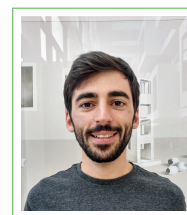


# Mirko Torrisi

*Data Scientist / PhD Candidate*

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📍 [mircare](#)



## Skill Set

Machine Learning	Supervised Learning, Transfer Learning, Ensembling, Stacking, Time series classification, Classification, 1D- and 2D-RNN, CNN, Deep Learning, Signal and Image Processing.
Software Engineering	Scientific Computing, Parallel Computing, High Performance Computing, Cloud Computing, Version Controller and Collaborative Integration (Git).
Programming	Python, Bash, C++, Java, MATLAB, MySQL.
Frameworks	Tensorflow, Keras, Scikit-learn, NumPy, Pandas.
Soft Skills	Critical Thinking, Problem Solving, Leadership, Project Management.

## Education

- 2015 – **PhD in Computer Science**, *University College Dublin*, Ireland.  
present My PhD project focuses on *Predicting Protein Structural Annotations by Deep and Shallow Learning* and is funded by the Irish Reserch Council. My PhD advisor is Dr. Gianluca Pollastri, who first introduced me to the Deep Learning world.
- Sep 2018 – **Visiting Scholar**, *University of California, Irvine*, US.
- March 2019 In Dr. Pierre Baldi's lab, a world-class scientist in Deep Learning and Bioinformatics, I performed cutting-edge research projects applying novel research practices.
- 2011–2015 **B.Sc. CS**, *University of Catania*, Italy, *110/110 cum laude*.  
I won a 1-year Erasmus scholarship to study at University College Dublin (Ireland), where I employed Apache Lucene/Sol, Java, jQuery and PHP for *Identifying Trends in Online Political Data* with Dr. Derek Greene. For my thesis, I processed, analyzed and evaluated viral miRNA and their target genes with Dr. Alfredo Ferro and his research group.

## Software

### Porter 5

- Description State-of-the-art Prediction of Protein Secondary Structure in 3 and 8 classes with Deep Recurrent Neural Networks. Over 35,000 unique queries.
- Web Server <http://distilldeep.ucd.ie/porter/>
- Docker <https://hub.docker.com/r/mircare/porter5/>

### Brewery

- Description Fast, state-of-the-art Prediction of 1D Protein Structure Annotations.
- Web Server <http://distilldeep.ucd.ie/brewery/>
- Docker <https://hub.docker.com/r/mircare/brewery/>

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## Experience

### Teaching

- Sep 2016 – **Teaching Assistant**, *UCD*.  
Dec 2019 Led 10 demonstrators, ran the lab and supervised the weekly submissions of 130 students while supporting Dr. Lorraine McGinty in planning and innovating the module.  
Jan – May **Facilitator - Advanced Machine Learning**, *UCD*.  
2018 Assisted postgrads with Keras, OpenAI Gym, Supervised and Reinforcement Learning, [...].

### Miscellaneous

- 2018 – **Journal Reviewer**.  
present I have reviewed 15+ journal articles for Bioinformatics (Oxford Academic), PeerJ, IEEE Transactions on Computers, and more; see details on [PubLons.com](https://publons.com).  
Oct – Dec **Tutor**, *IGB, UCI, Irvine, California*.  
2018 I defined and directly supervised the research internship of a master student, successfully enhancing and automatizing a sensible (proteomics) data pipeline.  
June 2018 **AI/Deep Learning Demo**, *UCD, Dublin, Ireland*.  
Invited to run a demo at the UCD School of Computer Science Summer School Programme.  
Mar – June **Capture The Flag**, *University of Catania, Catania, Italy*.  
2014 Part of the winning team of a *National Capture The Flag*.  
Mar – Aug **Stage Technician**, *University of Catania, Catania, Italy*.  
2014 I have been selected to support the IT Services at University of Catania.

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## Recent Journal Publications

- Mirko Torrisi, Manaz Kaleel, Gianluca Pollastri. **Deeper Profiles and Cascaded Recurrent and Convolutional Neural Networks for state-of-the-art Protein Secondary Structure Prediction**. *Scientific Reports, Nature Research* (2019). doi: 10.1038/s41598-019-48786-x.
- Manaz Kaleel, Mirko Torrisi, Catherine Mooney, Gianluca Pollastri. **PaleAle 5.0: prediction of protein relative solvent accessibility by deep learning**. *Amino Acids, Springer Nature* (2019). doi: 10.1007/s00726-019-02767-6.
- Mirko Torrisi, Gianluca Pollastri, Quan Le. **Deep learning methods in protein structure prediction**. *Computational and Structural Biotechnology Journal, Elsevier* (2020). doi: 10.1016/j.csbj.2019.12.011.
- Mirko Torrisi, Gianluca Pollastri. **Brewery: Deep Learning and deeper profiles for the prediction of 1D protein structure annotations**. *Bioinformatics, Oxford University Press* (2020). doi: 10.1093/bioinformatics/btaa204.

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## Invited Talks

- Mirko Torrisi, Manaz Kaleel, Gianluca Pollastri. **State-of-the-art ab initio prediction of protein secondary structure**, *8th Computational and Molecular Biology Symposium*, '17, IE.
- Mirko Torrisi, Manaz Kaleel, Gianluca Pollastri. **Brewery: state-of-the-art ab initio prediction of 1D protein structure annotations**, *15th Annual Meeting of the Bioinformatics Italian Society, June 2018, Italy*.
- Mirko Torrisi, Manaz Kaleel, Gianluca Pollastri. **Brewery: state-of-the-art ab initio prediction of 1D protein structure annotations**, *CASP13, December 2018, Mexico*.