

Conference Paper Title*

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Abstract—This document is a model and instructions for L^AT_EX.

Index Terms—component, formatting, style, styling, insert

REFERENCES

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I. INTRODUCTION

- 1) Whats morphology and whats its use
- 2) How's morphology mostly done [1]
- 3) Whats ML and what chances does it offer to morphology
- 4) How is ML currently used in biology (State of the Art?)
 - a) 7 cow breeds, no landmarks, SVM [2]
 - b) differentiate insects by mandible shape, automatic landmarks using PCA, VAE and SVM [3]
 - c) differentiate predators by toothmarks: fixed landmarks, bunch of different models [4]
- 5) What are the limitations of ML
- 6) Which of these limitations do we believe we can overcome using our architecture
- 7) (The data and why Tilapia) [5]

II. STATE OF THE ART

- CNN vs ViT [6]
- Autoencoders [7] and SVM [3]
- different approaches in explaining ML
 - Saliency maps: relevant pixel for image
 - CAM/ Grad-CAM: relevant pixel for class
 - explainable frameworks
 - 1) SHAP [8]
 - 2) LIME [9]
- How are phenotypes/landmarks? detected in biology
- GradCAM with CNN and ViT medicine [10]
- Counterfactual explanations: Change in result if regions are deleted [11]

III. METHODS

- System architecture [12] [13]
- compare to Devil in the Detail [14]
- using ViT as extractor [15]
- self attention and why it makes the model more explainable [16]
- data
- comparison of extracted landmarks and morphological landmarks
- quality vs quantity when training [17]

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