James Stainer, PhD

London, UK | stainerjames@hotmail.com
Jamsta.in | LinkedIn | Google Scholar

SUMMARY

PhD in AI-enabled Healthcare from UCL (viva passed October 2026, minor corrections), with a track record of building end-to-end data pipelines and forecasting systems on large, real-world data. Recent freelance work focuses on adversarial LLM-agent evaluation, using Claude Code, versioned agent skills, local proxy evals, transcript auditing, leak checks, and remote multi-model benchmark loops. Previously completed two AstraZeneca data science internships spanning large-scale data pipelines, NLP, model development, and validation. Published in *Communications Biology* (Nature).

TECHNICAL SKILLS

- **Languages:** Python, SQL, R, Bash
- **Data & Infra:** Data Pipelines, pandas, NumPy, Elasticsearch, Feature Engineering, SLURM, Git
- **ML / DL:** PyTorch, TensorFlow, scikit-learn, Graph Neural Networks, NLP, Ensemble Methods
- **Methods:** Time-series Forecasting, Statistical Inference, Bayesian Inference, Change-point Detection

EXPERIENCE

Freelance AI Evaluator & Data Science Consultant Dec 2023 – Present
Various AI Evaluation Clients Remote

- Delivered freelance AI evaluation and data science work across multiple projects, spanning model-output review, scientific reasoning benchmarks, failure-mode analysis, and applied AI workflows.
- **Selected current project:** ***Adversarial LLM evaluation for expert scientific reasoning.***
  - Authored adversarial evaluation tasks benchmarking frontier LLM agents on expert bioinformatics and scientific coding, with each task structured around a hidden oracle, golden answer, reference solver, grading contract, and reasoning trap.
  - Ran the task lifecycle through a versioned Claude Code agent skill, covering task scaffolding, local proxy evaluation, export, and remote multi-model benchmark calibration.
  - Audited agent transcripts to identify answer leakage, redundant reasoning shortcuts, data-access failures, and data-consistency bugs before submission.
  - Made targeted local fixes and upgrades to the agent skill's scaffolding tooling so task generation ran end-to-end more efficiently.

Data Science Intern Oct 2022 – Apr 2023
AstraZeneca – Centre for Genomics Research Cambridge, UK

- Engineered a PubMed-to-Elasticsearch data pipeline indexing 35M+ biomedical citations/abstracts from the NLM PubMed baseline, enabling fast, reliable downstream querying and relationship mining at scale.
- Built NLP pipelines to identify, prioritise, and validate candidate drug–target–disease relationships for expert review.
- Applied BioWordVec embeddings and semantic-similarity methods to surface relationships across disease, drug, and target ontologies.
- Replaced broad manual search with a ranked candidate-validation workflow, significantly accelerating curation for domain scientists.

Data Science Intern Jun 2020 – Sep 2020
AstraZeneca – Centre for Genomics Research Cambridge, UK

- Co-Developed the DrugnomeAI framework to predict protein-coding gene druggability across multiple therapeutic modalities.
- Owned the full ML pipeline end to end: data collection, feature engineering, model training, validation, and benchmarking.
- Designed ensemble ML models integrating multi-omic, structural, and functional data.
- Used ML-based prioritisation to streamline candidate identification and accelerate expert curation.

EDUCATION

PhD in AI-enabled Healthcare 2021 – 2026
University College London (UCL) London, UK

- Viva passed October 2026 with minor corrections.
- Integrated custom Graph Neural Networks to model physiological dependencies and forecast paediatric ICU patient trajectories on high-frequency 5-second time-series data.
- Reduced forecasting error versus baseline models; designed the framework for downstream clinical decision-support integration.

MRes in AI-enabled Healthcare 2020 – 2021
University College London (UCL) London, UK

- Dissertation: Unsupervised ML on time-series data for clustering patient subtypes and improving decision support.

MSc in Data Science 2019 – 2020
Lancaster University Lancaster, UK

- Dissertation: DrugnomeAI – an ensemble framework for predicting druggability of human genes in collaboration with AstraZeneca.

BSc (Hons) Mathematics 2016 – 2019
Lancaster University Lancaster, UK

PUBLICATIONS & PRESENTATIONS

Journal Articles

[1] A. Raies, E. Tulodziecka, **J. Stainer** et al. "DrugnomeAI is an ensemble machine-learning framework for predicting druggability of candidate drug targets." *Communications Biology* (Nature), 2022.

Conference Presentations

[2] **J. Stainer** et al. Poster presentation at the *IEEE Engineering in Medicine and Biology Society (EMBS) Conference*, 2024.

[3] **J. Stainer** et al. Poster presentation at the *IEEE International Conference on Biomedical and Health Informatics (BHI)*, 2024.

SELECTED PROJECTS

Multivariate ICU Forecasting with StemGNN PhD Thesis at UCL & Great Ormond Street Hospital

- Incorporated a PyTorch StemGNN model to jointly forecast heart rate and blood pressure from 5-second paediatric ICU bedside-monitor data at Great Ormond Street Hospital.
- Built the full clinical time-series pipeline: filtering from 4,120 raw admissions to 364 high-quality patients, age-aware normalisation, missing-data handling, outlier detection, and sliding-window segmentation across ∼12.5M observations.
- Modelled HR–BP dependencies as a learned graph and benchmarked performance against baselines.
- Achieved 2.30% / 3.49% MAPE (HR / BP) on 5-minute-ahead forecasts at 1-minute resolution, outperforming ARIMA (2.82% / 3.85%) and a persistence baseline.

DrugnomeAI – Gene Druggability Prediction GitHub | Web App

- Published ML framework predicting druggability across all 19,846 human protein-coding genes; integrated 324 features from 15 sources and outperformed three published benchmarks.
- Developed a stochastic semi-supervised ML framework that scores druggability likelihood for all protein-coding genes in the human exome.
- Top-ranked genes were significantly enriched for targets already in clinical development ($p < 1 \times 10^{-308}$) and for genome-wide significant hits in UK Biobank PheWAS of 450K exomes.
- Built specialised models stratified by drug modality (small molecule, antibody, PROTAC) and therapeutic area, outperforming three published benchmarks on independent validation sets.