

# KRISTINA ULICNA

PhD Candidate (final year) @ UCL

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## Computational Skills

Strongest programming language: **Python**

Experience with **deep learning** strategies for **image analysis** & computer vision apps

- **Fully supervised:** U-Net, ConvNet, TCN
- **Weakly supervised:** multiple-instance
- **Self supervised:** generative (VQ-) VAE
- **Unsupervised:** k-means clustering
- **Dimensionality reduction:** PCA, UMAP

Skilled in "image2seq" representations & time-sequence trajectory data analysis

- **Machine learning libraries:** skimage, sklearn, torch, pytorch lightning, tensorflow 2.0, keras, innereye-deeplearning, btrack, HPACellSegmentator, CSBDeep
- **Standard & scientific libraries:** numpy, scipy, pandas, matplotlib, seaborn, pyplot, h5py, tqdm, napari, dtadistance

Work comfortably in **conda** envs, **Git**Hub (git), **iPython** (jupyter) notebooks, **LaTeX** (overleaf) & **Sigmaplot Statistics** software

Analysis of **DNA sequencing** data :

- SnapGene software: vector construction
- CLC workbench: Sanger sequencing
- Nanopore sequencing platform interface

## Laboratory Skills

**Molecular biology & vector construction:**

- PCR (RT-, colony-, sequential-, nested-)
- Plasmid preparation (mini- & midi-prep)
- Restriction endonuclease gene cloning
- Gateway cloning & Gibson Assembly
- Preparation & purification of mRNA
- Cell-free protein synthesis (PURExpress)

**Cell engineering & tissue culture:**

- Stable cell transfection via lipofection or lentiviral & retroviral transduction
- Colony selection with antibiotic titration
- Tet(Dox)-inducible gene expression
- Cell fractionation & organelle isolation
- Induction of cell differentiation (DMSO)
- Cell culture (passaging) with cell lines: MDCK, HeLa, HL60, CHO, HEK-293, MCF-7 / 10A, MDA-MB-231, HMLER, LNCaP, HaCaT

**Cell-based assays & imaging platforms:**

- IncuCyte ZOOM live-cell analysis system cell proliferation assay with colorimetric cell viability, ratiometric  $[Ca^{2+}]$  release & fluorimetric protein release assays

**Gene expression detection methods:**

- SDS-PAGE, Western (dot) blotting
- Immunocytochemistry (IF cell staining)
- Extra- & intracellular flow cytometry
- FACS-sorted clonal cell line expansion

## Summary

As a **PhD researcher** at UCL, I apply my **programming & laboratory skills** in a multi-disciplinary project combining cell biology, computational single-cell tracking & interpretable **deep learning**. I focus on **Python research development** for **large image data analysis** to identify biological patterns influencing diverse **cell cycling** control mechanisms. I am a practical, detail-oriented wet-lab scientist with **cell engineering** background, experienced in dry-lab **machine learning research** applied to single-cell biology. I have demonstrated my **leadership skills** in individual & collective settings, which I gained through UK & US work experience in **academic biomedical research groups** & international bio-/medical & **microscopy imaging research teams** in leading **technological companies**, and through my involvement in **volunteering & community projects**.

## Education

- Oct 2018 – Nov 2022 (expected) **PhD in Biosciences, BBSRC LIDo DTP Programme, UCL | London, UK**
  - **Fully-funded Doctoral Thesis:** "Learning Meaningful Representations of Computationally Tracked Single-Cell Trajectories in Heterogeneous Cell Lines using Deep Generative Modelling", advised by [Alan Lowe](#) & [Guillaume Charras](#) (UCL & Turing)
  - 3x merit-based scholarships: Yale School of Medicine exchange visitor (postponed)
- Sep 2014 – Jul 2018 **BSc Biomedical Science (Hons), King's College London | London, UK**
  - First Class Hons (**76%**) Biomedical Science with Molecular Biology Extramural Year
  - Awards & Scholarships: Desmond Tutu Scholarship '14, Best Lay Article Award '15

## Research Experience

- Mar 2019 – Present **PhD Researcher, the "DeepTree" project @ UCL | London, UK**
  - Co-developed a robust, supervision-free, deep learning-based tracking pipeline for [deep lineage analysis](#) of large time-lapse live-cell microscopy data of 2D cell lines
  - Published two computational framework articles (*U-Net*, *CNN*, *bTrack* multi-object [tracking algorithm](#)) applicable for deep single-cell trajectory lineage reconstruction
  - Analysed multigenerational lineage trees (>20k single-cell tracks) to interpret [proliferation determinants](#) which predispose cells to commit to fast divider fates
  - Generated explainable image-based representations of single-cell time sequences
  - Directly supervised Masters project to develop an AI-based cell segmentation tool
- Apr 2021 – Sep 2021 **Research Intern @ Microsoft Research Cambridge | Cambridge, UK**
  - Developed an AI-based end-to-end pipeline to classify subcellular protein localisation in single cells from Human Protein Atlas' dataset of weakly labelled confocal [microscopy images](#) using Azure computing & [InnerEye Deep Learning](#) OS toolkit
  - Trained a competitively-performing model (MIL / SimCLR & BYOL architectures) upon evaluation with Kaggle competition authors (Prof. Emma Lundberg's Lab)
  - Summarised project to [Health Intelligence Lab](#) leadership at End-of-Internship talk
- Sep 2016 – Aug 2017 **Industrial Trainee @ Crescendo Biologics Ltd. | Cambridge, UK**
  - Engineered a novel, universal tool cell line for early drug discovery, i.e. phage display selection & functional screening of antibody fragment onco-therapeutics
  - Presented project outcomes to senior scientists & company management board
- Jun 2016 – Sep 2016 **Cancer Research UK Intern @ Cambridge University | Cambridge, UK**
  - S. Bohndiek Lab: Characterised anti-angiogenic drug effects via breast cancer cell-based growth, viability assays to evaluate oxygen role in cancer progression
- Jun 2015 – Aug 2015 **Visiting Scholar, Whitehead Institute @ MIT | Cambridge, USA**
  - R. Weinberg's Lab: Investigated determinants of cancer cell invasion, metastasis & tumour stroma immunomodulation upon epithelial-to-mesenchymal transition

## Teaching Experience

- Mar 2020 – Present **Graduate Teaching Assistant @ UCL BIOC0016 module | London, UK**
  - Co-designed an iPython-based [practical session](#) for 70+ undergraduate students for introductory concepts in bioimage analysis, bioinformatics & machine learning to hand-label image mini-dataset & train simplified classifier of cell mitotic state
- Jan 2021 – Dec 2021 **Google Certified Trainer for AI Tech & Tools | Bratislava, Slovakia**
  - Empowering non-tech professionals by leveraging their expertise & leadership in AI tech field via [AI-basics talks & workshops](#) with Google Slovakia outreach team
- May 2021 **"Smart Microscopy" Workshop @ ZEISS | Gothenburg, Sweden**
  - Trained 30+ intermediate-level attendees at "[Train Your Own Model](#)" hands-on workshop session to use (bio)image analysis tools (*napari*, *jupyter notebooks*) to annotate cell imaging data to train deep learning model to classify cell cycle state
- Jun 2020 **"Introduction to Deep Learning" @ UCL Cancer Domain | London, UK**
  - Delivered beginner-friendly [masterclass series](#) for 100+ interdisciplinary scientists with real-life examples of deep learning-based bioimage analysis from PhD project
  - Contrasted deep learning to other computer vision methods, demonstrated the utility & benefits, emphasised fundamentals of 'learning' component, outlined common evaluation metrics & listed current challenges in computer vision field

