

Michele De Cillis

Milan, Italy | decillismicheledeveloper@gmail.com | demic.dev | linkedin.com/in/michele-de-cillis
github.com/demic-dev

Education

- | | |
|--|-----------------------|
| BSc Computer Science , Università degli Studi di Milano | Sept 2022 – present |
| <ul style="list-style-type: none">• Focused on algorithms, systems design, and computational theory | |
| Erasmus+ Exchange , Université Paris-Saclay | Sept 2023 – June 2024 |
| <ul style="list-style-type: none">• Specialized in machine learning techniques and natural language processing• Developed cross-cultural collaboration skills in multinational academic teams | |

Experience

- | | |
|--|-----------------------|
| Front-End Engineer , Pane&Design s.r.l. | Oct 2021 – Dec 2022 |
| <ul style="list-style-type: none">• Developed and optimized high-traffic websites (200k+ monthly visits)• Integrated microservices into existing eCommerce• Created automation tools that reduced landing page creation time by 40% | |
| Full Stack Engineer , Online Impresa s.r.l. | July 2020 – Sept 2021 |
| <ul style="list-style-type: none">• Designed and built progressive web applications and mobile solutions for SMEs• Maintained client relationships and gathered requirements to ensure project success• Automated deployment pipeline, cutting publishing time from 45 to 10 minutes | |

Extracurricular activities

- | | |
|---|----------------|
| University Startup Challenge | April-May 2025 |
| <ul style="list-style-type: none">• Currently working with a multidisciplinary team (UniMi and Bocconi) to develop technology-driven solutions for urban challenges using data science and AI | |
| Cloudflight Coding Contest | April 2023 |
| <ul style="list-style-type: none">• Ranked in Top 10 amongst university teams in algorithmic problem solving under time constraints | |

Projects

- | | |
|---|--------|
| ALS Biomarker Identification | GitHub |
| <ul style="list-style-type: none">• Developed a computational pipeline to analyze RNA-seq data from ALS patients using Python, scikit-learn, and pandas• Implemented statistical methods to identify differentially expressed genes that could serve as potential biomarkers | |
| NixOS | GitHub |
| <ul style="list-style-type: none">• Configured a reproducible scientific computing environment using declarative system configuration with Nix | |

Open Source

- **PixelFed**: Contributed with bug fixes to an open-source federated image sharing platform (GitHub)

Skills

Technologies: Git, Nix, Jupyter, LaTeX, Docker, Linux/Unix

Programming Languages: Python, TypeScript/JavaScript, Go, Rust, SQL, Bash scripting

Spoken Languages: Italian (native), English (C1), French (B1)