EURATRANS uses state-of-the-art and emerging large-scale technologies and advanced computation in an expanded multi-disciplinary approach to identify gene networks underlying common diseases. We use the rat as model organism to identify the major gene pathways for human inflammatory, cardiovascular and metabolic, and behavioural disorders. Our programme will use next-generation sequencing technologies to generate genomic datasets and analyse the transcriptome across tissues in specialised rat resources. Genomic data will be integrated with cutting-edge, quantitative metabonomic, proteomic, and epigenomic datasets giving significant depth of coverage across molecular components of the gene, the cell, the organ and the organism. We shall gather, annotate and integrate these datasets in relational and dynamic models that can be used for comparative analysis to understand human gene function. These studies will reveal new biology enabling the understanding of human genes in the context of functional genomic networks that will result into comparative medicine.

We will incorporate our data into existing and new databases and establish repositories for models, reagents, discovery tools and specimens available to the scientific community. Our approaches will enable us to decipher gene function at large scale. Because we will focus on concepts and networks (rather than on single genes) we will produce results with relevance to fundamental mechanisms. Our results will contribute strategies to combat common diseases affecting human inflammatory, cardiovascular/metabolic, and behavioral disorders through identification of novel disease relevant networks that represent targets for diagnosis and drug therapy. This aim will be achieved by an integrated and interdisciplinary approach that brings together scientists with proven track records, albeit different areas of expertise. Our aim is to encourage rapid exchange of information between research fields and their immediate application in medicine and biotechnology.