Genetic and molecular markers of healthy aging and longevity

Our research

The Molecular Epidemiology group is part of the Epidemiology, Biostatistics and Biodemography (EBB) research unit at the Faculty of Health Sciences.

Overall, our research examines genetic and molecular markers and mechanisms that influence how long and how well we live. Our main focus is healthy aging, characterized by a long life with good physical and mental health, and age-related diseases.

Some of the specific topics that we focus on in our research are:

- Genetic studies of human aging and age-related diseases, e.g., cognitive function, including dementia and Alzheimer's disease.
- Using genetic variants to make predictions about an individual's risk of colorectal cancer, which is one of the most common types of cancer in the world.
- Functional genomic studies of human aging involving the analysis of one or multiple layers of biological variation, e.g., epigenome-wide, transcriptome-wide and proteome-wide omics data.
- Analysis of DNA methylation age, which is a proposed biomarker of biological age that has been linked to health- and lifespan.
- Studies of copy number variants (CNVs), where parts of the genome exist in fewer or more copies than the normal two.
- Studies of miRNAs, mitochondrial DNA copy number, and X-inactivation in women in relation to human aging and age-related diseases.

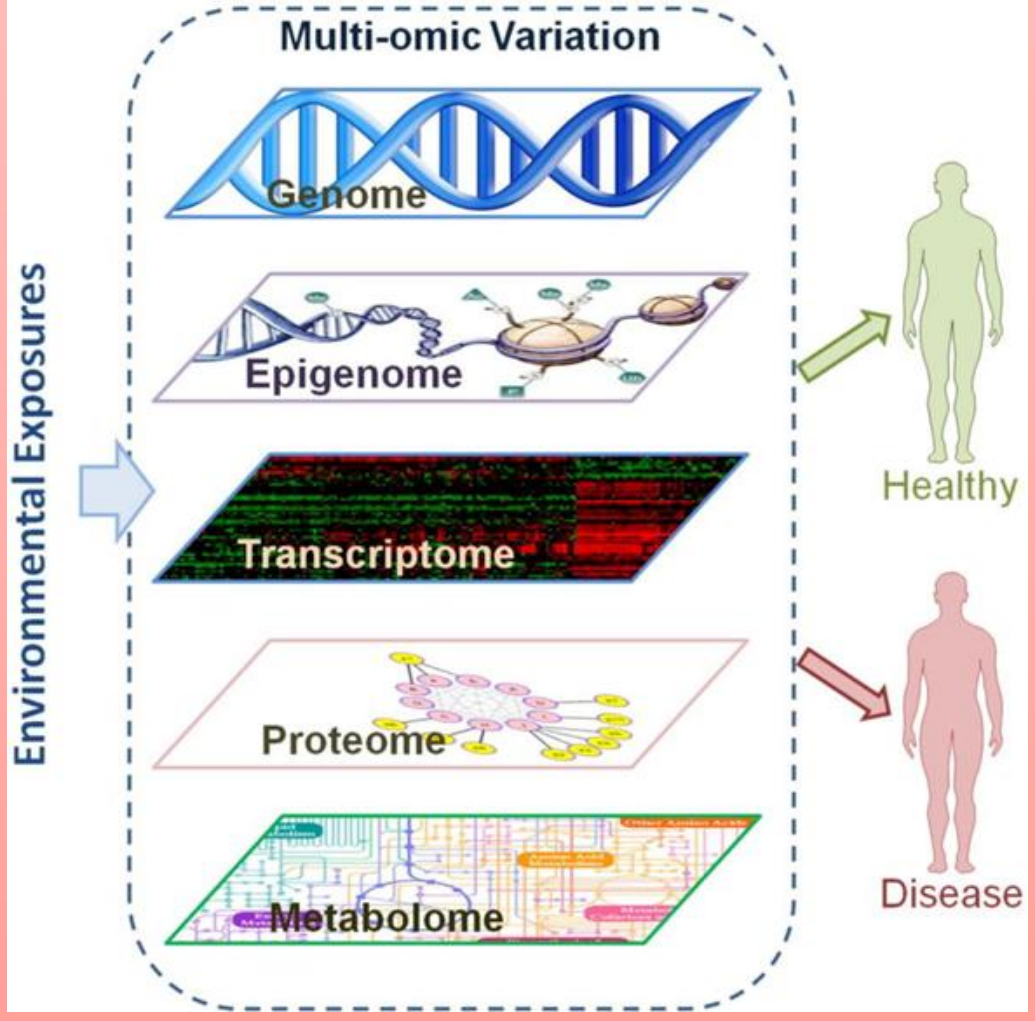
Our data and methods

In our research we primarily use data, i.e., phenotype and biological data, from the studies of twins and long-lived individuals conducted at EBB. Additionally, we use data from international biobanks, such as UK Biobank.

We have a large number of omics data sets (genetic, epigenetic, gene expression and protein data sets), which means that most of our projects involve biostatistical and bioinformatic analysis of already existing data.

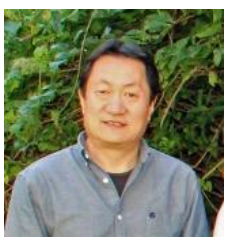
We use a wide range of analysis methods, e.g.:

- Genome-wide association studies of genetic data (GWAS), DNA methylation data (EWAS), gene expression data (TWAS), and proteome data (PWAS)
- Twin studies
- Genome-wide studies of copy number variants (CNVs)
- Mendelian randomization (MR) and Instrumental Variable (IV) approaches



Our group



Check out the EBB website for more information:

Scan me!

If you are interested in working on a project in our group, please contact: mnygaard@health.sdu.dk