Vergouwe, Y. (2014) 'Towards better clinical prediction models: seven steps for development and an ABCD for validation', *European Heart Journal*, 35(29), 1925-31.