# EpiGene2Sys – The Journey Continues

Monday 15th January – Wednesday 17th January, 2018  
Botanische Staatssammlung, Munich, Germany

### Monday 15th January

<table>
<thead>
<tr>
<th>Time</th>
<th>Event</th>
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<tbody>
<tr>
<td>13:00-14:00</td>
<td>Registration</td>
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<tr>
<td>14:00-14:15</td>
<td>Opening Remarks</td>
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### Session 1 - Computational Frameworks, Quantitation and Modelling

Chair: Stephen Beck

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<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
<th>Affiliation</th>
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<tbody>
<tr>
<td>14:15-14:25</td>
<td>Stephen Beck</td>
<td>University College London Cancer Institute</td>
<td>Introduction</td>
</tr>
<tr>
<td>14:25-14:40</td>
<td>Till Bartke</td>
<td>Helmholtz Zentrum München</td>
<td>Decoding Chromatin Modification States Using Chemical Biology and Proteomic Approaches</td>
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<tr>
<td>14:40-14:55</td>
<td>Cecilia Lövkvist</td>
<td>John Innes Center, Norwich</td>
<td>Spatiotemporal modelling of DNA methylation in mammals</td>
</tr>
<tr>
<td>14:55-15:10</td>
<td>Zahra Fahmi</td>
<td>Babraham Institute, Cambridge</td>
<td>Diverse protein occupancy drives 3D genome organisation through heterogeneous Brownian motion</td>
</tr>
<tr>
<td>15:10-15:30</td>
<td>Michiel Vermeulen</td>
<td>Radboud University, Nijmegen</td>
<td>Proteome-wide affinity quantification by mass spectrometry</td>
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<tr>
<td>15:30-18:00</td>
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<td>Break and Poster Session</td>
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<tr>
<td>18:00-19:00</td>
<td>Keynote Speaker</td>
<td>Martin Howard, John Innes Center, Norwich, UK</td>
<td>A new approach to dissecting the fundamentals of epigenetic regulation: fusing mechanistic mathematical modelling with experiments</td>
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<td>19:00</td>
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<td>Welcome Reception</td>
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### Tuesday 16th January

### Session 2 - Environmental and Metabolic Regulation and Disease

Chair: Andrew Pospisilik

<table>
<thead>
<tr>
<th>Time</th>
<th>Speaker</th>
<th>Affiliation</th>
<th>Title</th>
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<tbody>
<tr>
<td>09:00-09:05</td>
<td>Andrew Pospisilik</td>
<td>MPI of Immunology and Epigenetics, Freiburg</td>
<td>Introduction</td>
</tr>
<tr>
<td>09:05-09:25</td>
<td>Marcus Buschbeck</td>
<td>Universitat Autonoma Barcelona</td>
<td>The histone variant macroH2A histones links metabolic sensing to nuclear architecture</td>
</tr>
<tr>
<td>09:25-9:45</td>
<td>Ritwick Sawarkar</td>
<td>MPI of Immunology and Epigenetics, Freiburg</td>
<td>The role of stress proteins in regulation of chromatin at repetitive elements</td>
</tr>
<tr>
<td>09:45-10:00</td>
<td>Duncan Sproul</td>
<td>University of Edinburgh</td>
<td>Analysis of a longitudinal cohort delineates the genetic control of age associated epigenetic changes</td>
</tr>
<tr>
<td>10:00-10:15</td>
<td>Raffaele Teperino</td>
<td>Helmholtz Zentrum München</td>
<td>Models and modes of epigenetic inheritance in mammals</td>
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Session 3 – The Non-Coding Genome

Chair: Robin Allshire

10:50-11:10  **Valerio Orlando, KAUST**  
*Regulated somatic L1 retrotransposition is required for adult mammalian cell differentiation and reprogramming*

11:10-11:30  **Jaqueline Mermoud, IMT Marbourg University**  
*Chromatin remodeller SMARCAD1 is a functional co-factor of KAP1 in embryonic stem cells and regulates retrotransposon*

11:30-11:50  **Manolis Papamichos, Newcastle University**  
*Chronakis: Transcriptional regulation by a chromatin checkpoint for selective early termination of mRNA synthesis*

12:00-13:00  **Lunch**

13:00-15:30  **Poster Session**

Session 4 - Epigenetic Memory, Replication and Chromatin Disassembly

Chair: Peter Becker

15:30-15:50  **Marcel Mechali, Institute of Human Genetics, Montpellier University**  
*Metazoan DNA replication origins: genetic elements, epigenetic features, and links with transcription*

15:50-16:05  **Alessandro Scacchetti, Ludwigs Maximillian University, Munich**  
*CHRAC/ACF Contribute to the Repressive Ground State of Chromatin*

16:05-16:20  **Sophie Polo, University Paris Diderot**  
*Epigenome maintenance in response to DNA damage*

16:20-16:35  **Angela Taddei, Institute Curie, Paris**  
*Expanding heterochromatin reveals discrete subtelomeric domains delimited by chromatin landscape transitions*

16:35-16:50  **Sigurd Braun, Ludwigs Maximillian University, Munich**  
*Anchoring the histone acetyltransferase Mst2 to chromatin via a PWWP protein ensures integrity of chromatin domains*

16:50-17:20  **Break**

17:20-17:40  European initiatives for funding, new networks, outlook beyond H2020  
Genevieve Almouzni and Maria Elena Torres-Padilla

17:40-18:40  **Keynote Speaker**  
**Cedric Feschotte, Dept of Molecular Biology and Genetics, Cornell University, Ithaca, USA**  
*Transposable Elements as Catalysts of Regulatory Evolution*

19:00  **Conference Dinner**
Wednesday 17th January

Session 5 - Genome Organization

Chair: Juanma Vaquerizas

09:00-09:20  Juanma Vaquerizas –MPI for Molecular Biomedicine, Münster
  Transposable element-driven reorganisation of 3D chromatin during early embryonic development

09:20-09:40  Jane Skok, New York University School of Medicine, NY
  The Impact of Endogenous Retroviruses on Nuclear Organization in Mammalian Cells

09:40-10:00  Sara Buonomo, University of Edinburgh
  Rif1 a hub connecting nuclear architecture and replication timing

Session 6 –Low Input and Single Cell Approaches

Chair: tba

10:00-10:15  Poonam Bheda, Helmholtz Zentrum München
  Approaching single-cell epigenetic memory using microfluidics

10:15-10:30  Tineke Lenstra, Netherlands Cancer Institute, Amsterdam
  A single molecule understanding of the connection between activator binding dynamics and transcriptional bursting

10:30-10:45  Sriharsa Pradhan, Genome Biology Division New England Biolabs, MA
  High resolution open chromatin profiling of cancer cells

10:45-11:15  Break

Session 7 -Epigenetics and Developmental Plasticity

Chair: Fred van Leeuwen

11:15-11:35  Fred van Leeuwen, Netherlands Cancer Institute, Amsterdam
  Decoding the chromatin proteome of a single genomic locus in yeast by DNA sequencing

11:35-11:55  Nicola Iovino, MPI Immunology and Epigenetics, Freiburg
  Epigenetic inheritance through the germline in Drosophila

11:55-12:15  Bernard de Massy, Institute of Human Genetics, University of Montpellier
  PRDM9 methyltransferase activity regulates key steps in meiotic DSB formation

12:15-12:30  Closing comments

12:30  Departure