

Functional Genomics Times



Functional Genomics Workshop

Ljubljana, October 15-16

The Workshop is about the techniques for large-scale functional genomics data generation and consequent data analysis. It features distinguished guest lecturers that study model organisms yeast and worm, or focus on mammalian cell genomics. Guest lecturer's laboratories have been spearheading the development of both experimental and computational analysis of biological networks. The workshop also features a hands-on course on computational analytics and data mining, and selected presentations of the research projects by the students — attendees. Informal discussions of all attendees with the lecturers are encouraged. And finally, everybody should taste šmorn!

Getting around

On foot. During a break, go for a walk with your colleagues. Even Aristotle preferred discussions while walking.

Bus. Buses 18 and 18L stop at the Zoo station, a 7 minute bus ride from the center. The bus heading towards the center ("Kolodvor" station) leaves every 15 minutes until 18.00, and afterwards every half an hour. The bus heading towards the faculty from the center (named "Center Stožice P+R" station) leaves every 15 minutes. Warning: you can not pay with cash—you will need the Urbana card, which you can buy at newspaper kiosks and news-stands. Every bus ride costs 1,20 euro.

Taxi. The venue address is "Večna pot 113".

Taxi društvo Ljubljana	+386 1 234 9000
Taxi Laguna	+386 80 12 33
Taxi Metro	+386 41 240 200

Internet

There is internet. Check your bag for the password.

Chad Myers

Insights from mining large-scale genetic interaction networks in yeast

Recent developments in experimental technology have enabled the rapid construction and phenotyping of combinatorial genetic perturbations in a number of different organisms. Certain combinations of harmless single perturbations can result in dramatic phenotypes, suggesting redundancy is a ubiquitous property of biological systems. While the data derived from these large-scale screens have proven to be highly informative for characterizing gene function, many challenges remain in the mechanistic interpretation of genetic interactions.

I will describe our recent efforts to understand large-scale genetic interaction networks in the context of the model organism yeast, where we have now measured quantitative phenotypes for more than 10 million double mutants. I will address the general question of how we can learn systems-level biology from these data and demonstrate their utility for characterizing global cellular function and organization. Lastly, I will describe our progress in leveraging insights from the yeast network to improve our understanding and treatment of human disease.

Charlie Boone

Global Genetic Interaction Networks

Genetic interactions can play an important role in determining the relationship between genotype and phenotype and may underlie a significant component of the "missing heritability" in current genome-wide association (GWAS) studies. To explore the general principles of genetic networks, we've taken an unbiased and global approach to map digenic interactions in the budding yeast *Saccharomyces cerevisiae*. We developed Synthetic genetic array (SGA) analysis, which automates yeast genetics, enabling the combinatorial construction of defined mutants and the mapping of genetic interactions quantita-

tively. We are generating a comprehensive genetic landscape for yeast, examining networks derived from an analysis of all gene pairs, covering both nonessential and essential genes. Constructing a higher order network driven by genetic interaction profiles reveals the roles of specific genes and traces a global functional wiring diagram of the cell. Ultimately, our findings in yeast may allow us to explore genetic interactions underlying the heritability of traits in other organisms, including humans, and the design of synthetic lethal cancer therapies.

The Venue

Faculty of Computer and Information Science



In the beginning of the early seventies, computer science was taught at the University of Ljubljana as an elective program of the Faculty of Electrical Engineering. A separate Faculty of Computer and Informa-

tion Science was founded in 1996. Since then, it has become by far the largest institution of its kind in Slovenia, with more than 1300 students enrolled in its undergraduate and graduate programs. For almost

twenty years, it shared a building with its parent faculty, despite the quickly growing number of students and personnel, study programs and research projects. Just two months ago, it finally moved to its own new building on the beautiful green outskirts of Ljubljana.

Yet the faculty is not a building: the faculty is its people. And the Faculty of Computer Science thrives with life. At almost any time, one can run into a meeting of world-class scientists, or into a group of primary school kids learning about the magic of computer science. In the week before the Functional Genomics Workshop, graduate

students and high school students competed in the final round of a year-long competition in robotics. Using sets of Lego Mindstorms, they simulated teams operating a vehicle on Mars. The workshop itself coincides with the EU Code Week, and the faculty hosts a number of free courses in programming for diverse age groups, from primary school children to the elderly, as well as a TEDx event dedicated to answering why everybody in the 21st century should learn to code.

The doors of the Faculty of Computer Science never close. Feel free to drop by anytime.

Ljubljana

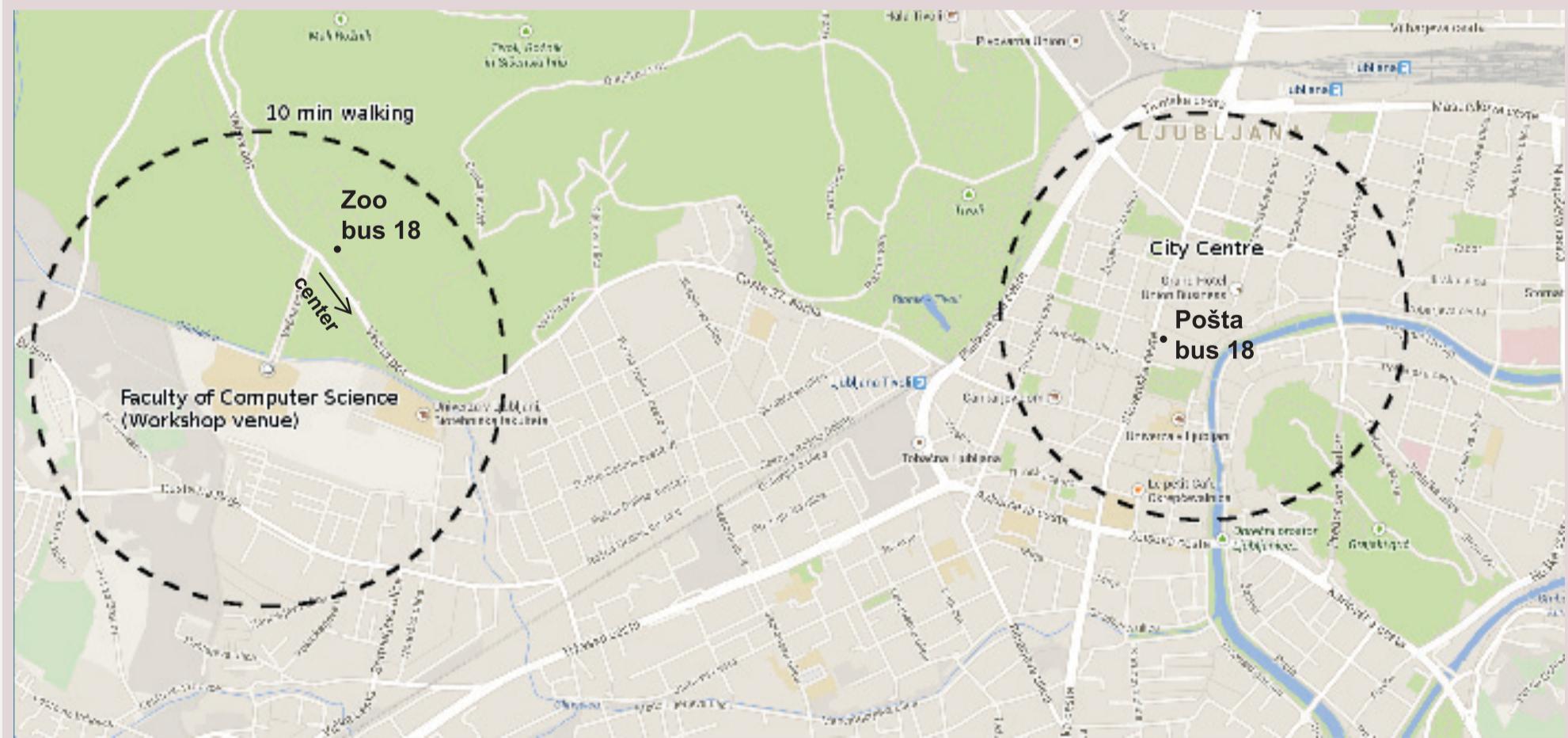
Ljubljana is the capital and the largest city of Slovenia and has few, if any, world-famous attractions. This doesn't bother its mere 300,000 inhabitants, who very much enjoy the city and everything it has to offer. The symbol of the city is the Ljubljana dragon, which has its origins in the legend of Jason and the Argonauts. Once upon a time, the Greek hero Jason and his Argonaut comrades stole a golden fleece, the coat of a golden ram, from the King of Colchis on the Black Sea. On board the Argo they fled their pursuers and found themselves at the mouth of the River Danube. There was no way back, so they went on, up the Danube and then along the River Ljubljanica. They had to stop at the source of the Ljubljanica and overwintered there. They then took the Argo apart and in the spring carried



it on their shoulders to the Adriatic coast, where they put it back together again and went on their way. According to the legend, on their ar-

rival between what is now Vrhnika and Ljubljana, the Argonauts came across a large lake with a marsh alongside. The marsh was inhabited

by the Ljubljana dragon that Jason slayed and in doing so destroyed the last of the city's world-famous attractions.



Organizers

Slovenian Biochemical Society

The Society is the mother organisation for all in Slovenia that do biochemistry or molecular biology, and is also friendly to its members that do math and computer science for application in natural sciences. This is not the first time the Society has hosted scientists from the Donnelly Centre. We would here like to thank it for its financial and social network support.

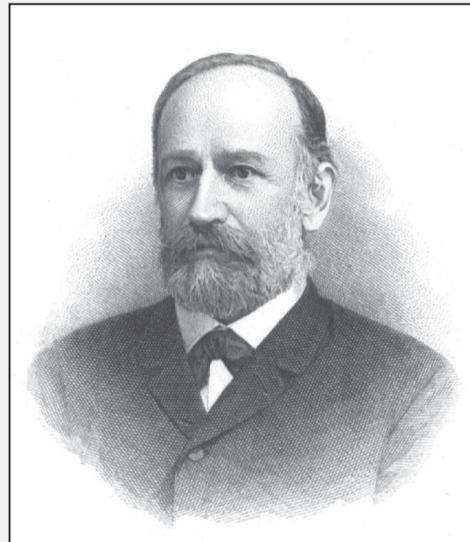


Jožef Stefan Institute



The Jožef Stefan Institute is the leading Slovenian scientific research institute. It is responsible for a broad spectrum of basic and applied research in the fields of natural sciences and technology. Physics, chemistry and biochemistry, electronics and information technologies, reactor engineering and energetics comprise the Institute's research departments. The establishment of the Institute dates back to 1949, at which time the focus of the research was on the peaceful use of nuclear energy. The basic goals of the Institute are to provide expert scientific and applied output in the form of processes, products and consultancy, and to produce well-trained young scientists. Nowadays, the Institute is closely connected with Slovenian universities and cooperates with many leading scientific research institutions worldwide.

The Jožef Stefan Institute is named after the distinguished



Slovenian 19th century physicist Jožef Stefan, most famous for his work on the Stefan-Boltzmann law of a black body radiation. Stefan deduced from experimental measurements that the total radiation from a black body (e.g. star) is proportional to the fourth power of its absolute temperature. With his law Stefan determined the temperature of the Sun's surface as 5703 K, which was off by less than 1.3% (5778 K). The law was later derived theoretically and extended in the framework of thermodynamics by Stefan's student Ludwig Boltzmann.

The Institute's logo originates from a Slovenian spelling written in the 5-bit teleprinter code (ITA2).

Functional genomics workshop is locally organized and coordinated by Uroš Petrovič and Blaž Zupan. They would not come very far without the assistance of Jerca Tekavec, Jernej Šribar and Aleš Berlec.

We would like to thank distinguished guest lecturers, professors Brenda Andrews, Charlie Boone, Andy Fraser, Jason Moffat, Chad Myers and Fritz Roth. Also, thanks to the four student speakers Areejit Samal, Alenka Baruca Arbeiter, Ines Oršolič and Marinka Žitnik.

Hands-on part of the workshop was prepared by Bioinformatics Lab from University of Ljubljana. Thanks to Aleš Erjavec, Marko Toplak, Jure Žbontar, Miha Štajdohar, Anže Starič, Tomaž Hočevar, Martin Stražar, Lan Žagar, Maja Vodopivec, Mojca Mattiazzi Ušaj, Matej Ušaj and Andrej Čopar, and instructors Janez Demšar and Tomaž Curk.

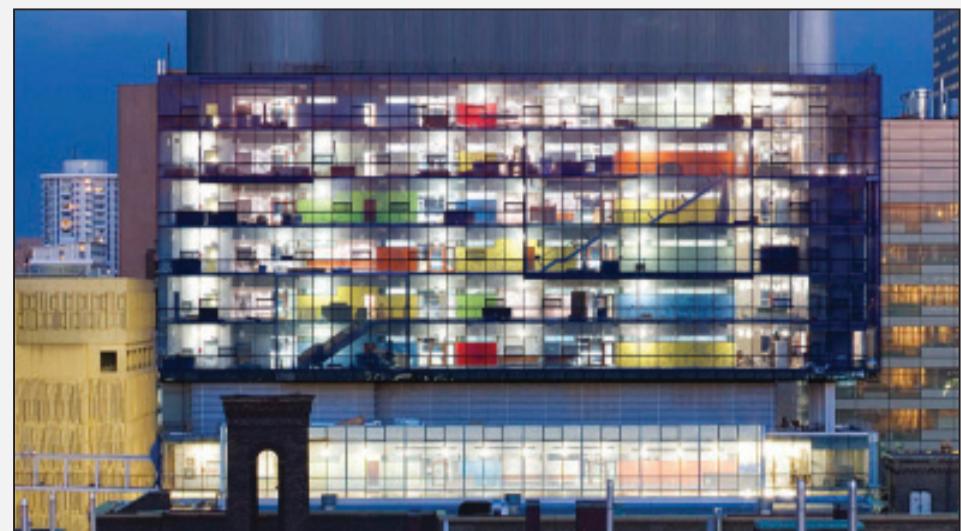
The workshop is co-organized by the Donnelly Centre for Cellular and Biomolecular Research (CCBR) of the University of Toronto, Jožef Stefan Institute, Ljubljana, University of Ljubljana, and the Slovenian Biochemical Society. Additional financial support came from Interdisciplinary Doctoral Study Programme in Biomedicine and Bioinformatics Lab at University of Ljubljana.

This workshop leaflet was designed by Agnieszka Rovšnik. The printing was organized by Primož Javornik at CH4. Agnieszka also designed Orange bags and t-shirts for workshop attendees. Agnieszka is now working on Orange pillows that will be available exclusively to whoever comes by the Faculty of Computer Science in Ljubljana (check with us later).

Images and some writing for this leaflet came from various web sources, like home pages of speakers and organizers and pages of Slovene tourist institutions. We acknowledge them all. The rest was written by Bioinformatics Lab members, and quite some was at the last minute proofread by Philip Nagel and Lara Zupan. Thanks!

Finally, many thanks to the staff of the Faculty of Computer Science.

Donnelly Centre for Cellular and Biomolecular Research (CCBR) of the University of Toronto



A part of Toronto Faculty of Medicine, founded in 1843, the Terrence Donnelly Centre for Cellular and Biomolecular Research opened its doors in 2005 with the goal of identifying the causes and cures of diseases. Since then, the centre attracts interdisciplinary scientists from fields such as chemistry and computer science, employing 30 principal investigators and about 500 staff members.

The Donnelly Centre takes a holistic approach to biomedical

research: by integrating technology, expertise and thought from a diverse array of disciplines, it aims to unravel some of the great complexities of biology. In the process, the Centre is poised to make some significant future advances in medicine and health. Researchers at the Centre are beginning to produce breakthrough insights on a key frontier—understanding the complex ways in which genes and proteins interact with each other.

University of Ljubljana



The University of Ljubljana is a public university located in Ljubljana, Slovenia. It is considered one of the most prestigious universities in Slovenia and is listed amongst the top 500 universities in the world according to the ARWU Shanghai, Times THES-QS and WEBOMETRICS rankings. Apart from its academic prestige, the University of Ljubljana is also well known for producing a high number of social studies graduates.

The university campus* occupies 9.8km² (2,420 acres) including parts of the Tivoli park to the west and parts of Castle hills to the east. The seat of the university is located

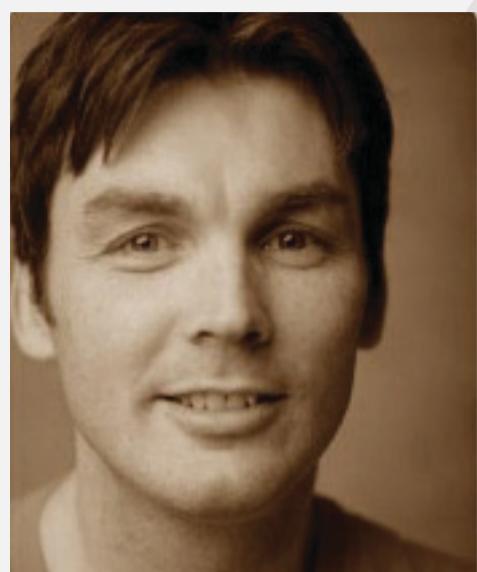
in the city centre in a prominent corner of the Congress Square. Nearby lies the largest university library, designed by the famous Slovenian architect Jože Plečnik. The three academies and some of the older of the twenty-three faculties are also located in the city centre. Some of the most recent and modern buildings were constructed on the outskirts of Ljubljana, giving the university and its students a ubiquitous presence in the city.

* Slovenian universities do not have strictly defined campus areas; the convex hull of all member faculties was used instead.

Wednesday, October 15

Prof. Jason Moffat

The Donnelly Center is all about interactions. So is Dr. Moffat's lab. But instead of yeast or worms, they focus on mammalian cancer cells. Using RNA interference to suppress gene expression of target genes, they hunt for essential genes, that is genes that are indispensable for life. A collection of essential genes could constitute the minimal gene set required for a living cell. The essentiality of a gene depends on the context, and nonessential genes may become essential under certain growth conditions, or under a certain combination of mutations. Through systematic studies of genome alterations through RNA interference, Dr. Moffat maps genetic interaction networks, which are a rich source of functional information.



tion and can lead to identification of conserved genetic interactions, functions for uncharacterized genes, targetable vulnerabilities, and functional modules.

Prof. Brenda Andrews

Dr. Brenda J. Andrews, current director of the Donnelly Centre (Terrence Donnelly Centre for Cellular and Biomolecular Research) at the University of Toronto, acquired her diploma in Zoology in 1980. She later pursued a doctorate in Medical Biophysics at the same university and started her training in genetics, which led to a position at the Department of Medicine at the University of Toronto (1991). By 1999 she succeeded in becoming the Chair of the Department, a position she held for 5 years before assuming her current position. An interesting quote of Dr. Andrews states that "All disease has a genetic basis, whether in genes inherited by the affected individual, environmentally-induced genetic changes that produce a cancer, or the genes of a virus and their interaction with an infected person. But, despite astounding advances in biomedical research, the cause of common human diseases remains largely unknown." As it turns out,



the single-celled budding yeast is an excellent model for understanding the basics of human biology and the complex networks of gene interactions responsible for most diseases. That is why Dr. Andrews' research interests lie in the fields of genetics, human disease, functional genomics and proteomics. The Andrews lab group is excellent at interdisciplinary research, integrating biology, computer science, engineering and chemistry and therefore pioneering the field of yeast systems biology.

Prof. Charles Boone



Dr. Charles Boone is a professor and Canada Research Chair at the University of Toronto's Banting and Best Department of Medical Research. His research focuses on mapping yeast genetic networks on a large scale in order to assign gene function. The function of many yeast genes is conserved in humans. Observation of cell growth and division in yeast is relevant to a molecular understanding of a number of diseases, including cancer.

His lab identifies genes that work together in the cell to carry out essential functions which may provide insight into our understanding of the molecular basis of inherited traits. In collaboration with Brenda Andrews' lab, they have built up a unique facility for automated and large-scale genetic analysis in yeast. The results of Dr. Boone's work can be used to study highly conserved disease genes and to decipher drug mode of action. Dr. Boone has

received many awards, including the Ontario Government's Premier's Research Excellence Award, William E. Rawls Award for Research Excellence of the National Cancer Institute of Canada, the 2003 Merck Frosst Award of the Canadian Society of Biochemistry, and the 2006 Ira Herskowitz award at the Yeast Genetics and Molecular Biology Meeting. Ask him whether it is easier to catch a fish or a genetic interaction. Which one's cheaper?

9:00	Welcome address
9:15	Charlie Boone Global Genetic Interaction Networks
10:15	Coffee break & Orange Installation Clinic
10:45	Brenda Andrews High throughput phenomics in budding yeast
11:45	Jason Moffat The Hunt for Essential Genes and Genetic Interactions in Cancer Cells
12:45	Lunch break
14:00	Areejit Samal Reconstruction and systems analysis of plant cell wall deconstruction network in filamentous fungus <i>Neurospora crassa</i>
14:25	Alenka Baruca Arbeiter Development and characterization of novel microsatellite markers from ESTs of developing olive fruit (<i>Olea europaea L.</i>)
14:50	Ines Oršolić The Role of Ribosomal Proteins L5 and L11 in Tumor Suppression
15:15	Marinka Žitnik Biomedical Data Fusion
15:40	Coffee break & Orange Installation Clinic
16:15	Fritz Roth Using yeast as a platform for assessing functionality of variation in human disease genes
16:45	Blaž Zupan & Janez Demšar Data mining without programing—hands-on workshop (part 1, until 18:00)
18:15	Charlie Boone Dinner intro
18:20	Dinner with fluffy shredded pancakes and sangria

Thursday, October 16

9:00	Andy Fraser: Why background matters—insights from RNAi and drug screens in <i>C. elegans</i>
10:00	Coffee break
10:30	Fritz Roth Exploiting next-generation sequencing to map protein interactions
11:30	Chad Myers Insights from mining large-scale genetic interaction networks in yeast
12:30	Lunch Break
14:00	Fritz Roth Next-generation protein interaction mapping, and yeast as a platform for personal human genomics
14:30	Blaž Zupan & Janez Demšar & Tomaž Curk Data mining without programing—hands-on workshop (part 2)
15:30	Coffee break
16:00	Blaž Zupan & Tomaž Curk: Data mining without programing—hands-on workshop (part 3)
16:50	Workshop wrap-up

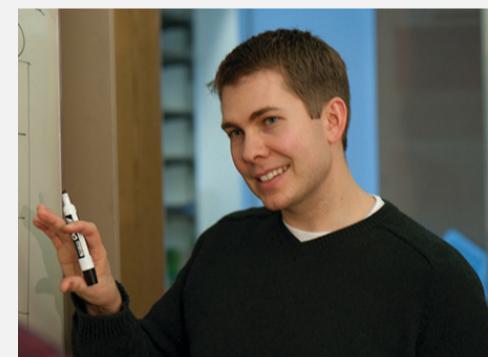
Prof. Andy Fraser



make for an excellent model for functional genomics. Dr. Fraser uses RNA interference to make single gene knock-outs and observes the resulting phenotypes, and uses the same technique to study combinations of mutations. There are many different combinations of gene mutations in worms, and in humans, and the study of their effects is an open problem in modern genetics and a major inspiration to researchers at the Donnelly Center.

Caenorhabditis elegans is a free-living, non-parasitic, transparent nematode, about 1 mm in length. Each adult has only 959 cells, and we know every cell division that occurs during its development. Despite its simplicity of form, the worm is genetically complex—the worm has 20,000 genes, half of which have very close matches in humans. This makes the worm a perfect organism to study how inherited mutations could affect health in humans.

Prof. Chad Myers



Dr. Myers, now a faculty member at the University of Minnesota, was not interested in biology at first. As a high school student in North Dakota, he liked math and physics. In college, those strengths expanded into computer engineering. Then, in graduate school at Princeton, he was exposed to the quickly growing fields of genomics and systems biology. Until that point, says Myers, he thought biology was mainly about memorizing facts that had mostly been worked out. Suddenly, he realized how much uncharted territory was out there. Myers' research emphasis includes computational methods for analysis and interpretation of large-scale genetic interaction networks and methods for integration of diverse genomic data. His lab is developing approaches for analyzing and leveraging interaction networks to answer biological questions in a variety of systems, including yeast, plants, worms and humans.

Prof. Fritz Roth



Dr. Roth has a diverse background in physics, molecular and cell biology, and biophysics, but also excels in computer science and data analytics. In the six-pack of invited lecturers, if we would by any means try to sort them in a line (performing a one dimensional projection, say, through multidimensional scaling), he would most likely stand between Dr. Myers and the rest of the pack. Though,

like any low-dimensional projection, that would obscure many interesting details. Experimentally, his lab develops technologies for phenotyping yeast mutants under multiple growth conditions, is inventing approaches for large-scale protein interaction screening technologies using next-generation sequencing of recombinant DNA barcodes, and develops yeast complementation assays to assess human functional variation. Among his computational interests are approaches to analysis of genetic interaction to reveal redundant systems and the order of action in genetic pathways. He also likes huge collection of data sets and uses them in integration studies. Ask him how to assign gene function and drive disease association studies from data on phenotype, genetic epistasis, protein-protein and transcription-regulatory interactions and sequence patterns.

Jason Moffat

Mapping essential genes and genetic interactions in human cancer cells for therapeutic target discovery

Technological advancement has opened the door to systematic genetics in mammalian cells. Genome-scale loss-of-function screens can assay fitness defects induced by partial gene knockdown, using RNA interference, or

complete gene knockout, using new CRISPR techniques. We are leveraging these approaches to reveal the basic blueprint and context-dependencies required for cancer cell proliferation.

Fritz Roth

Next-generation protein interaction mapping, and humanized yeast as a platform for personal genomics

I will describe analysis of an unpublished map of 14,000 new binary human interactions, and a new "barcode fusion genetics" interaction mapping technology that enables library x library screening using barcode recombination and next-generation sequencing. Also,

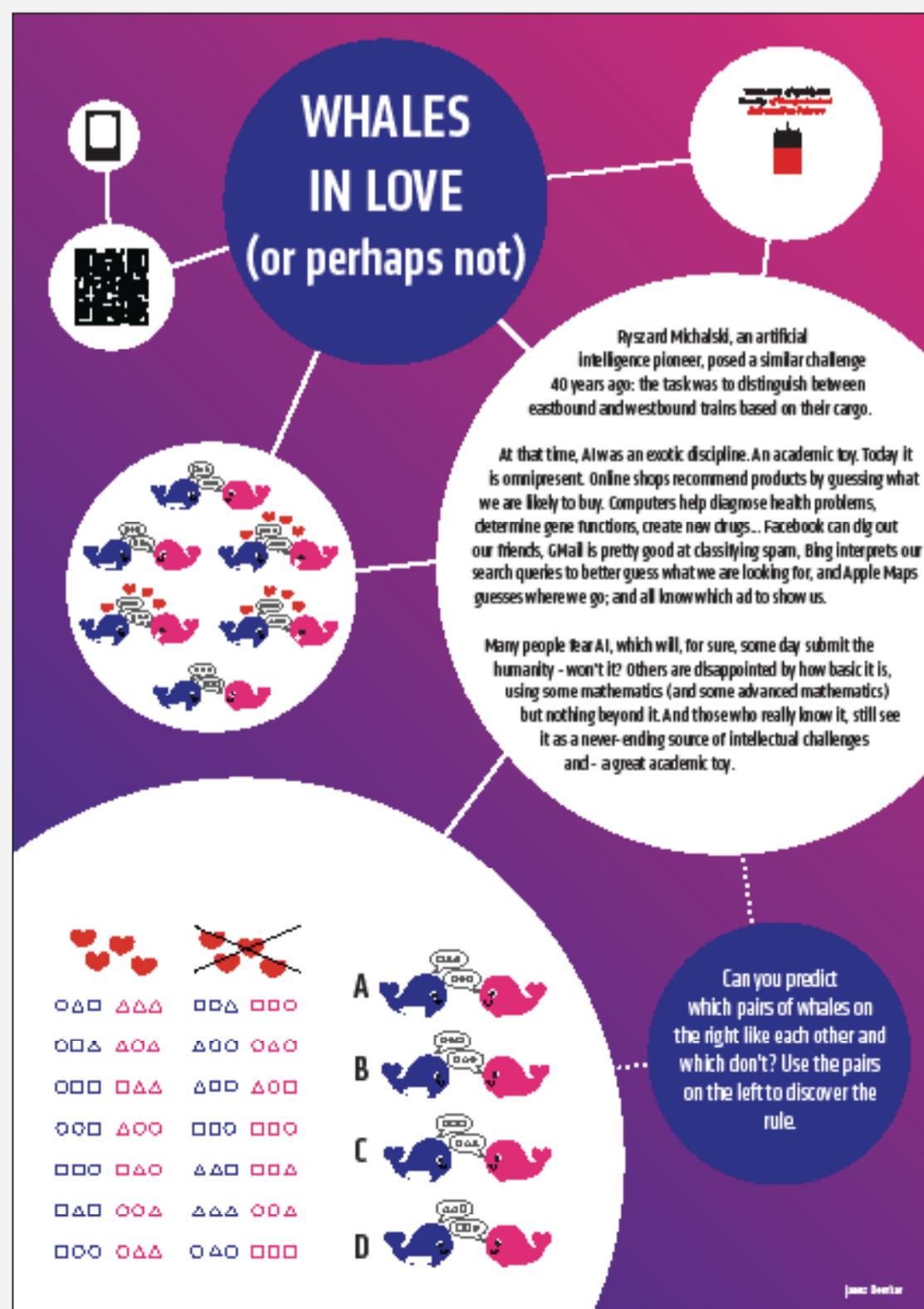
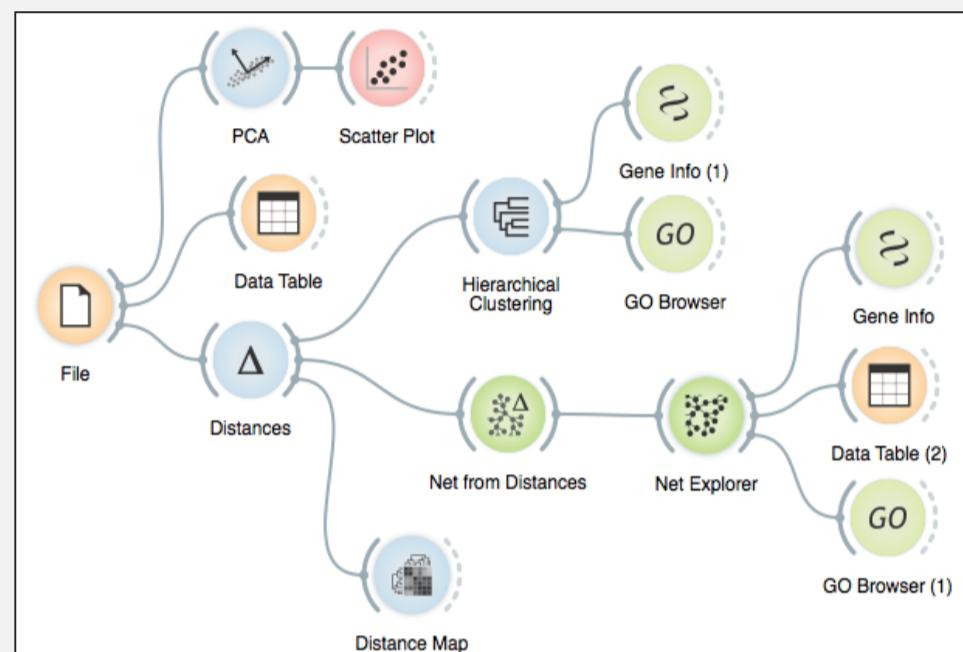
I will describe systematic development of yeast as a platform for assessing the functionality of human variation, and exhaustive mutagenesis and phenotyping to assess the functionality of rare human variants before they have been seen in the clinic.

Blaž Zupan, Janez Demšar, Tomaž Curk

Data Mining without Programming

This is a strange title for the hands-on part of our workshop. And it is also a false one. We will actually program data processing pipelines, but not with R or Python. Instead, we will program visually; we will create workflows that process genomics data and render interesting visualizations. We will use Orange, a data mining software package from your host, Bioinformatics

Lab at University of Ljubljana. Orange was initially designed as a general-purpose data mining environment. But then we met Gad Shaulsky, a biologist from Houston, and promised him we will design a tool that any biologist can use with no knowledge of any computer language. In this workshop you will be able to test if we kept the promise.



Horoscope



The PCA analysis that you planned to look into may reveal something interesting. Pay attention to the third principal component.



Have you backed up all your data? There may be a catastrophe on the horizon.



Nobel prize in three years. Guaranteed. No, no, wait, I thought your sign was Pisces. Sorry. No prize for you, it's for the guy in the second row.



About that experiment you thought about the last week ... Well, forget about it. It's not gonna work. Ever.



Beware of the second reviewer.



Carefully plan your meals, as your intestinal microbiota might be acting moody.



One of your PhD students should work harder. Much much harder.



Before submitting that manuscript, check the caption for Fig. 2 again. Just in case.



Do not trust horoscopes and weather forecasts written by charlatans.



Never again prepare agar plates on the full moon!



That brilliant idea you had last year, but never pushed it through, will appear in this month's Science issue.



The next batch of experiments will yield excellent results. Recommendation: give your technicians a lesson about the difference between Fahrenheit and Celsius.

Beer in Slovenia

Unlike the varied selection of top-quality wines, the beer market in Slovenia is dominated by the two largest brands: Laško and Union. Most Slovenes can be divided into two camps—as is (too) often the case—the red supporters of Union, and the green die-hard fans of Laško. The slightly comic twist to this division comes from the fact that both brands have now been owned by the same company for several years.



Fortunately for beer aficionados, Slovenia is also discovering the charms of fine craft beer and slowly opening up to less known trade names from local microbreweries. These offer a range of unique tastes and add different types of ales to the ubiquitous, but quite generic, lagers produced by the main brands.

While sometimes a bit more effort is needed to find these, the reward is that much sweeter (or should we say bitter). In Ljubljana you can get homemade beer accompanied by good food in the Kratochwill pub and the Eksperiment bar. Beer from several top microbreweries scattered around Slovenia (Human Fish, Carniola, Bevog, Pelicon, Vizir, Rokovnjač, ...) can also be found in selected bars in the centre of Ljubljana. If Google is not your thing, just ask for directions to one of the following (or many others): Sir William's pub, Zlata Ladjica, Irish pub, Petkovšek bar, TOZD, Caffe Bar Bangladesh, or visit the beer shop Pivoteka. And remember, you will not know which one you like the most until you try them all.

Šmorn



The history of Šmorn goes back to the 19th century in these lands, when Emperor Francis Joseph I. attempted to impress the Empress Elisabeth of Bavaria. The result of his cook's efforts to prepare a "light" dessert was unsuccessful however. As the Emperor had to eat both portions, the dessert is sometimes called "Ceasar schmarn" ("Šmorn" or "Carski praženec" in Slovene). In Slovenia Šmorn is often served as a breakfast or dinner dish and is easily made and consumed.

Šmorn is a light, caramelized pancake made from a sweet batter of flour, eggs, sugar, salt, and milk, baked in butter. Šmorn can be prepared in many different ways, but it is usually made as a consequence of an unsuccessful attempt to flip a regular pancake. The main difference is thus a thicker batter, which allows the addition of berries, fruits and nuts, such as blueberries, cherries, plums, and almonds.

Input:
eggs = 3
milk = 500 ml
sugar = 2 teaspoons
salt = 1/2 teaspoon
flour = 350 g
raisins = 1 handful
rum = 1 dl
mineral_water = 30 ml
butter = 30 g
powdered_sugar = 2 spoons
favourite_fruit_jam = 3 spoons
Possibly nuts, cherries, plums,
almonds, etc.

Output:
Šmorn, a delicious breakfast/dinner meal.

Algorithm:
wash(raisins)
dry(raisins)
for 10 mins:
soak(raisins, rum)

mix = stir([egg yolks, milk,
sugar,
 mineral water, salt])
add(mix, flour)
mix.stir() # until smooth

egg_whites = mixer.mix(egg_
whites)
add(mix, egg_whites) # slowly

frying_pan.melt(butter)
frying_pan.set_
temperature("medium")
frying_pan.add(mix)
smorn = frying_pan.get_contents()

while smorn.upper_side not nice_
crust:
 wait()
 frying_pan.flip()
while smorn.upper_side not nice_
crust:
 wait()

add(smorn, powdered_sugar)
enjoy() # Serve with your fa-
vourite
 # jam, such as blueberry
 # or lingonberry.

Palačinke

My father rarely cooked (Marko from Biolab wrote this section). In fact, throughout my childhood I only remember him making "palačinke", or Slovenian pancakes. These are so thin that you can almost see through them. In fact, if they are properly made, they have holes a few millimeters wide that you actually can see through. The French would call them crepes.

Flipping pancakes in a pan is a skill one masters slowly. Beginners should start with a flat and wide spatula. First, loosen the edges by going around the pancake in a circle and then slide the spatula under the pancake, lift it and turn it. If the pancake tears, do not panic—tear it a few more times, mix, and—you've

made "Šmorn". For the next stage, try flipping the pancakes in the air with a small elegant move of the wrist holding the pan. If the pancake sticks to the ceiling, do not worry—it will fall down eventually—just make another.

Slovenian pancakes are traditionally served topped with jam made by your grandmother, but these days, some prefer Nutella. Roll them up and eat them with your hands. To surprise your significant other, wake up earlier and start making pancakes. Their scent will spread through the house and softly wake your significant other up. Then, serve warm pancakes in bed. Enjoy.

RECIPE

For four pancakes (one person), mix two eggs, a pinch of salt, a small spoon of sugar, a deciliter of white flour, a deciliter of milk and a deciliter water. Mix well.

Heat your largest pan. Add some oil or butter into the pan. Then, add about a scoop of batter to the side of the pan and turn the pan slightly to the other side so that the batter spreads evenly. When the pancake surface completely dries, flip the pancake. After a while remove it from the pan. Repeat until you run out of batter.

Do not skimp on the oil—enough guarantees crunchy edges. Also, instead of water, try Cocta (a Coca-Cola clone) or Donat Mg (a sparkling water with a tremendous amount of Magnesium; please do not drink too much of it during the workshop).



Three hidden treasures

Slovenia is a small but very diverse country with just two million inhabitants on 20,273 km² of land. It is sometimes referred to as the land on the sunny side of the Alps. The current parliamentary republic is relatively young (independence in 1991) and used to be a part of the former Yugoslavia. It is incredible that Slovenia falls among the more developed countries of Europe, yet over half of its land area is covered by forest. It is therefore no wonder that there are many beautiful natural retreats in Slovenia and because of their easy accessibility, Slovenians are very involved in outdoor activities—we love to go hiking, climbing, cycling, skiing, snowboarding, jogging, swimming and more.



Škocjan caves

Slovenia has many caves, the most famous of which is definitely Postojnska cave. However, the Škocjanske caves should not be overlooked as they are incredibly rich in cave formations and offer a far more authentic underworld experience. The highest chamber in the caves is 150 m high, and there are some particularly nice views of waterfalls, rapids and pools as the path through the cave goes along an underground river. Škocjanske caves are on UNESCO's list of natural and cultural world heritage sites.



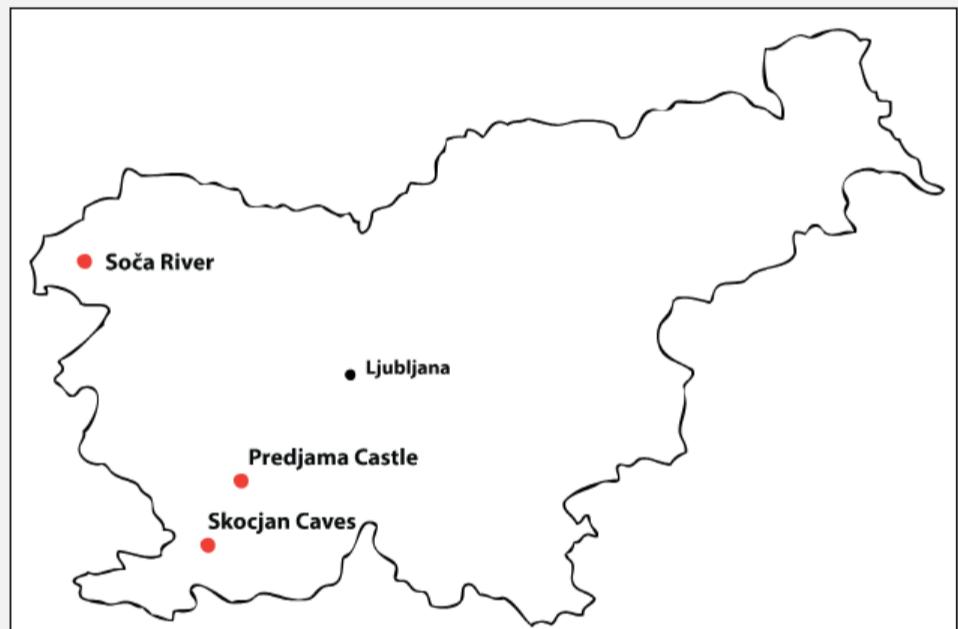
Predjama castle

This romantic castle dates to the 13th century and is famous for its location and for the annual Knight's Tournament festival held there every August. The protagonist of most stories about Predjamski grad is the knight Erasmus who was said to have protected the besieged castle for over a year by smuggling food and supplies through a secret cave passage.



Soča river

The Soča River flows through a glacial valley under the Alps in the northwestern part of Slovenia. It is famous for its striking green color, deep canyons and scenic views. The Soča is actually very cold (12.0 °C), so we do not recommend bathing. It is, however, an incredible place for picturesque walks, with the steep mountain slopes of the Alps rising high above the river canyon.



Wednesday

Sunny and dry weather will allow you to take a walk to the center of Ljubljana. There are many exciting locations to explore—try the hidden path to the castle and don't forget to enjoy the view! If you get low on energy, stop at the excellent restaurant Prekmurska Gužvina and enjoy some traditional Slovenian cuisine.



Thursday

Partly cloudy and a bit moist. A wonderful day for mushroom and chestnut picking—essential ingredients for Slovenian fall cuisine. The forests are a palette of wonderful colors during the short but still warm October afternoons.



Friday

Chilly morning and a foggy afternoon. Winter is coming. But do not fret—Slovenian borovničke (blueberry schnapps) will certainly warm up your cold feet. Other local spirit drinks for you to try are medica (honey), smrekovec (spruce tree buds), hruškovec (pear) and pelinkovec (wormwood).

