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Profile

Computational Biologist Researcher and Engineer. co-Founder of PiPle, I am mission-driven and have a lifelong passion for Research and Science.
Highly independent, I am interested in improving Genomics & Biomedical research using Artificial Intelligence. I am now doing a Ph.D. at ENS & Pasteur. I worked in many research institutes and multiple startup companies.

Skills

BigData: *GCP*, *AWS*, *batch*, *snakemake*, *terra*, *nextflow*, *HPC*, ...

Biology: Systems biology, Cancer Biology, epigenomics, *Neuroscience*...

Datatype: single cell, RNAseq, *DNAseq*, *ChIP-seq*, *ATACseq*, *slam-seq*, *bisulfite-seq*, *Perturb-seq*, *bi-photon imaging*...

Packages: *Numpy*, *Scipy*, *Pandas*, *Seaborn*, *Bokeh*, *scikit-learn*, *Pytorch*, *DGL*, *WandB*, *pysam*, *DESeq2*, *MACS2*, *scVI*, *scanpy*, *seurat*, *pyMOL*, *RDkit*, *smina*...

Code & frameworks: *python*, *javascript*, *java*, *R*, *matlab*, *firebase*, *SQL*, *Neo4j*, *nodeJS*, *react*...

Datasets: *CCLE*, *TCGA*, *GTEX*, *Gnomad*, *GWAS*, *ENCODE*, *Human Cell Atlas*, ...

ML: *VAEs*, *GNNs*, *CNNs*, *NMF*, *optimization*...

Languages: *English*, *French*, *Spanish*

Leadership: *team lead*, *project lead*, *project management*, *mentorship*

Education

ENS ULM, Pasteur Institute, CNRS	PARIS, FR	2023-2026
Ph.D. in Artificial Intelligence, ED130		
Harvard University	CAMBRIDGE, USA	2019-2021
Graduate Certificate in Biology		
University of Kent	CANTERBURY, UK	2017-2018
Master of Science, Machine Learning		
ECE Paris	PARIS, FR	2013-2018
Tec de Monterey	QUERETARO, MX	2014
French Diplôme d'ingénieur (M.sc.), Biomedical Engineering		

Experience

WhitelabGx - Team Leader in Computational Biology
Aqemia - Research Scientist for Target Discovery (2022)

- Cellular Atlas & Knowledge Graph for target discovery & cell surface marker discovery. AI for Cellular therapies. Hit Discovery.
  ML, BIG DATA, GENOMICS, STRUCURAL BIO   2022-2023

Broad Institute of MIT and Harvard - Senior Associate Computational Biologist (Project Lead)

- DepMap Omics, Predicting cancer dependencies from genetic sequences of cancer cell lines.
  ML, BIG DATA, GENOMICS   2019 - 2022
- AMLproject, deciphering AML from deep epigenetic profiling, with Dana Farber Cancer Institute & Boston Children's Hospital
  ML, BIG DATA, GENOMICS
- Celligner, Alignment of cancer models to patient tumors using conditional VAEs on multi omics data.
  ML, DL, GENOMICS   2021 -2022

PiPle - co-Founder - CEO

- Co-Founder of PiPle, A startup focused on bringing the next-generation communication platform. PiPle. INSEEC incubator
  PROJECT DEV, ENTREPRENEUR   2016 -

Flatiron Institute, Simons Found. - Research Associate

- Member of the CalmAn project, Neural spike inference from calcium imaging. Flatiron Institute under the supervision of Dmitri Chklovskii
  RESEARCH, IMAGING, ML, VISION   2017

University of Kent - Master Thesis in the C.U.B. group

- Developed PyCUB, Master Thesis in ML for the analysis of the Codon Usage Bias across the fungi kingdom.
  ML, BIG DATA, RESEARCH, GENOMICS   2017

HighLife Med - R&D

- Stage in HighLife Med, A Parisian Biomedical Startup developing the world's first no-surgery mitral heart valve replacement.
  SIMULATION, DATA ANALYTICS

Interests

Awards

- *2x Broad Spotlight Awards, For outstanding contribution. 2020, 2022.*
- *ECE innov' Awards, 2nd Place for the PiPle project, innovative Chat app introducing the concept of message-mapping. 2017*
- *Berger-Levrault Innovation Awards, 2nd Place for the PiPle project, innovative Chat app introducing the concept of message-mapping. 2017*

Events

- *Human Brain Project symposium, 2017*
- *BioIT World conference, 2023*
- *Broad retreat, 2019, 2020, 2021*
- *Paris AI for Biosciences symposium, 2023*
- *Paris Lego Group conference, 2023*

Publications

Scholar: https://scholar.google.com/citations?user=zyXiydsAAAAJ

- *Leukemia core transcriptional circuitry is a sparsely interconnected hierarchy stabilized by incoherent feed-forward loops. J. Kalfon, T. Harada, Y Heshmati, in review, 2022.*
- *A distinct core regulatory module enforces oncogene expression in KMT2A-rearranged leukemia, J. Kalfon, T. Harada, Y Heshmati, Genes & Development, 2021. https://doi.org/10.1101/2021.08.03.454902*
- *Transcriptional Immunoediting of AML Cells after Allogeneic Hematopoietic Stem Cell Transplantation, K Eagle. T. Harada, J. Kalfon, Blood, 2021. https://doi.org/10.1182/blood-2021-151180*
- *Repeat expansions confer WRN dependence in microsatellite-unstable cancers, N. Wietmarschen, S. Sridharan, W. J. Nathan,…, Nature, 2020. https://doi.org/10.1038/s41586-020-2769-8*
- *Synthetic Lethal Interaction between the ESCRT Paralog Enzymes VPS4A and VPS4B in Cancers Harboring Loss of Chromosome 18q or 16q, J. E. Neggers, B. R. Paolella, A. Asfaw, M. V. Rothberg, Cancer Research, 2020. https://doi.org/10.1016/j.celrep.2020.108493*
- *Broad retreat, An overview of research happening in DepMap Omics, 2021. https://docs.google.com/presentation/d/1zgQixZjqV8VtGK_2ErYXvHpCt9ZcJ6gLHnRZag872Xw*
- *Hidden Patterns of the Codon Usage Bias across kingdoms, Y Deng, J. Kalfon, T Von der Harr, D. Chu, RSIF, 2019. https://doi.org/10.1098/rsif.2019.0819,*
- *Master Project, PyCUB, python package for the kingdom-level analysis of the codon usage bias, 2018. https://github.com/jkobject/pycub/blob/master/docs/PyCUB.pdf,*
- *Broad retreat, Poster Session presentation, on the analysis of AML specific super enhancer and AML dependencies, 2019. https://jkobject.com/projects/predicting-dependencies-from-enhancers/*