JUSTYNA GREDECKA

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PROFILE

Motivated Bioinformatics graduate with experience in developing computational tools using Python. Proficient in full-stack web development including up-to-date knowledge of Flask, Bootstrap, Celery and Redis technologies. Experienced in data cleaning, manipulation and analysis using Pandas and NumPy. Skilled at team collaboration and working on own initiative while meeting strict deadlines.

TECHNICAL SUMMARY

Languages	Python, Bash, HTML5, CSS3, JavaScript, R
Tools/Frameworks	Flask, pandas, NumPy, seaborn, matplotlib, Celery, RQ, SQLAlchemy, redis-py Bootstrap, jQuery, JSON, Gunicorn, Docker, Heroku
Databases	Redis
Version Control	Git/GitHub
O/S	UNIX (Mac OS X, Linux) and Windows
Big Data Analysis	High Performance Computing (HPC)
Software	Jupyter Notebook, Adobe Illustrator, Sublime Text

PROJECT HIGHLIGHTS

KSEAPlus
- Web application implementing various algorithms for the quantification of protein kinase activity from experimental data. Architecture includes Flask as the web-framework coupled with Celery and Redis for running analyses in the background.
- Available at: https://ksea-plus.herokuapp.com
- Source code: https://github.com/jgredecka/KSEAPlus

KinBase
- Web-based resource of protein and protein inhibitor information. Main components include Flask and SQLite database, with SQLAlchemy used as an object-relational mapper.
- Available at:
- Source code:

PDBParser
- Python-based tool that allows for analysing and visualising protein structural information from PDB (Protein Data Bank) files.
- Source code: https://github.com/jgredecka/PDBParser

KiNet
- Python program that retrieves information from UniProt RESTful API via urllib/urllib2 libraries to generate simple-interaction-files (SIF) suitable as input to Cytoscape, a graphical network generator software.

- Source code: https://github.com/jgredecka/KiNet

EDUCATION

Sep 2018 - Aug 2019 **Queen Mary University of London, London, UK**
Master of Science in Bioinformatics (award pending)

- Coursework covered Python programming, web development, bash shell scripting, use of Apocrita HPC cluster and supervised and unsupervised machine learning using R.
- Developed the web application *KinBase* as part of a software development group project. Practised skills include version control, back-end/front-end development and collaborative teamwork.
- For a final project, developed the web application *KSEAPlus*, improving problem-solving skills and ability to work independently.
- Developed good presentation and written communication skills by presenting both web applications to fellow students/supervisors and by writing extensive software documentation as part of a team.

Sep 2012 - Jul 2015 **Anglia Ruskin University, Cambridge, UK**
Bachelor of Science in Biomedical Science (First Class)

- Developed excellent numerical and analytical skills by undertaking a module on statistical data analysis in R.
- Practised teamwork, written and oral communication skills by participating in group projects and poster presentations.

EMPLOYMENT HISTORY

Oct 2015 - Aug 2018 **MRC Laboratory of Molecular Biology, Cambridge, UK**
Research Support Assistant

- Worked independently and as part of a team to generate, analyse and report high-throughput genetic data, developing an excellent attention to detail, communication skills and ability to work under pressure.
- Worked effectively with people from a variety of backgrounds by regularly liaising with technicians, researchers and PhD students.
- Supervised students and newer members of staff.

REFERENCES

Available on request.