12 full-time PhD positions

HOST INSTITUTIONS:

- Agencia Estatal Consejo Superior de Investigaciones Científicas (CSIC). Spain (Valencia)
- Stockholms Universitet (SU). Sweden (Stockholm)
- Centre National de la Recherche Scientifique (CNRS). France (Évry)
- Fondazione Istituto Italiano de Technologia (IIT). Italy (Milan)
- Nacionalni Institut la Biologijo (NIB). Slovenia (Ljubljana)
- Fundació Centre de Regulació Genòmica (CRG). Spain (Barcelona)
- Max-Planck Gesellchaft sur Forderung der Wissenschaften EV (MPG). Germany (Berlin)
- Commissariat a l'energie atomique et aux energies alternatives (CEA; Genoscope). France (Saclay)
- BioBam Bioinformatics. Spain (Valencia)
- Oxford Nanopore Technologies Ltd. United Kingdom (Oxford)
- Earlam Institute. United Kingdom (Norwich)

RESEARCH PROFILE: First Stage Researcher (R1[1])

APPLICATION DEADLINE: 16 January 2023

EU RESEARCH FRAMEWORK PROGRAME: HORIZON MSCA – 2021- DN

MARIE SKOLODOWSKA CURIE GRANT AGREEMENT NUMBER: 101072892

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[1] First Stage Researcher (R1) PhD candidate or equivalent. Early stage researcher with less than 4 years FTE research experience.

About the LONGTREC network

LongTREC is a Doctoral Network of the Marie Sklodowska-Curie action program (MSCA-DN) that will develop methods and tools for the analysis of transcriptomic data obtained with the most recent single-molecule, long-reads sequencing technologies. The **LongTREC** MSCA-DN will train 12 Doctoral Candidates (DC) who will perform research in top European computational biology laboratories guided by current European leaders of the lrRNA-seq technologies, both at experimentation and computation. Each candidate will develop a specific project under the supervision of a Principal Investigator within the **LongTREC** network.
All **LongTREC** DCs will enroll in local PhD programs from top-tier universities. Taking part in local programs will allow our DCs to be embedded in their respective graduate environments, gaining access to seminars, graduate retreats, training, and local scientific activities. Moreover, LongTREC DCs will be fully integrated in the research lab and R&D departments of their host institutions, participating in the day-to-day scientific life of their groups, which includes project discussions, journal clubs, interaction with visiting scientists, co-supervision of undergraduate or master's thesis, institutional seminars, etc. DCs will be encouraged to enroll in local/national/European Young Scientist Organizations to promote peer engagement, leadership, and networking skills. Moreover, **LongTREC** will structure doctoral training as an intersectoral endeavor by systematically involving the academic and private sector of the training of our DCs. Every DC will carry out at least two research-based, intersectoral and international secondments. The recruitment procedure will be through an international and open call in which future candidates who possess less than 4 years of research experience and are interested in the lrRNA-seq transcriptomics are welcome to apply.

Offer Description

The Doctoral Network of the Marie Sklodowska-Curie action program (MSCA-DN) **"LONGTREC - The Long-reads TRanscriptome European Consortium: The next generation transcriptome biology revealed by single molecule sequencing technologies"** is recruiting 12 highly motivated PhD candidates. The offered positions are available with a duration of 36 months. The fellowships are funded as part of the Marie Skłodowska-Curie Actions (MSCA) Doctoral Network under the European Commission's Horizon program. MARIE CURIE GRANT AGREEMENT NUMBER: 101072892.

See more info at: https://ec.europa.eu/research/mariecurieactions/actions/research-networks_en

Scientific project

lrRNA-seq is an effervescent field, where new experimental protocols, biological applications and analysis solutions are constantly emerging in pace with the rapid improvements in third-generation sequencing technologies. lrRNA-seq has already displayed great potential, but much work is still needed. e lrRNA-seq technology can unravel novel biological insights which have been hidden until now due to technological limitations. Because of their potential for full-length transcript sequencing, lrRNAseq can improve genome annotation by providing an accurate representation of transcript start and end sites, as well as alternatively spliced sites and discover novel genes and transcripts. lrRNAseq is triggering a paradigm shift in transcriptome biology

research by progressively moving away from a gene focus to embrace a transcript-centric view. A new generation of computational biologists is essential to consolidate current methods, develop new tools, envision new applications, and lead the unstoppable transition of transcriptome analysis to effectively become LRS-based. The **LongTREC** network will provide all the key expertise, training, skills, values and infrastructure to support the scientific excellence of our PhD candidates.

PhD Positions

PhD Project 1: Alternative splicing regulation at the single cell resolution: Protocols and computational developments for long read RNA-Seq in single cell.

Nearly 95% of multiexonic genes in humans undergo alternative splicing1, the process by which multiple isoforms are transcribed from a single gene through differential inclusion of exons and splice sites. Alternative splicing is a highly regulated process with evidence for the developmental stage-, tissue-, and cell-specific isoforms. The development of long-read RNA sequencing has opened the unique opportunity to gather a much more comprehensive understanding of the existing transcript diversity and its regulation. Work by ourselves and others, mainly conducted at the tissue level demonstrated that the current transcript diversity in human is severely underestimated. Although already extremely informative, this work was conducted on thousands to millions of cells, obfuscating transcripts that are found in specific cell types including rare cell types such as stem cells. Recent molecular developments by ourselves and others aiming to bring long-read sequencing to single cells already provided unique insights on transcript regulation but also fundamental events such as VDJ recombination. Methods so far have been suffering from relatively low throughput leading to the recovery of genes with mid to high expression. Additionally, there is limited availability of computational tools for their analysis and visualization. We offer a highly collaborative PhD project between the Haerty (bioinformatics) Macaulay (molecular biology, technology development) groups. The main aim of the project is to develop protocols and computational solutions to further enable the applications of long-read RNA sequencing to single cells, with a specific focus on rare cell types such as hematopoietic stem cells, and genes fundamental to our physiology and of primary interest in disorders and diseases but expressed at low levels. The student will work in a rapidly developing field and gain unique expertise in computational biology, large dataset analysis, genomics, transcriptomics, sequencing technologies, molecular biology, technology development, and therapeutic target identification. The project will be conducted at the Earlham Institute, a UKRI-BBSRC strategically supported research centre of excellence for bioinformatics and sequencing technology development. In addition to the training offered through the LongTrec network, the student will have access to training and career development opportunities at EI and on the Norwich Research Park.Host: Earlham Institute, United Kingdom.

The ideal candidate must hold an undergraduate degree (2:1 equivalent) or a Master's degree in biology, biotechnology, or molecular biology as well as experience in wet lab.

Supervisor: Wilfried Haerty (https://www.earlham.ac.uk/profile/wilfried-haerty), Iain Macaulay (https://www.earlham.ac.uk/research-group/macaulay-group).

Envisioned secondments: Uppsala University (SciLifeLab) (Adam Ameur), Biobam (Stefan Götz)

PhD Project 2: Develop an improved adaptative sampling method for Nanopore dRNA and cDNA sequencing.

RNA base modifications and transcript isoform usage have major and critical impact on basic gene function, viral infection, and applications such as RNA vaccines. However, little is known about transcriptome-wide epi-transcriptomic modifications and isoform diversity, especially of low abundance and biomedical relevant transcripts. The goal of the project is to develop experimental and informatic tools for in silico targeted sequencing (aka "adaptive sampling" or "read until") of RNA isoforms and modifications using direct RNA sequencing and the Nanopore sequencing platform. The student will apply these tools to in-depth transcriptome analysis both in fundamental biology and clinical research relevant contexts. The project builds on the Loose lab's prior work on adaptive sampling and its applications (Payne et al. Nat Biotechnol. 2021)

The ideal candidate should have a minimum 2.1 BSc (UK) or an MSc in biological sciences, bioinformatics or related disciplines. Previous laboratory-based experience in a relevant area (experimental cell biology, molecular biology or biochemistry techniques; genomics or transcriptomics; and bioinformatics and/or software) will be advantageous. Overseas applicants should fulfil the University of Nottingham English Language Requirements.

Host: Oxford Nanopore Technologies. United Kingdom

Supervisors: Aino Järvelin (https://nanoporetech.com/), Matt Loose (https://www.nottingham.ac.uk/Life-Sciences/people/matt.loose)

Envisioned secondments: Wobble (Richard Kuo), CRG (Eva María Novoa), CSIC (Ana Conesa)

PhD Project 3: Algorithm development for splice alignment of long-read sequence data.

Long-read sequencing technologies have revolutionized the area of RNA biology through their capacity to sequence the RNA in full length. However, the data needs computational processing. Current methods cannot accurately identify transcripts (RNA products) from such data, which has been demonstrated in recent studies that found thousands of low-quality and potentially spurious transcript predictions from state-of-the-art tools. Such erroneous predictions cause mistakes in analysis and conclusions. This project aims to develop computational methods to process long-read transcript data, particularly for the computational problem of splice alignment of long-read data. The project will have both theoretical and practical components. The theory part focuses on algorithm and data structure design for efficient text search aimed at biological sequence data. The practical part involves implementing the ideas into software that can be used by biologists. The ideal candidate must have completed courses equivalent to at least 60 credits in a mathematical subject (e.g., computer science, statistics, physics, or applied mathematics), of which at least 30 credits must be related to either numerical analysis or computer science having solid mathematics and/or Computer Science background.

Host: Stockholms Universitet. Sweden.

Supervisor: Kristoffer Sahlin (https://sahlingroup.github.io/), Adam Ameur (https://www.katalog.uu.se/profile/?id=N3-1440)

Envisioned secondments: Wobble Genomics SL (Dr. Richard Kuo), Commissariat a l'energie atomique et aux energies alternatives (Jean-Marc Aury, France Denoeud), Spanish National Research Councill (Ana Conesa).

PhD Project 4: Long read RNA sequencing to annotate the genomes across the eukaryotic tree of life.

Identifying and mapping genes into genomes is essential to relate the genome sequence to the biology of species. Producing high-quality gene annotations, however, is more difficult than usually thought, as illustrated by the fact that twenty years after the publication of the first drafts of the human genome sequence we still do not know the number of human genes. Long-read RNAseq is becoming an appealing approach to produce high quality annotations of eukaryotic genomes. These are essential, as plans are under way to sequence the genome of about the 1.8M know eukaryotic species on Earth. The Doctoral candidate will develop computational methods to obtain accurate gene and transcript annotation from long read RNAseq data. In the lab, we plan to develop experimental RNA-seq methods specifically aimed to genome annotation, and we plan to produce long-read RNAseq data in about 40 eukaryotic species strategically placed along the eukaryotic phylogeny. The candidate will use this data (and data produced elsewhere) to develop and test the computational methods. In addition, the candidate will analyze the data to investigate the evolution of the exonic structure of genes and of gene expression across eukaryotes. The ideal candidate must hold or be in the process of gaining a Master's degree in Bioinformatics, Computational Biology, Computer Science, or a similar field, as well as familiarity with basic evolutionary and molecular biology concepts, and good statistical (data analysis) and programming skills. Familiarity with mathematical and quantitative approaches is preferable.

Host: Center for Genomic Regulation (CRG). Spain.

Supervisor: Roderic Guigó (https://www.crg.eu/roderic_guigo)

Envisioned secondments: Wobble Genomics (Richard Kuo), Stockholms Universitet (Kristoffer Sahlin), Commissariat a l'energie atomique et aux energies alternatives (Jean-Marc Aury, France Denoeud)

PhD Project 5: Investigation of allele-specific expression in stress-challenged polyploid potato plants using long read transcriptomics.

Allele-specific expression and expression of gene families contribute to phenotypic variation and complex traits. Unraveling the function of different transcript variants is especially challenging in polyploid species, which most crop plants are, due to multiple highly similar transcripts. Long reads substantially simplify differential expression analysis of such highly similar transcripts. The Doctoral candidate will benchmark existing methods and those developed within the doctoral network for analysis in polyploid species. The candidate will build an analysis pipeline that can be applied for differential expression of allele isoforms and gene families in tetraploid potato genotypes and will study the function of different isoforms in potato leaves under diverse stress conditions. The host group is composed of a highly multidisciplinary and motivated group of biologists, microbiologists, biotechnologists, mathematicians, engineers, and bioinformaticians. The candidate will have access to excellent equipment and facilities as well as training in soft skills required for reaching research independence. The ideal candidate must hold or be in the

process of gaining a Master's or equivalent degree in Natural sciences, such as Bioinformatics, Biology, Biotechnology, or Biochemistry as well as possess strong communication skills and teamwork abilities within and outside the host team. Interest in both wet and dry lab techniques is required, and experience with high-throughput sequencing is highly recommended, as well as some basic knowledge of programming languages, such as R or Python.

Host: National Institute of Biology, Department of Biotechnology and Systems Biology (NIB). Slovenia.

Supervisor team: Kristina Gruden and Marko Petek

(http://www.nib.si/eng/index.php/component/directory/?view=details&id=77
https://www.nib.si/component/directory/?view=details&id=102&Itemid=12)

Envisioned secondments: University of Florida, USA (Lauren McIntyre); BioBam Bioinformatics S.L. (Stefan Goetz).

PhD Project 6: Long-read single-cell and spatial transcriptomics to explore the diversity of isoform expression.

Single-cell technologies are becoming central to understand complex biological systems. Different microfluidic assays provide, in routine, high-quality experiments that shed light on complex biological processes. Our team introduced the use of long-read Nanopore sequencers in single-cell and spatial transcriptomics, providing the necessary workflows to obtain in-depth full-length profiles at single cell (Lebrigand et la., Nat. Comm., 2020) and spatial resolution (Lebrigand et la., bioRxiv, 2022). These developments provide new opportunities to better explore the mechanisms that control isoform-level and full-length heterogeneity of the transcriptome. The aim of this project is to introduce AI approaches to better define and explore the gene expression pattern in terms of splicing usage, bi-allelic expression, and splicing quantitative trait loci (sQTL) in complex biological samples at single-cell and spatial resolutions. The PhD student will develop innovative computational approaches based on machine learning to explore and decipher the biology of those mechanisms. The ideal candidate must hold or be in the process of gaining a Master's degree in Bioinformatics, Biotechnology, or Biochemistry as well as possess experience with wet and dry lab techniques as well as knowledge of R or Python programming languages.

Host: Centre National de la Recherche Scientifique (CNRS). Institute of Molecular and Cellular Pharmacology (IPMC, Sophia Antipolis). France.

Supervisor: Pascal Barbry (http://www.ipmc.cnrs.fr).

Envisioned secondments: Nanopore, UK (Aino Järvelin), WCM (Hagen Tilgner)

PhD Project 7: Interactome predictions from long-read transcriptome sequencing data.

The Max-Planck-Institute for Molecular Genetics in Berlin is a leading research organization in genome research and is aiming to discover how genes and their regulatory landscapes give rise to organismal function. The institute is home to over 200 scientists from over 40 different countries, who collaborate in 20 different research groups. The Herwig group is developing computational

methods i) for the analysis of molecular sequencing data with a focus on human diseases, in particular cancer, and ii) for the integration of these data in the context of biological networks. Recently, we have developed IsoTools, a Python-based software package for the analysis of long-read sequencing data. We are interested in uncovering the role of alternative splicing in cancer, and we are looking for an outstanding PhD candidate to further develop our computational methods in the field of long-read RNA sequencing in particular tools for the functional interpretation of isoforms. The ideal candidate must have a master's degree in Computational Biology, Mathematics, or Computer Science as well as have excellent programming skills in Python and the ability to work under a Unix/Linux operating system, experience in software development and shared, interactive work environments such as Jupyter, Notebooks, experience in statistical methods and bioinformatics applications (R, BioConductor), good knowledge of molecular biology and genetics, as well as excellent communication skills and willingness to work in an interdisciplinary team.

Host: Max-Planck Gesellchaft sur Forderung der Wissenschaften EV (MPG). Germany.

Supervisor: Ralf Herwig (https://www.molgen.mpg.de/156820/Bioinformatics-Group).

Envisioned secondments: Earlham Institute (Wilfried Haerty), Biobam (Stefan Goetz)

PhD Project 8: Exploring the transcriptional landscape of environmental samples using metatranscriptomics long reads.

Marine environments remain largely unexplored and unobserved. Planktonic eukaryotes have been shown to harbour non-canonical splice sites and original splicing mechanisms1, but a lot are uncultivable. Recently, long-read sequencing technologies have emerged and their current costs make them eligible for sequencing metagenomics and metatranscriptomics environmental samples2. The PhD project we propose is aiming at solving pending questions on transcriptome biology by exploring intron structure, organization, and evolution in a broad set of eukaryotes, taking advantage of the fact that long reads provide the complete set of introns in a single read (without biases inherent to assembly). Our project represents the first attempt to use meta-omics data directly (with no assembly steps, and no reference genome) to obtain full transcript structures and coding sequences. We also propose to discover new introns and splicing mechanisms in the still poorly explored marine eukaryotic world. Nanopore long-read sequencing allows such a strategy, providing that suitable pipelines are developed. This work will be made at an unprecedented scale and will take advantage of the large-scale sampling realized during Tara expeditions. The project is a combination of several expertise in bioinformatics (software development and assessment), genomics (sequencing, functional transcriptomics) as well as evolutionary analysis. The ideal candidate must hold or be in the process of gaining a Master's degree in Bioinformatics as well as have experience with genomics, as well as knowledge of Unix-type environments, scripting languages (Perl, Python, Awk, or R), and genome analysis tools. Knowledge of workflow management systems (such as Snakemake) and task managers (such as Slurm) would be an asset.

Host: Genoscope, CEA Institut de Biologie François Jacob. Genoscope (UMR8030, Metabolic Genomics lab), Université Paris Saclay, France.

Supervisors: France Denoeud and Jean-Marc Aury (https://www.genoscope.cns.fr/lbgb/).

Envisioned secondments: Stockholm University (Kristoffer Sahlin); Centre de Regulació Genòmica, Barcelona (Roderic Guigo)

PhD Project 9: Analysis of tRNA dynamics using native RNA nanopore sequencing.

Transfer RNAs (tRNAs) are abundant small non-coding RNAs that play a pivotal role in decoding genetic information, determining which transcripts are highly and poorly translated at a given moment. Dysregulation of tRNA abundances and their RNA modifications is a well-known feature in cancer cells, which leads to enhanced expression of specific oncogenic transcripts and proteins. Our laboratory has recently developed a novel approach to studying tRNA populations using native RNA Nanopore sequencing technologies (Nano-tRNAseq), providing tRNA abundance, length, and tRNA modification information from the same individual molecules. Nano-tRNAseq generates powerful and information-rich data, which can in turn be used to predict the biological status (e.g. health, disease, stress) of the cells. The Doctoral candidate will develop novel bioinformatic algorithms and tools to integrate tRNA modification and abundance information, as well as alignment-free classification methods of Nanopore current intensity signals. Once these tools have been built, the PhD candidate will train novel machine-learning algorithms to classify and stratify samples based on different characteristics (disease, exposure to stress, cancer, metastasis, etc). The Doctoral candidate will also be responsible for preparing and sequencing Nanopore native RNA libraries, which will be used to train the candidate's machine learning models, together with other existing datasets previously generated in the lab. The ideal candidate must hold or be in the process of gaining a Master's degree in Bioinformatics, Biotechnology, or Biochemistry as well as have experience with wet and dry lab techniques as well as knowledge of R or Python programming languages.

Host: Center for Genomic Regulation (CRG).

Supervisor: Eva Maria Novoa (https://www.crg.eu/ca/programmes-groups/novoa-lab).

Envisioned secondments: Oxford Nanopore Technologies (Aino Järvelin), Italian Institute of Technology (Francesco Nicassio, Tommasso Leonardi)

PhD Project 10: Characterization of microRNA primary transcripts by Nanopore direct RNA sequencing.

The project will consist of the development and application of state-of-the-art genomics methods based on Nanopore direct RNA sequencing, with the underlying aim of characterizing the regulatory features of a subset of ncRNAs involved in cancer. This is a highly interdisciplinary project that will require a combination of experimental (wet-lab) and analytical (dry-lab) work. Based on their interest and prior experience, the applicant will be responsible for either the experimental or bioinformatics component of the project, and the other one will be carried out by another experienced researcher in the host lab. Candidates with a computation background will apply advanced analytical strategies and develop new methods to push the boundaries of what can be achieved with Nanopore direct RNA Sequencing. On the other hand, candidates with an experimental background will have the opportunity to apply existing techniques as well as develop and/or optimize new approaches for Nanopore Direct RNA Sequencing. In both cases, this Ph.D. program will provide solid and interdisciplinary training on modern, long-read sequencing technologies for the study of the non-coding genome. The ideal candidate must hold

or be in the process of gaining a master's degree in Biology, Biotechnology, Bioinformatics, Computational Biology, Mathematics, Physics, Statistics. Candidates with a computational background will need to have familiarity with bioinformatics and analysis of genomics data as well as with scientific programming in R or Python. Candidates with an experimental background will need to have prior hands-on laboratory experience as well as familiarity with bioinformatics and analysis of genomics data (preferred but not required).

Host: Istituto Italiano di Technologia, Italy.

Supervisor: Francesco Nicassio (https://www.iit.it/people-details/-/people/francesco-nicassio) and Tommaso Leonardi (https://www.iit.it/web/guest/people/-/people/tommaso-leonardi).

Envisioned secondments: Nanopore (Aino Järvelin), CRG (Eva Maria Novoa)

PhD Project 11: Long Reads multiomics methods to understand isoform regulatory biology.

Transcript variant expression is the combination of transcriptional and post-transcriptional regulation. The regulatory environment at promotor regions is studied by short reads, but these do not reveal the contiguous promoter methylation landscape, which could be captured by LRS. Moreover, methods for integration of multi-omics long reads data do not exist. The Doctoral candidate will develop a wet-lab protocol for long reads ATAC-seq and Nascent-seq using Nanopore and apply them to H1 human cell line. The candidate will develop an analysis pipeline to process lrATAC-seq data to identify chromatin accessibility and methylation. Methods will be implemented in the SQANTI and tappAS software tools. The ideal candidate must hold or be in the process of gaining a Master's degree in Bioinformatics, Biotechnology or Biochemistry. Experience with wet and dry lab techniques are highly recommended, as well as knowledge of R or Python programming languages.

Host: Spanish National Research Councill (CSIC). Institute for Integrative Systems Biology

Supervisor: Ana Conesa (http://conesalab.org).

Envisioned secondments: Italian Institute of Technology (Francesco Nicassio); Nanopore, UK (Aino Järvelin), University of California at Santa Cruz (Angela Brooks).

PhD Project 12: Development of a user-friendly software solutions of lrRNA-seq data analysis. From mapping to pathway analysis.

lrRNA-seq data analysis is poorly accessible to users without bioinformatics expertise. OmicsBox is a user-friendly software with modules for RNA-seq and functional enrichment analysis. lrRNA-seq is not yet supported. The candidate will compare existing long reads analysis pipelines for mapping, quantification, and differential expression analysis in non-model species, and develop a novel pathway analysis method for isoform-resolved data. The newly developed methods will be implemented in OmicsBox as user-friendly analysis features. The ideal candidate must hold or be in the process of gaining a master's degree in bioinformatics or a related field with a background in biological sciences (biology, biotechnology) as well as possess a strong technological interest in software development as well as a solid knowledge of languages used in scientific programming (R, python, bash, etc.).

Host: BioBam Bioinformatics, Spain.

Supervisor: Stefan Götz (https://www.biobam.com/about/?cn-reloaded=1).

Envisioned secondments: UU-SciLifeLab (Adam Ameur), CNRS (Pascal Barbry).

REQUIREMENTS:

Eligibility criteria:

We welcome applications from PhD candidates from any country fulfilling the following criteria:

- Eligible candidates must not have resided or carried out their main activity (work, studies, etc.) in the country of their host institution for more than 12 months in the 3 years immediately prior to their recruitment by the host institution (i.e. the starting date indicated in the employment contract/equivalent direct contract). This is applicable to all jobs except for the PhD position 2 in which the mobility criteria is not required.
- Eligible candidates shall at the date of recruitment by the host institution (i.e. the starting date indicated in the employment contract/equivalent direct contract), be in the first 4 years (full-time equivalent research experience) of their research careers and not have been awarded a doctoral degree.
- Eligible candidates must hold or be in the process of gaining a master's degree relevant to the chosen position (including biology, medicine, biochemistry, bioinformatics or a related discipline, depending on each PhD project) by June 2023 or an equivalent experience, or must hold an official university qualification from a country of the European Higher Education Area with a minimum of 300 ECTs of official university studies.
- In all cases, employment will be conditioned to acceptance by the Doctoral school of the associated PhD awarding institution.

Successful candidates must have a high level of proficiency in written and spoken English, which will be assessed with the motivation letter and the interview, respectively.

ADDITIONAL INFORMATION:

Application and selection process

The application will be done through an online application platform to be found on the LONGTREC website: https://longtrec.eu/. Applications must be in English. Each applicant may apply to a **maximum of three individual research projects**.

Applications must contain the following documents (in pdf):

- a CV (including publications, if any),
- a motivation letter,
- 2 reference letters,
- Statement in diversity, inclusion and sustainability
- Copies of Bachelor's and Master's degree certificates. Candidates should include the transcripts in English of academic records for the studies that make them eligible for a doctoral programme. If these studies have been completed by the deadline for

applications, the total number of credits for the degree and the credits awarded must also appear.

Eligible applications will be ranked on the basis of CVs and merits by a selection committee: up to 30 points for the CV, up to 15 points for the motivation letter and up to 5 points for the two reference letters.

The 3 best candidates for each position will be invited to a recruitment workshop in February 2023 (date to be confirmed) where the final candidates will be selected.

Applicants with a positive evaluation but not selected will be included on a reserve list to cover eventual future positions and might be contacted at a later stage.

Timeline

- Application deadline: 16 January 2023
- Announcement of preselection results and call for interviews: 1 February 2023
- Recruitment workshop: Short-listed candidates will be interviewed at the end of February 2023 (date to be confirmed). To give same opportunities to all candidates, we anticipate that workshop and interviews will be run in a virtual format. Full details regarding the interview process will be sent to invited candidates during the arrangement of interviews.
- Communication of the final results: 1 April 2023
- Hiring process: between June and September 2023 (depending on end of Master's degree)
- Enrolment on Doctoral school deadline: October 2023

Benefits

- 3-year full-time employment contract (salary depends on the country of the recruitment considering both the local and MSCA regulations for Early Stage Researchers and their family status at the time of the recruitment).
- Enrolment in a PhD program.
- Shared research and innovative multidisciplinary and multisectoral training by experts and experienced trainers from two sectors (academia and industry).
- A structured training programme consisting of soft skill courses, targeted workshops, retreats, social events and networking.
- Secondments at other institutions within the LONGTREC consortium.
- Gaining experience abroad.
- Opportunities for participation in national and international meetings.
- Enlarged professional network and improved future scientific career perspective in academia and the private sector.

For further information on the LONGTREC MSCA-DN and the application process, please visit https://longtrec.eu/.

This project has received funding from the European Union's Horizon research and innovation program under the Marie Skłodowska-Curie grant agreement No 101072892.