Heng Yang

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OBJECTIVE

Seeking a research position in AI and NLP, leveraging expertise in biological sequence modeling, sentiment analysis, and adversarial attacks to drive innovation and contribute to impactful research projects.

EDUCATION

• University of Exeter

PhD in AI/NLP

Sept. 2021 - Sept. 2025 (Expected) Exeter, UK

• South China Normal University

Master's in Computer Science (AI/NLP)

Sept. 2018 - June 2021 Guangzhou, China

Yangtze University

Sept. 2014 - June 2018

Jingzhou, China

Bachelor's in Computer Science

AWARDS

- Chinese National Graduate Scholarship 2020
- Outstanding Graduate of Yangtze University 2018

Publications

- OmniGenBench: Automating Large-scale Benchmarking for Genomic Foundation Models Heng Yang, Jack Cole, Ke Li (Arxiv 2024)
- OmniGenome: Aligning RNA Sequences with Secondary Structures in Genomic Foundation Models Heng Yang, Ke Li (Arxiv 2024)
- PlantRNA-FM: An Interpretable RNA Foundation Model for Exploration Functional RNA Motifs in Plants Haopeng Yu#, Heng Yang#, et al. (Co-first Author, Nature Machine Intelligence, 2024)
- Modeling Aspect Sentiment Coherency via Local Sentiment Aggregation Heng Yang, Ke Li (EACL 2024)
- The Best Defense is Attack: Repairing Semantics in Textual Adversarial Examples Heng Yang, Ke Li (EMNLP 2024)
- PyABSA: A Modularized Framework for Reproducible Aspect-based Sentiment Analysis Heng Yang, Cheng Zhang (CIKM 2023)
- Evolutionary Multi-objective Instruction Optimization via Large Language Model-based Instruction Operators Heng Yang, Ke Li (EMNLP 2023)
- DaNuoYi: Evolutionary Multi-Task Injection Testing on Web Application Firewalls Ke Li, Heng Yang (IEEE TSE, 2023)
- Boosting Text Augmentation via Hybrid Instance Filtering Framework Heng Yang, Ke Li (ACL 2023)
- A Multi-task Learning Model for Chinese-oriented Aspect Polarity Classification and Aspect Term Extraction Heng Yang, Biqing Zeng (Neurocomputing 2021)

Personal Open-source Projects

• OmniGenBench – 4.7k Downloads

Sept. 2023 - Present

First large-scale in-silico benchmarking framework for genomic foundation models

GitHub

• PyABSA – 340k Downloads, 1k GitHub stars

 $June\ 2020\ -\ Present$

Aspect-based sentiment analysis framework, serving commercials, developers and scholars

GitHub

COMMUNITY STATISTICS

- GitHub: 1.5k stars, ≈ 160 commits and 60 PRs /year. I am a open-source lover since the beginning of my research. I am grateful to the developers whose projects helped me a lot. Therefore, I am committed to share all my open-source projects on GitHub with friendly MIT lenience.
- Huggingface: 8 Models and 10 Spaces with $\approx 400 k downloads and 10 k access, respectively$. Thanks to the Hungingface platform, I am glad to share all my pretrained and fine-tuned state-of-the-art sentiment analysis and genomic foundation models. e.g., deberta-v3-base-absa-v1.1 and OmniGenome-186M. Moreover, I have been to releasing demos for low-resource research topics, like RNA secondary structure prediction and RNA Design.
- PyPi: 8 python wheels with 800k downloads. I have made efforts to simplify the workflows and pipelines by packing and releasing open-access Python wheels. My wheels have been widely used in by the community. These wheels can be easily distributed via PyPi and installed via the pip tool.