



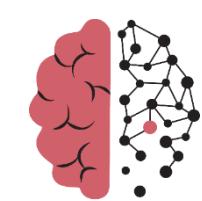
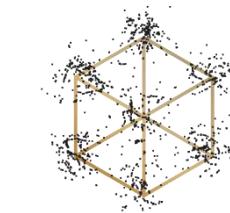
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# The NO-Age and NO-AD Seminar Series 013

09:30-12:00 (CET), Monday, 22<sup>nd</sup> Feb 2021

09:30-10:45: 'Heterogeneity of Aging in Human Populations', by **Prof. Jackie J.D. Han**, Peking University, China

10:45-12:00: 'What is ageing? Lessons from C. elegans' by **Prof. David Gems**  
Institute of Healthy Ageing, University College London, UK

Register in advance for this webinar:

[https://uio.zoom.us/webinar/register/WN\\_Y0RejMUATnmBkiTMqPgufA](https://uio.zoom.us/webinar/register/WN_Y0RejMUATnmBkiTMqPgufA)

Organizers:

Evandro F. Fang (UiO), Jon Storm-Mathisen (UiO), Menno P. Witter (NTNU),  
Lene Juel Rasmussen (KU), W.Y. Chan (CUHK)

Queries: [e.f.fang@medisin.uio.no](mailto:e.f.fang@medisin.uio.no)

Previous recorded talks are available here: <https://noad100.com/videos-previous-events/>



**Speaker:** Jing-Dong Jackie Han (韩敬东)

**Title:** Heterogeneity of Aging in Human Populations

**Abstract:**

We have always been interested in finding quantitative aging biomarkers to accurately assess the aging status by focusing on epigenetic changes (Cheng et al., 2018; Han et al., 2012; Jin et al., 2011). Recently by analyzing the 3D facial images, we generated the first comprehensive mapping of the aging human facial phenotype. We found quantitative facial features, such as eye slopes, highly associated with age. We constructed a robust age predictor and found that on average people of the same chronological age differ by +/- 6 years in facial age, with the deviations increasing after age 40. The predictor is as accurate as the most accurate to-date physiological age predictor – the one based on blood cell DNA methylation sites. Using this predictor, we identified slow- and fast-agers that are significantly supported by health indicators (Chen et al., 2015). By extending the study to a large Northern Chinese cohort of 5,000 people we can now use deep learning AI approaches to precisely estimate aging status based on 3D facial images and their associations with individuals' lifestyle and health. We further profiled blood cell mRNA and lncRNA expression by RNA-seq of this cohort and computationally predict their regulatory networks and their contributions to the variation in aging rate among different individuals, and those that are modifiable by their lifestyles (Xia et al., 2020). I will also share some of our newest results on microbiota aging rate association and ethnic group differences on facial aging rate.

**Biography:**

Prof. Jing-Dong Jackie Han obtained Ph.D. degree from Albert Einstein College of Medicine. She had her postdoctoral training at The Rockefeller University and Dana-Farber Cancer Institute. In 2004, she became an investigator/professor at the Institute of Genetics and Developmental Biology, Chinese Academy of Sciences. In 2010-2019, she was a director of the CAS-Max Planck Partner Institute for Computational Biology. In 2019, she became a tenured professor at Peking University, and an adjunct professor at National University of Singapore. Her research focuses on the structure and dynamic inference of molecular networks, using a combination of large-scale experiments and computational analysis to explore the design principles of the networks and to find how the complex phenotypes, such as aging, cancer and stem cell development are regulated through molecular networks. She was awarded the NSFC Outstanding Young Scientist Award in 2006, and the Hundred Talent Plan Outstanding Achievement Award in 2009, selected as a Max Planck Fellow in 2011 and a MaxNetAging Fellow in 2014, F1000 faculty in developmental biology in 2016.

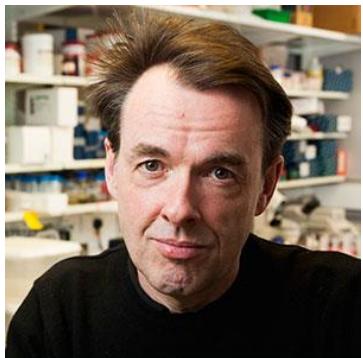
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Photo: from Jackie Han



**Speaker: Prof. David Gems, Professor of Biogerontology, University College London**

**Title: What is ageing? Lessons from *C. elegans***

**Abstract:**

Ageing is really bad: it is now the main cause of chronic disease and death in the world, and yet its causes remain poorly understood. For example, ageing is the main cause of cardiovascular disease, neurodegenerative disease (e.g. Alzheimer's), chronic obstructive pulmonary disease, cancer, and many, many other diseases. It could be argued that discovering the primary causes of ageing is the greatest challenge for biomedical research. One approach to discover the causes of ageing is to study them in simple, tractable laboratory models, such as the short-lived nematode *Caenorhabditis elegans*. In this organism it has been shown that a number of signalling pathways exert powerful effects on lifespan, suggesting the presence of central mechanisms controlling the entire ageing process; however, these mechanisms have proven difficult to identify using standard genetic approaches. My lab has been taking new approaches and exploring and developing new theories to try to understand *C. elegans* ageing. From this new work new perspectives on ageing are emerging. Our working hypothesis is that the diversity of diseases of ageing across the animal kingdom result from a limited set of broad pathophysiological principles. These principles are expressed differently and to differing degrees in different organisms; thus, although diseases of ageing appear very different in *C. elegans* and humans, studying the former can help understand the principles governing the latter. In *C. elegans*, programmatic rather than stochastic damage etiologies play a particularly large role, which can take the form of futile programme run on (or quasi-programmes), or of costly programmes that support reproductive fitness. Our recent work also supports the presence of reproductive death and adaptive death in *C. elegans*, mechanisms that are not typical of animal ageing - at least, not superficially.

**Biography:**

David Gems is a Professor of Biogerontology (the scientific study of the biology of ageing) at the Institute of Healthy Ageing, University College London. He graduated from Sussex University and then conducted research at Glasgow University, Imperial College, and the University of Missouri-Columbia, where in 1993 he began working on the biology of ageing in *C. elegans*, with Don Riddle. He set up his own research group at UCL in 1997 with the support of a fellowship from the Royal Society. Much of his work uses the nematode worm *C. elegans* to understand the fundamental mechanisms that cause the ageing process. He has also contributed to studies of aging in other nematodes, *Drosophila*, and the mouse, and penned articles on the ethics of aging research. He is a founder member and Research Director of the UCL Institute of Healthy Ageing, and has contributed to some 140 articles. Ageing is now the main cause of serious illness worldwide, yet its underlying biology remains poorly understood. Research using animal models has shown that it is possible to intervene in ageing and slow it down, thereby increasing late-life health and extending lifespan. It is envisaged that this work will contribute to the future development of preventative approaches to diseases of human ageing, such as cardiovascular disease, late life dementias, cancer and many others, thereby achieving major gains in terms of improved late life health and well being.

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Photo: UCL