**Master Project Proposal**

**Title: Modelling single-cell transcriptomic data from healthy human CD4 T cells**

**Synopsis:** CD4 T cells are the organisers of immune responses. They sequentially differentiate from thymocytes into circulating naïve and memory T cell subsets, while committed to conventional or regulatory lineages, and define an ecology of cell types efficiently limiting autoimmunity and pathology of the immune responses.

We propose to explore single-cell RNA-seq datasets previously generated in the lab and uncover the biological pathways required for the homeostasis and activity of human CD4 T cells. The candidate will make use of the latest computational methodologies to identify different populations of cells, respective gene signature, and their putative developmental timeline.

Our long-term aim is to identify relevant targets to modulate T-cell imbalances in future therapies for immune diseases.

**Key words:** scRNA-seq, T cells, human health, Molecular Biology, Computational Biology

**Supervisor:** *Alexandre Raposo, Ana Espada Sousa Lab, alexandre.raposo@medicina.ulisboa.pt*
**Co-Supervisor:** *Ana Espada de Sousa, Ana Espada de Sousa Lab, asousa@medicina.ulisboa.pt*
*Webpage of the group*