



Eduardo Conde-Sousa



europass

Date of birth: 23/10/1979 | **Nationality:** Portuguese | **Gender:** Male |

eduardo.condesousa@p-95.com | econdesousa@gmail.com

WORK EXPERIENCE

04/04/2022 – CURRENT – Leuven, Belgium
ANALYTICAL PROGRAMMER – P95

- Data Analysis
- Pipeline Automation

01/04/2018 – 30/03/2022 – Porto, Portugal
BIOIMAGE ANALYST – INEB – INSTITUTO NACIONAL DE ENGENHARIA BIOMÉDICA

Extract numerical data from biological images

01/02/2016 – 30/03/2018 – Braga, Portugal
BIOINFORMATICS SCIENTIST – CBMA - CENTRE OF MOLECULAR AND ENVIRONMENTAL BIOLOGY

05/12/2014 – 31/10/2015 – Vairão, Portugal
BIOINFORMATICS SCIENTIST – CIBIO-INBIO - RESEARCH CENTER IN BIODIVERSITY AND GENETIC RESOURCES

01/09/2011 – 29/09/2011 – Porto, Portugal
TEACHING ASSISTANT – EVMAT 2011 SUMMER SCHOOL, CENTER OF MATHEMATICS OF UNIVERSITY OF PORTO (CMUP), PORTUGAL

01/01/2008 – 31/12/2013 – Porto, Portugal
EXTERNAL COLLABORATOR AND CONSULTANT – PORTO EDITORA

01/09/2004 – 31/08/2010 – Portugal
HIGH SCHOOL TEACHER OF MATHEMATICS – PORTUGUESE MINISTRY OF EDUCATION

01/09/2003 – 31/08/2004 – Bragança, Portugal
TEACHER OF MATHEMATICS – POLYTECHNIC INSTITUTE OF BRAGANÇA

01/09/2001 – 31/08/2002 – Porto, Portugal
HIGH SCHOOL TEACHER OF MATHEMATICS (INTERNSHIP) – PORTUGUESE MINISTRY OF EDUCATION

● EDUCATION AND TRAINING

01/09/2009 – 12/11/2014

PHD IN APPLIED MATHEMATICS – Faculty of Sciences of University of Porto (FCUP), Porto, Portugal

01/09/2002 – 22/10/2004

MSC IN MATHEMATICS – FUNDAMENTALS AND APPLICATIONS – Faculty of Sciences of University of Porto (FCUP), Porto, Portugal

01/09/1997 – 29/05/2002 – Portugal

BSC IN MATHEMATICS – EDUCATIONAL BRANCH – Faculty of Sciences of University of Porto (FCUP), Porto, Portugal

● LANGUAGE SKILLS

Mother tongue(s): **PORTUGUESE**

Other language(s):

	UNDERSTANDING		SPEAKING		WRITING
	Listening	Reading	Spoken production	Spoken interaction	
ENGLISH	C2	C2	C1	C1	C1
SPANISH	C2	C2	C1	C1	B1

Levels: A1 and A2: Basic user; B1 and B2: Independent user; C1 and C2: Proficient user

● DIGITAL SKILLS

Python | Linux | MATLAB | R

● PROJECTS

01/06/2018 – 31/05/2021

eCSI-barcode – Efficient computational solutions for integrated DNA barcoding, metabarcoding, and associated high-throughput sequencing data analysis

co-PI

01/01/2022 – CURRENT

BioCoat: Engineered biomimetic hydrogel coating for improved biocompatibility of chronically-implanted neural electrodes

10/2018 – 09/2022

COMULIS: Correlated Multimodal Imaging in Life Sciences

10/2018 – 09/2021

NIS-DNA: Early detection and monitoring of non-indigenous species (NIS) in coastal ecosystems based on high-throughput sequencing tools

09/2018 – 08/2021

From Portugal back to Africa: uncovering the african roots of present-day Portuguese

05/2017 – 04/2020

PPBI: Plataforma Portuguesa de Bioimagem

05/2016 – 04/2020

NEUBIAS: A new Network of European BioImage Analysts to Advance life Science Imaging

12/2014 – 09/2015

Assessing The Whole-Genome Structure and Variation of the Tropical Adapted Zebu Cattle (*Bos indicus*) using Dense SNP Maps

● PUBLICATIONS

MCL1 alternative polyadenylation is essential for cell survival and mitochondria morphology

Cellular and Molecular Life Sciences 79, 164. ; DOI: 10.1007/s00018-022-04172-x
2022

Pereira-Castro I., Garcia B., Curinha A., Neves-Costa A., **Conde-Sousa E.**, Moita L., Moreira A

4SpecID: Reference DNA Libraries Auditing and Annotation System for Forensic Applications

Genes, 12, 61.; DOI: 10.3390/genes12010061
2021

Neto L., Pinto N., Proença A., Amorim A., **Conde-Sousa E.**

Characterization of the striatal extracellular matrix in a mouse model of Parkinson's disease

Antioxidants, 10(7), 1095; DOI: 10.3390/antiox10071095
2021

Freitas A., Aroso M., Barros A., Fernandez M., **Conde-Sousa E.**, Leite M., Carvalho E., Ribeiro C. C., Ferreira R., Pêgo A. P., Vitorino R., Gomez-Lazaro M.

QUAREP-LiMi: A community-driven initiative to establish guidelines for quality assessment and reproducibility for instruments and images in light microscopy

J. Microscopy; DOI: 10.1111/jmi.13041
2021

Nelson G. et al.

Detection of HER2 from Haematoxylin-Eosin Slides Through a Cascade of Deep Learning Classifiers via Multi-Instance Learning

J. Imaging, 6(9), 82; DOI: 10.3390/jimaging6090082
2020

La Barbera D., Polónia A., Roitero K., **Conde-Sousa E.**, Della Mea V.

Population analysis and evolution of *Saccharomyces cerevisiae* mitogenomes

Microorganisms, 8(7), 1001; DOI: 10.3390/microorganisms8071001
2020

Vieira D., Esteves S., Santiago C., **Conde-Sousa E.**, Fernandes T., Pais, C., Soares P., Franco-Duarte R.

Reference DNA databases for forensic species identification: Auditing algorithms

Forensic Science International: Genetics Supplement Series, 7 (1), pp. 564-566. DOI: 10.1016/j.fsig
2019

Conde-Sousa E., Pinto N., Amorim A.

Underestimation and misclassification of mutations at X chromosome STRs depend on population's allelic profile

Forensic Science International: Genetics Supplement Series, 7 (1), pp. 718-720. doi: 10.1016/j.fsig
2019

Antão-Sousa S., **Conde-Sousa E.**, Gusmão L., Amorim A., Pinto N.

Engineering hydrogels with affinity-bound laminin as 3D neural stem cell culture systems

Biomaterials Science, 7 (12), pp. 5338-5349. Doi: 10.1039/c9bm00348g
2019

Barros D., **Conde-Sousa E.**, Gonçalves A.M., Han W.M., García A.J., Amaral I.F., Pêgo A.P.

A dispersal of *Homo sapiens* from southern to eastern Africa immediately preceded the out-of-Africa migration

Scientific Reports, 9 (1), 4728, DOI: 10.1038/s41598-019-41176-3
2019

Rito T., Vieira D., Silva M., **Conde-Sousa E.**, Pereira L., Mellars P., Richards M.B., Soares P.

Optimizing the information increase through the addition of relatives and genetic markers in identification and kinship cases

Forensic Science International: Genetics, 40, pp. 210-218. DOI: 10.1016/j.fsigen.2019.02.019
2019

Pinto N., Simões R., Amorim A., **Conde-Sousa E.**

An affinity-based approach to engineer laminin-presenting cell instructive microenvironments

Biomaterials, Vol 192, 2019, doi:10.1016/j.biomaterials.2018.10.039
2019

Barros D., Parreira P., Furtado J., Ferreira-da-Silva F., **Conde-Sousa E.**, García A.J., Martins M.C.L., Amaral I.F., Pêgo, A.P.

The influence of the different mutation models in kinship evaluation

Forensic Science International: Genetics Supplement Series <http://dx.doi.org/10.1016/j.fsigss.2017.2017>
2017
Machado P., Gusmão L., **Conde-Sousa E.**, Pinto N.

Key individuals for discerning pedigrees belonging to the same autosomal kinship class

Forensic Science International: Genetics, 19 March 2017, DOI: 10.1016/j.fsigen.2017.03.018
2017
Goncalves J., **Conde-Sousa E.**, Egeland T., Amorim A., Pinto N.

Mitogenome diversity in Sardinians: a genetic window onto an island's past

Mol Biol Evol. 2017 Feb 8. doi: 10.1093/molbev/msx082
2017
Olivieri A., Sidore C., Achilli A., Angius A., Posth C., Furtwängler A., Brandini S., Rosario Capodiferro M., Gandini F., Zoledziewska M., Pitzalis M., Maschio A., Busonero F., Lai L., Skeates R., Giuseppina Gradoli M., Beckett J., Marongiu M., Mazzarello V., Marongiu P., Rubino S., Rito T., Macaulay V., Semino O., Pala M., Abecasis G.R., Schlessinger D., **Conde-Sousa E.**, Soares P., Richards M.B., Cucca F., Torroni A.

N3DFix: an Algorithm for Automatic Removal of Swelling Artifacts in Neuronal Reconstructions

Neuroinformatics, 2016 doi:10.1007/s12021-016-9308-7
2016
Conde-Sousa E., Szücs P., Peng H., Aguiar P.

A working memory model for serial order that stores information in the intrinsic excitability properties of neurons

Journal of Computational Neuroscience, Volume 35, Issue 2, October 2013, pp 187-199
2013
Conde-Sousa E., Aguiar P.

Assessing paternities with inconclusive STR results: the suitability of bi-allelic markers

Forensic Science International: Genetics, Volume 7, Issue 1, January 2013, Pages 16-21
2013
Pinto N., Magalhães M., **Conde-Sousa E.**, Gomes C., Pereira R., Alves C., Gusmão L., Amorim A.

● ORGANISATIONAL SKILLS

HEROHE grand-challenge

Main organizer of the 2020 HEROHE grand-challenge (<https://ecdp2020.grand-challenge.org/>), a parallel event of the 16th European Congress on Digital Pathology, with more than 800 participants.