

PRESS RELEASE

Understanding How Genes Interact

Bonn Researchers Play Key Role in Mapping Gene Interactions

Bonn, April 30 – How do our genes determine our appearance and our susceptibility to disease? This question is central to biomedical research, and today we can sequence thousands of human genomes to identify these genes. However, genes work in complex networks. In a major transdisciplinary collaboration, an international team of geneticists and bioinformaticians set out to create a so-called genetic interaction (GI) map of a human cell. With significant contributions from the Canadian Donnelly Centre, the University of Minnesota, the Hospital for Sick Children in Canada, the University Hospital Bonn, and the University of Bonn, a first draft has now been published in the journal *Cell*. This draft currently covers about 2.5 percent of all possible gene pairs.

Most genes in the genome can be removed without consequences for the cell—an observation that fits only partially with our understanding of evolution. One explanation is that these genes are dispensable since another gene takes over their function. In this case, consequences for the organism would be observable only if two genes are lost simultaneously. This so-called gene-gene relationship is referred to as a genetic interaction (GI). Nearly three decades ago, corresponding authors Charles Boone and Brenda Andrews from the Donnelly Centre at the University of Toronto in Canada, and Chad Myers from the University of Minnesota began to co-deplete nearly all possible gene pairs in the genetic model system yeast, which confirmed the GI hypothesis. With the discovery of the CRISPR-Cas9 gene-editing tool, similar studies became possible in the human genome—a field that co-author Jason Moffat of the Hospital for Sick Children played a key role in developing.

With the recently published first draft of the GI map, a team led by first author Assistant Professor Maximilian Billmann from the Institute of Human Genetics at the UKB established a gene-editing platform to study gene pairs in a cultured human cell line on an unprecedented scale. The team also developed a computer-based algorithm to identify approximately 90,000 GIs among the four million gene pairs examined. These GIs included gene pairs that link drug targets and genes that are mutated in human diseases. “This showed us that genes that may appear dispensable in the human genome are actually part of a more complex regulatory system that evolution has built to make a cell more robust,” says Billmann, who is a member of the Transdisciplinary Research Areas (TRA) “Modeling” and “Life and Health” at the University of Bonn. “We believe that our map contains many more gene-gene relationships that can also be used to combat human diseases. In fact, the GI map also made it possible to predict a function for genes that were previously unknown.”

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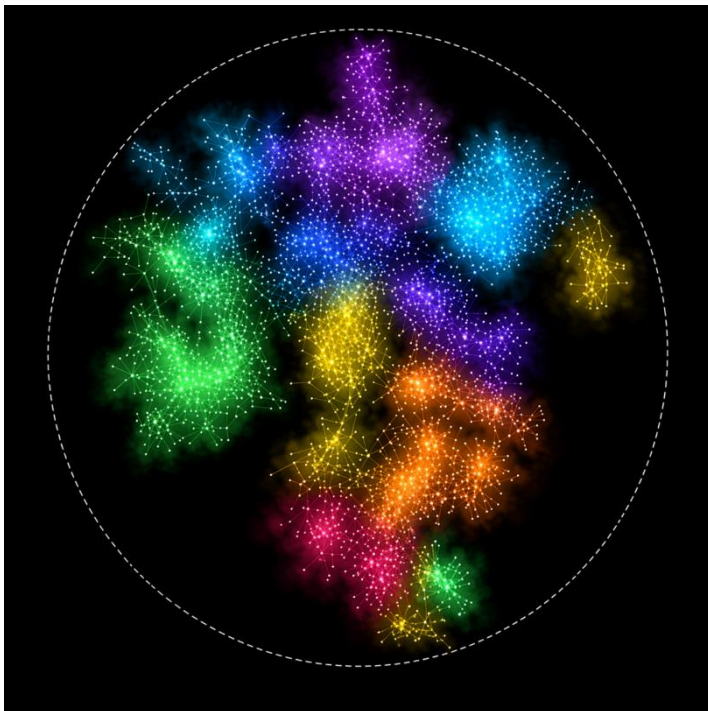
The first draft of the human GI map currently covers about 2.5 percent of all possible gene pairs. Many more gene pairs still need to be investigated to complete our understanding of the human genome. “However, we cannot simply measure all gene pairs. Instead, we must learn from the principles of our first draft of the GI map and predict the most promising GIs,” says Billmann, who is developing computer-aided algorithms for this purpose. “Artificial intelligence has transformed many disciplines. However, the functional interpretation of the human genome has so far been limited by a lack of data. We are eager to see how the data we began collecting nearly a decade ago can fill this gap.”

Publication: Maximilian Billmann, Michael Costanzo, Xiang Zhang, Arshia Z. Hassan, Mahfuzur Rahman, Kevin R. Brown et al.: A global genetic interaction network of a human cell maps conserved principles and informs functional interpretation of gene co-essentiality profiles, *Cell*; DOI: <https://doi.org/10.1016/j.cell.2026.03.044>

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Image:



Caption: A first map of gene-gene interactions in the human cell

Image credit: Chad Myers, University of Minnesota



Caption: Understanding how genes interact:

Bonn-based researcher Jun-Prof. Maximilian Billmann is playing a key role in creating a map of gene interactions.

Image credit: Institute of Human Genetics, UKB / Andreas Stein

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About the University Hospital Bonn: As one of Germany's leading university hospitals, Bonn University Hospital (UKB) combines excellence in medical care and research with high-quality teaching. Every year, UKB treats more than half a million outpatients and inpatients. Around 3,500 students are enrolled in medicine and dentistry, and over 600 individuals receive training in healthcare professions annually. With around 9,900 employees, UKB is the third-largest employer in the Bonn/Rhein-Sieg region. In the „*Focus* hospital rankings“, UKB is rated the top university hospital in North Rhine-Westphalia and has the second-highest case mix index (an indicator of treatment complexity) of all university hospitals nationwide. In 2025, UKB secured nearly €100 million in third-party funding for research, transfer, and teaching. For the fourth consecutive year, the F.A.Z. Institute recognized UKB as both “Germany's Training Champion” and “Germany's Most Desirable Employer.” For current figures and further information, please refer to the annual report at:

[geschaeftsbericht.ukbonn.de](https://www.ukbonn.de/geschaeftsbericht)