

Mihai Chelaru-Centea

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[Website](#)
[GitHub](#)
[Stack Overflow](#)

Objective

Data scientist with background in neuroscience and bioinformatics looking to join a dynamic data science team and apply data mining and machine learning to uncover actionable business insights and optimize decision-making. Experienced Python practitioner, fast learner, and driven self-starter.

Software, Environment, and Methodologies

- ❑ Languages: Python (proficient), R (prior experience), Java (prior experience)
- ❑ Python libraries: pandas, numpy, scikit-learn, matplotlib, keras, plotly, fastai
- ❑ Database: SQL, relational database development, Oracle, PostgreSQL
- ❑ Environments: Jupyter, RStudio, PyCharm, Visual Studio Code, sqlplus, Unix CLI

Relevant Projects

- ❑ Conducted churn analysis on a telecom customer dataset through performing exploratory data analysis, feature engineering, data transformation, and tuning of multiple random forest models. Also analyzed feature importance and explored variable relationships using partial dependence plots to derive actionable insights for customer retention. [\[Source code\]](#)
- ❑ Scraped aggregated reviews for over 2,000 different plant strains from Leafly.com and employed association rule learning to identify potential relationships between chemical profile and medicinal effects. [\[Source code\]](#)
- ❑ Created the website intelligencerefinery.io, written in Django and hosted on Heroku, a curated professional blog focused on data science and machine learning resources. [\[Source code\]](#)
- ❑ Conceptualized and developed [BenchMate](#), a Java Android app that provides a dynamic interface for laboratory scientists to organize and track their molecular biology experiment workflow. [\[Source code\]](#)
- ❑ Designed and constructed a [custom plant genome browser platform](#) for the agricultural consulting firm Aether Research and their collaborators, Sunrise Genetics, in accordance with business requirements as defined in collaboration with key company stakeholders. The platform integrates the web-based alignment tool BLAT, written in C, with JBrowse, an open-source JavaScript-based genome browser. [\[Source code\]](#)

Education/Training

- ❑ **2017-2018: Bioinformatics Post-graduate Certificate, High Honours**, Seneca College
- ❑ **2009-2013: Honours Bachelor of Science with High Distinction**, University of Toronto
Neuroscience Specialist with Minors in Psychology and Physiology
French and Spanish Language Citations

Relevant Courses

Programming

- | | |
|---|--------------------|
| ❑ Algorithms I | Princeton (online) |
| ❑ Python Bioinformatics | Seneca |
| ❑ Programming with Java | Seneca |
| ❑ Concepts of Programming with Perl | Seneca |
| ❑ Operating Systems | Seneca |
| ❑ Data Systems | Seneca |
| ❑ Introduction to Computer Science and Programming Using Python | MITx (online) |
| ❑ Introduction to Computer Science | HarvardX (online) |

Statistics

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|------------------------------|-----------------------|
| ❑ Statistical Learning | Stanford (online) |
| ❑ Statistics and R | HarvardX (online) |
| ❑ Applied Statistics | Seneca |
| ❑ The Practice of Statistics | University of Toronto |

Machine Learning

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|---------------------------|--------------------------------------|
| ❑ FastAI Machine Learning | University of San Francisco (online) |
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Awards and Honors

- ❑ **2018: Seneca College Dean's List Award**
- ❑ **2010 – 2013: University of Toronto Dean's List Award**
- ❑ **2012: University of Toronto Chancellor's Award**