In this seven-day course at the idyllic Fraueninsel Abbey in southern Germany, we discussed and used many neuroinformatics tools and public data resources in the context of neurogenomics and brain diseases. The mornings and evenings were filled with lectures on areas of neuroscience in which large data sets are becoming available, such as the synaptic complex and the proteome, synaptic plasticity, impulsivity, mRNAs, neuro-ontology, neurogenomics, and neurogenesis. In the afternoons, all participants worked together to apply the new tools and datasets to address and even answer specific research questions. By the end of the course we had six jointly written draft papers for each of the questions. When participant left the island, they did so with hands-on experience in applying the available online tools to study the brain in health and disease as good extra baggage.
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On the 14th of September 2013, 37 scientists from all over the world assembled on the lovely Fraueninsel, in the Chiemsee lake in Bavaria. There they would be staying for a week in the Frauenwörth Benedictine sisters convent for the first Neuroinformatics Jamboree. Funded by the International Neuroinformatics Coordinating Facility and the University of Tennessee’s Center for Integrative and Translational Genomics, the aim of the meeting was to introduce participants to core neuroinformatics and neurogenomics data sets and tools. On the program were a series of tutorials on these tools and resources and companion lectures by leaders in the field. The bulk of the program, however, was devoted to applying these tools and to learn how to mine the publicly available data in an ambitious attempt to get to nearly-submittable manuscripts by the end of the week. We used a classic collaborative group learning structure, but in this case each group included one more senior scientist to help catalyze progress.

The jamboree started with dinner and a welcoming speech by Sister Scholastica, head of the seminar program at the convent. In her entertaining manner, she informed the participants, that in fact their goal was not only to achieve great science, but even more ambitiously, to work toward world peace. The remainder of the evening was spent at the football and ping pong table, the last bit of leisure time before the work really would commence the next day.

After breakfast, the next morning, all participants assembled in the aula, where traces of its previous life as a high school gym were still visible on the walls. The aula was transformed in a modern hub in the world wide neurogenomics web with high-speed internet access and power sockets for every attendant. School started with a tutorial on systems neurogenetics online resources in general and GeneNetwork in particular. After breaking for lunch, research started. Participants assembled in groups with the titles, Neural Development, Addiction & impulsivity, Brain Disorders, Synapse & Plasticity, Neurodegeneration and Adult Neurogenesis. These groupings were roughly based on common interests and assembled to have a mix of expertise and experience. The afternoon was spent exploring possible research questions. With only one week to complete draft papers, it was essential to quickly find tractable questions. After breaking for dinner, participants returned for introductions. All
participants prepared a one-slide presentation about their background and research interests. After these introductions were over, more informal introductions ensued, and also work on the research projects resumed. Most people chose to stay in the aula and work in groups on defining good research questions. This general pattern was repeated for 5 of 7 days: lecture in the morning, lunch break, joint research, dinner, presentation and more research.

By Monday afternoon, most groups had formulated research questions. These were presented to the other groups for open discussion. The questions not only varied by topic, but also by the approaches suggested to attack them. Common in all topics, however, was the attempt to mine public data sets with online tools. The Development Group, for instance, focused on using correlations in the Allen Institute’s gene expression data sets, the Addiction and Impulsivity Group used mouse genetic and phenotypic data set available on GeneNetwork, the Synapse and Plasticity Group used human microarray data.

By Tuesday, all groups had really dug into their topic. Students and our seven faculty members also occasionally joined other groups to share their knowledge and expertise. In the afternoon, a participant, spontaneously gave a tutorial on several online databases (Gemma and Cytoscape?) and tools that had not been covered yet. On Tuesday, September 17, broadband access temporarily halted. Apparently, the Jamboree teams had already downloaded 30 Gbs of data—the abbey’s whole allotment for the month of September. Fortunately, it was possible to increase the limit and by the end of the week close to 100 Gbs of data were sent to the island. On Wednesday, research intensified, with only a single lecture in the morning. Groups were now really cracking, and the Jamboree was in full swing. Data were pouring in again, and the first lines of manuscripts were started using a simple Jamboree advice template each group was given.

Thursday was devoted to writing drafts. Documents were shared online via Dropbox or the very interactive Google documents interface. People proofread and corrected each others text while it was being typed. In the evening, the keyboards were temporarily left untouched while all teams presented the results of their labor. Friday morning was the deadline for submitting a first draft manuscript for open Jamboree review and editing. Students were frantically trying to finish drafts, with all sections being edited simultaneously. By 1 pm on Friday, manuscripts were submitted. Work was not over yet, as all these manuscript were then reviewed by teams of other participants. In a nice contrast to the usual review process, the reviewers were then on hand to orally explain their critiques and give constructive feedback on how to improve the draft for publication. By Friday 8 pm, the scientific part of the Jamboree was over. Music, drinks, and an ping pong tournament finally managed to distract the participants from their research and celebrate the end of an intense, but marvelous week exploring the neuroscience and neurogenomics online databases and tools, and their work toward world peace by creating lasting links with research from around the world.

More photographs, information and the lecture slides are available at the jamboree website: https://sites.google.com/site/neuroinformaticsjamboree/
Program

Saturday September 14 (day 0)
6:00 pm Dinner
7:00 pm Introduction, Rob Williams, Rupert Overall and Alexander Heimel

Sunday September 15 (day 1)
9:00 am Tutorial “Genetic Resources for Neuroscience”, Rob Williams
12:30 pm Lunch
2:00 pm Defining research topics
4:00 pm Lecture “Neurogenetics of impulsivity”, Sabine Spijker
6:00 pm Dinner
8:00 pm Single-Slide-Introductions

Monday September 16 (day 2)
9:00 am Tutorial “Allen Institute Resources”, David Feng
12:00 pm Lunch
1:30 pm Defining research topics
3:00 pm Research topic presentations
6:00 pm Dinner
7:30 pm Lecture “Neurodevelopment”, Richard Nowakowski

Tuesday September 17 (day 3)
9:00 am Lecture “m(i)RNA and Neurodegenerative Diseases”, Ruth Luthi-Carter
11:00 am Lecture “mRNA, Neuro-ontology, Neurogenetics”, Rupert Overall
12:00 pm Lunch
1:30 pm Tutorial “Online Genomic Resources”, Victoria Perreau
2:00 pm Research workshop
6:00 pm Dinner
8:00 pm Lecture “The Synaptic Proteome”, Louie van de Lagemaat
Wednesday September 18 (day 4)
9:00 am Lecture “Genetics of Neural Plasticity”, Alexander Heimel
11:00 am Research workshop
12:00 pm Lunch
1:30 pm Research workshop
6:00 pm Dinner
7:30 pm Research workshop

Thursday September 19 (day 5)
9:00 am Write drafts
10:30 am Tutorial “miRNA Resources”, Andre Pietrzykowski
12:00 pm Lunch
1:30 pm Write drafts
6:00 pm Dinner
7:30 pm Presentations

Friday September 20 (day 6)
9:00 am Finish drafts
12:00 pm Lunch
1:00 pm Review drafts
3:00 pm Present reviews
6:00 pm Dinner
8:00 pm Party

Saturday September 21 (day 7)
Departure
Participants

The course was attended by participants of 16 different nationalities currently working in 10 different countries, spanning the world from Australia to the USA, from Singapore to Portugal. All career stages were present: 5 professors, 10 scientists, 7 postdoctoral fellows, 14 PhD students and 1 practicing psychiatrist. In total, there were 18 females and 19 males representing a wide range of research backgrounds.

Standing, left to right: Michaela Fenckova, Alexander Heimel, Victoria Perreau, Patrick Schaefer, Louie van de Lagemaat, David Feng, Alberto Capurro, Florian Freudenberg, Rob Williams, Jose Lopez-Moreno, Andre Pietrzykowski, Alexandre Raposo, Amit Lotan, Alexandre Colville, Evan Graf, Liviu Bodea, Rupert Overall, David Ashbrook, Yuting Wang, Shivakumar Keerthikumar, Richard Nowakowski, Anna Delprato.

Sitting, left to right: Janita Bralten, Aet Alttoa, Carrie Wright, Claudia Grellmann, Danielle Bosch, Bonnie Nijhof, Alexandra Badea, Mahdokht Nodehi, Ruth Luthi-Carter, Cynthia Vied, Luanna Dixon

Not on photograph: Marieke Klein, Sabine Spijker, Monique Vandervoet, Richard Wetzel
Feedback

"I had fantastic time. It was really something special and I'll remember it for a long time (until my Alzheimer will kick in). I've learned a lot and immediately applied that knowledge to my work, which was awesome. I also met really cool people and learned that Chiemsee can be really cold (but swimmable) in September."

“I think format and place is excellent and you have achieved your goals: 1/ teach participants about different bioinformatical approaches, 2/ give them immediately hands-on opportunities to use the tools, 3/ produce real results, 4/ have fun, 5/ create life-long friendships."

“I also enjoyed the meeting immensely. I think that Fraueninsel was a perfect working environment that supported to get to know each other better. For me it was a really productive week. I learned to apply different helpful online tools and met interesting people with different backgrounds from all over the world.”

“What an international group we are! I felt that the opportunities to build collaborative relationships were at least as important as the stuff we learnt, and hopefully long lasting and productive. I built more than one type of network.”

“The interaction has been a key value so I find this format much better than a 100% lecture format.”

“I also enjoyed the meeting immensely. For me, it was intellectually stimulating and very productive and as bonus, I had the opportunity to work directly with highly motivated and diverse scientists. I hated to see it end.”

“It has been fun and an intensively informative week.”

“I felt that the meeting was a great success and the knowledge that I gained in just a week was amazing. I feel one of the strongest points of the meeting was the availability of people that are directly involved with online resources, such as Rob Williams with Genenetwork.org and David Feng with the Allen Brain Institute, to name a couple. Working with people like that for the entire week really enforced the ability to use these resources not only for the meeting but in my daily research as well.”

“The group that I was a part of will continue to work on our paper and hopefully submit this paper for publication in the coming months.”

“As a result of the Jamboree, I will be providing a short workshop with members of my department to introduce them to the great online resources that I was introduced to by the organizers and the participants of the meeting.”
“As a newcomer to genomics I had a great opportunity to get a general view of what is going on in the field and meet with leading scientists, as well as establish contacts and even start a new collaboration article. The organizers did everything to make us feel welcome and I got a great boost of enthusiasm as a scientist and as a person.”

“I have attended several workshops in the past, both clinical and basic science oriented, but this workshop was unique in that it involved multi-dimensional learning through first-hand self and group experience. I think the organization was excellent and the non-formal interaction with faculty highly inspiring.”

“From a clinician’s perspective, every patient is a unique world in their own. Nevertheless, this workshop helped me realize that there are common pathways underlying neuropsychiatric disorders, so that in a way understanding these disorders from a database-driven approach may be complementary in many ways to more traditional clinically-based approaches.”

“I have shared with some of my colleagues the opportunities available by combining clinical experience with the vast array of neuroinformatic resources, and I hope to convey more on this topic in the near future.”

“I think I have never been so productive in my life as during the jamboree”

“I had a fantastic time at the Jamboree, it was great to interact with such a creative and multidisciplinary bunch and I hope to directly apply some of the things I learnt to my own work.”

“I talked about the course to my colleagues, and they were impressed by how much fun I had with science during that week, especially some lab mates from Europe who had no idea there is such a nice and quiet island where we could be so concentrated in research.”

“I think every lecturer did an excellent job. The clear explanation and demonstration on different databases/tools made it easy to catch even for a beginner (like me) in that area. I enjoyed working in our small group, as the interaction and teamwork went very well. And also I could see that you made a great effort to arrange the group. The group leader played an essential role, and each member moved forward the progress with their own expertise. As a student I learnt a lot from the senior research fellows, and everyone was very friendly and helpful.”

“I love the idea of drafting a manuscript by the end of the course, and I was impressed by how efficient we were”

“It has been said that “we are drowning in information, but starving for knowledge” (John Naisbitt). The Neuroinformatics Jamboree has managed to bring together a diverse group
with a common and strong interest in learning how to mine information to further the current knowledge about the brain – in healthy and disease states."

“The workshop has certainly enhanced my knowledge about public resources for gene expression data as well as various brain phenotypes, and has provided me with information on how to use them. From the excellent instructors to the youngest students, I feel everybody has contributed towards enriching the methodologies we had at our disposal when we started the workshop."

“I personally do not like to travel much. But the ambitious scope of the workshop, and the quality of the instructors were so compelling, that I took a little more than one week off from work and family to join the Jamboree. I feel extremely fortunate to have been able to participate, as I have learned in a very short time about neurogenesis in the adult brain, and was able to work in a small group to write the basis of what I believe will become a peer reviewed publication."

“The group was a nice mix of enthusiastic students and more experienced researchers that joined forces to work on well-thought, predefined projects. The project-based approach has generated a high level of motivation for learning, and the projects were shaped and reshaped in a fast paced, dynamic process – modulated by frequent feedback from the whole group. This is just one of the factors that contributed to what I think was a successful first Neuroinformatics Jamboree."

“I am not sure how you measure success – but if I were to score it according to my level of enthusiasm – this has been the best workshop I have attended yet! I wish it can become a tradition and continue to grow to match and surpass the initial success.”

“I really enjoyed the workshop and I have already used some of the tools that I learned about in my own research and helped spread the knowledge to my lab-mates. Additionally, this was a really wonderful networking opportunity and a very informative experience in working with others.”
Suggestions

As can be seen from the quotes in the previous section, the participants were overwhelmingly positive about their experience at the jamboree. When asked for suggestions on how to make future jamborees even better, two common themes were clear:

- The tutorials by Rob Williams, David Feng and participants Victoria Perreau and Andre Pietrzykowski were seen as some of the most valuable parts of the jamboree. Unanimously, the participants would like a future version to feature even more tutorials and hands-on lectures on online resources and tools.

  “I liked the presentations followed by in the afternoon/evening trying it out yourself (in a group). However if I would organize a school like this I would make it somewhat more practical. For example plan in an hour after the presentation where everybody is working on the same database, followed by a question hour/most frequently asked questions explained. In that way the expert can help during the practical hour, and people can discuss the same instruments used.”

  “I thought that all presentations were very high quality. Although seminars with more of a tutorial format would be well received I feel that one or two "key note" seminars which illustrate the integration of informatics analysis into larger research projects are very valuable for conveying the "big picture" and should not be lost entirely.”

- The attempt to write draft papers was seen as a nice feature of the jamboree, but the time course of one week was very ambitious. Some participants suggested to make the meeting a few days longer to allow for more time. Others suggested to organize the research groups and define the problems longer before the meeting. Also some people suggested to be less ambitious and produce a poster instead.

  “The manuscript aim of the course was very demanding and I think that we didn’t quite have enough time to achieve a satisfactory document. I felt rather disappointed in sending on my manuscript as it plainly need a lot of remedial work. I feel that an extra half day or whole day would have been necessary.”

All the feedback is available at request from the organizers.
## Finances

### Income

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<th>Source</th>
<th>Amount</th>
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<tr>
<td>INCF</td>
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<tr>
<td>UTHSC CITG</td>
<td>€ 7,232.86</td>
</tr>
</tbody>
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### Fees

€ 100.00 pp x 28

### Drinks cash deposits

€ 308.60 +

### Total

€ 30,341.46

## Expenses

### Lodging

€ 10,050.00

### Seminar rooms

€ 900

### Coffee

€ 585

### Drinks

€ 300

### Water

€ 180

### Breakfast

€ 2,331

### Lunch

€ 3,663.75

### Dinner

€ 3,999

### Extra broadband access

€ 299.39

### Party

€ 118.22

### Coffee mugs INCF

€ 280.00

### Travel stipends

€ 4,250.00

### Travel faculty

€ 3,285.10

### Folders

€ 100.00 +

### Total

€ 30,341.46

## Acknowledgments

The neurojamboree would not have been possible first and foremost without the financial support of the **International Neuroinformatics Coordinating Facility** and the **UTHSC Center for Integrative and Translational Genomics**, but also required the help and assistance of Terry Mark-Major (CITG), Annelies Wijle (NIN), Cock Koeleman (NIN), Ernst Rijvordt (NIN), Rikesh Balgobind (NIN), Sister Scholastica and the sisters and personnel of Abtei Frauenwörth and Klosterwirt, Gerd Kempermann, Terri Gilbert (ABA), Mathew Abrams (INCF), Raphael Ritz (INCF).
Draft abstracts
All groups produced a draft manuscript by the end of the course. After the course people continued to work on a number of these projects, and at the time of writing this report, the manuscript were still improved with the aim to be submitted to scientific journals.

A Multi-Resource Data Integration Approach: Identification of Candidate Genes Regulating Cell Proliferation during CNS Development

David Y Feng, Florian Freudenberg, Alexandre A Raposo, Cynthia M Vied, Yuting Wang and Richard S Nowakowski

We have analysed publically available databases to identify candidate genes that are potentially involved in regulating mammalian neocortex development. Proliferating cells located in the ventricular zone of the neocortex lining the lateral ventricles pass through 11 cell cycles over a 6 day period to produce the neurons of the neocortex. Using transcriptome data from the human brain we found high levels of expression of TEAD2, FOXM1, KIF23 and AurKA at 8-9 weeks post-conception (Allan Brain Atlas). The levels of all four genes were greatly reduced by 12 weeks post-conception. Microarray expression datasets from the neocortex of post-natal day three mice also show that AurKA, KIF23, FOXM1, and TEAD2 expressions are tightly correlated. Both TEAD2 and FOXM1 are highly expressed at early stages of mouse neurogenesis (E11.5-15.5), specifically by proliferating cells at the ventricular zone of the neocortex, and then significantly reduced at later stages (P4 and onwards)(ref ISH, Allen Atlas). Additionally, meta-analysis of differential expression studies are consistent with co-expression and interaction of TEAD2, FOXM1, AurKA and KIF23 in the brain of both human and mouse (ref. GEMMA, String-db). Taken together, these data show a temporal and spatial correlation between expression of TEAD2 and key components of the AurKA/Centralspindlin machinery. The Aurora kinases and the kinesin family member 23, KIF23, work together to assure the correct formation of the mitotic spindle for symmetric cell division. AurKA expression is controlled by the transcription factor FOXM1, a known enhancer of key mitotic regulators. These findings strongly suggest that the interaction of the 4 candidate genes at early stages of corticogenesis is conserved between mice and humans.
Major psychiatric diseases are highly heritable and there is mounting evidence that these disorders share common molecular and cellular causes. Here we systematically test the degree of genetic commonality of six neuropsychiatric disorders—attention deficit hyperactivity disorder, anxiety, autism, bipolar disorder, major depression, and schizophrenia. We generated comprehensive and well vetted list of genes independently associated to each of these six disorders in human genetic studies (primarily GWASs). A total of ~1700 genes were accepted into the analysis primarily on the basis of low but liberal GWAS p values (<10^{-4}). About 15% of genes (n = 229) overlap two or more diseases. The most widely shared subset—common to 5 of 6 diseases—include AS3MT, CACNB2, GRIN2A, GRIN2B, NPAS3, NTRK3, and ITIH3. We used a suite of bioinformatic data sets and on-line resources to evaluate common and unique biological network attributes unique to each set of genes and diseases. The shared subset form coherent networks with common patterns of expression including high expression in the amygdala of humans and mice. The overlap set also has comparatively dense protein-protein interactions that highlight glutamatergic neurotransmission as a common denominator. In contrast approximately 85% of genes are associated with single disorders and this is likely due to underlying biological differences as well as higher false discovery. Each set is significantly enriched in distinct gene ontology categories. The analysis reveals both a common etiologic core, but clearly highlights distinct gene subsets specific to each disorder. Better resolution of shared and unique genetic, molecular, and environmental factors should translate into improved diagnosis and treatment of these common debilitating disorders.
Bioinformatical attempt to uncover regulatory, genetic, and protein pathways connecting Nrg3 and mir-346 to impulsivity

Alexandre Colville, Evan Graf, Andre Pietrzykowski, Carrie Wright, Sabine Spijker

Cell type specific processes in neurodegenerative diseases.

Liviu Bodea, Alberto Capurro, Ruth Luthi-Carter, Victoria Perreau, Patrick Schaefer

The characterization of molecular changes in diseased tissues can provide crucial information about pathophysiological mechanisms and is important for the development of targeted drugs and therapies. However, changes in the numbers of neuronal and glial cells that occur in brain diseases can confound the analysis of brain samples, particularly human materials, where sample availability and control is limited. Here we apply our recently developed method, ‘Population Specific Expression Analysis’, to expression studies of human neurodegenerative disease brain. The PSEA method successfully identified cell type-specific contributions of neurons, astrocytes, oligodendrocytes and microglia from cerebral cortical tissue samples. Moreover, similar changes could be identified in additional neurodegenerative disease datasets produced by other groups.
Integration of data from multiple mouse genetic reference populations identifies Myo1b as a candidate regulator of proliferation in the adult hippocampus

David Ashbrook, Alexandra Badea, Anna Delprato, Claudia Grellmann, Marieke Klein, Richard Wetzel, Nancy Hayes, Richard Nowakowski, Rupert Overall

Reduced inhibition underlies excitation-inhibition imbalance in autism

Bonnie Nijhof, Danielle GM Bosch, Mahdokht Kohansal-Nodehi, Shivakumar Keerthikumar, Louie van de Lagemaat, J. Alexander Heimel

In the healthy brain there is a tight balance between the level of excitation and inhibition. A disruption of this balance has been hypothesised to underlie a number of neuropsychiatric disorders, in particular autism spectrum disorders. We devised a new method to quantify excitatory and inhibitory signalling in the brain from gene expression data. Using these measures, we establish that indeed the balance of excitation and inhibition is disturbed in autism cerebral cortex, but that this disturbance is primarily due to changes in inhibitory signaling.