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REPUBLIKA SLOVENIJA
MINISTRSTVO ZA IZOBRAŽEVANJE,
ZNANOST IN ŠPORT



EVROPSKA UNIJA
EVROPSKI SKLAD ZA
REGIONALNI RAZVOJ
NALOŽBA V VAŠO PRIHODNOST

Podatki za življenje

Sodelovanje raziskovalnih infrastruktur

A. Kastrin, J. Dimec, B. Leskošek

Mreža znanja 2017, 22. november



SIO · 2020 

Operacijo delno financira Evropska unija iz Evropskega sklada za regionalni razvoj ter Ministrstvo za izobraževanje, znanost in šport.

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Univerza v Ljubljani

Medicinska fakulteta

Inštitut za biostatistiko in medicinsko informatiko

ibmi Inštitut za biostatistiko in medicinsko informatiko
Univerza v Ljubljani, Medicinska fakulteta

domov novice **Izobraževanje** storitve raziskave centri o ibmi

Izobraževanje
izobraževalni programi in prispevki

Biostatistični center
namen centra je širiti kvaliteto in obseg biostatističnega znanja

Storitve
storitve, ki jih omogoča IBMI

Hitri meni

- Biostatistični center
- Statistika po domače
- Izobraževanje
- O ibmi
- Storitve
- Biomedicina Slovenica

Zadnje novice

<http://ibmi.mf.uni-lj.si>

- Organizacija, ki združuje ustanove na področju znanosti o življenju
- Viri in storitve:
 - podatkovne zbirke
 - programska orodja
 - učni materiali
 - superračunalniki
- Cilj:
 - koordinacija virov in storitev
 - enotna infrastruktura



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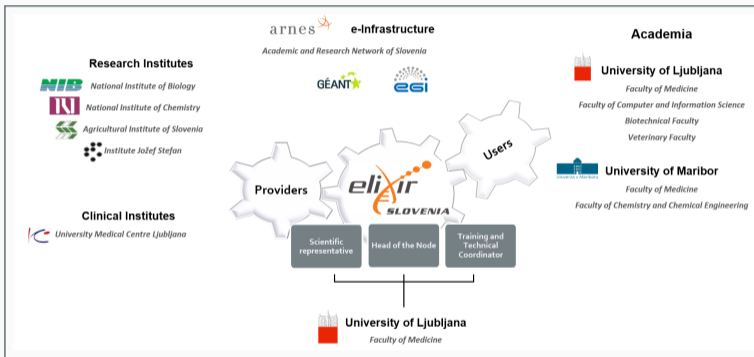




<https://www.elixir-europe.org>



<https://www.elixir-slovenia.org>



Videokonferenčni sestanki



<https://mcu.arnes.si>

ELIXIR-SI izbor nacionalnih aktivnosti

- Nacionalna podatkovna in informacijska infrastruktura temelječa na FAIR
- Ustanovitev nacionalnega ELIXIR-SI podatkovnega vozlišča
- Ustanovitev regionalnega izobraževalnega središča
- Bioinformatika:
 - orodja in storitve za boljše upravljanje podatkov
 - pomoč in svetovanje pri podatkovni analizi in načrtovanju raziskav
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ELIXIR-SI English (en) ▾

elixir
SLOVENIA

NAVIGATION ☰

- Home
- ▶ Courses



ONLINE USERS ☰



(last 5 minutes: 0)
None



Available courses

🔖 Genome assembly and annotation course 3

Teacher: Joelle Amselem
Teacher: Mahesh Binzer-Panchal
Teacher: Laurent Bouri
Teacher: Victoria Dominguez Bohler
Teacher: Erik Hjerde
Teacher: Christophe Klopp
Teacher: Henrik Lantz
Teacher: Daniel Sobral
Teacher: Lucile Soler
Teacher: Lieven Sterck

23-27 Oct 2017, Portugal

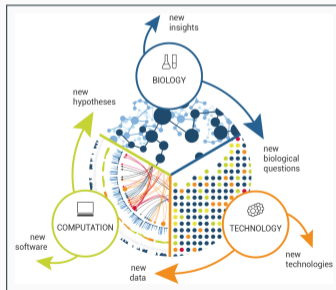
A course is being organized in Ljubljana, hosted by the Slovenian ELIXIR Node leading organisation and in cooperation with the nodes involved in ELIXIR-EXCELERATE task 10.3 "Capacity Building in Genome Assembly and Annotation". Some of the most experienced assembly and annotation experts in Europe will be teaching at the course.

The course is aimed at researchers interested in learning more about genome assembly and annotation. It will include information useful for both the beginner and the more advanced user. We will start by introducing general concepts and then continue to step-

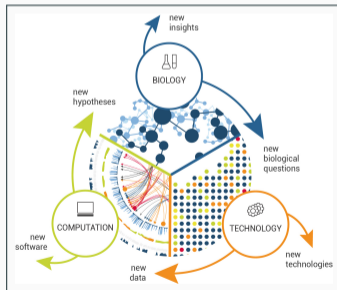
<https://elixir.mf.uni-lj.si>

- *Genome assembly and annotation (3 izdaje)*
- *UNIX / Linux tutorial for beginners*
- *How to get the most out of your microarray experiment*
- *Linux command line*
- *RNA-seq data analysis using Chipster*
- ...

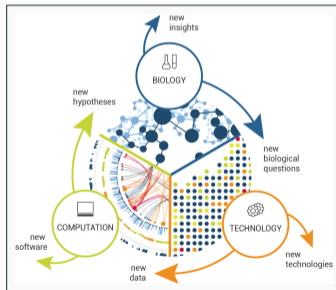
- Cilj: razumeti razumevanje živih organizmov na sistemskem nivoju
- Interdisciplinarnost
- Kvantitativna znanost



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Chipster: sodobna podatkovna analitika

The screenshot displays the Chipster 3.0.0 (build 1436) interface, which is divided into several functional areas:

- Datasets:** A list of files including 'column-value-filter.tsv', 'UniqueSymbolsFinalListLenburg.tsv', 'foundByLenburgAndChipster.tsv', 'DEG_foundByChipsterOnly.tsv', 'annotations.tsv', 'extracted-from-GO.tsv', 'variance.tsv', 'pca.tsv', and 'loadings.tsv'.
- Analysis tools:** A menu with categories like 'Microarrays', 'NGS', and 'Misc'. The 'Statistics' category is expanded, showing options such as 'Linear modelling using user-defined design', 'Test proportions', 'Correlate with phenodata', 'Correlate miRNA with target expression', 'Time series', 'Association analysis', 'Adjust p-values', 'PCA', 'DCA', 'NMDS', 'Sample size estimation', and 'Sample size calculations with an adapted B...'. The 'PCA' tool is currently selected.
- Workflow:** A visual representation of a data processing pipeline. It starts with a root node '17' (tsv) which branches into 'pht' (pdf) and several 'pdf' nodes. These further lead to 'tsv' nodes, which then lead to 'tsv' nodes, and finally to 'tsv' nodes.
- Visualisation:** A 3D Scatterplot for PCA. The plot shows data points in a 3D space defined by axes X, Y, and Z. The X-axis is labeled 'PC1', the Y-axis is labeled 'PC2', and the Z-axis is labeled 'PC3'. The plot includes a legend with two series: '1' (blue sphere) and '2' (green sphere). The plot is titled '3D Scatterplot for PCA' and has a legend on the right with settings for 'Automated rotation', 'Black background', 'Symbol' (Sphere), and 'Settings | Selected | X-axis: PC1, Y-axis: PC2'.

<http://chipster.csc.fi>

Galaxy: podatkovna analitika v oblaku

The screenshot displays the Galaxy web interface. At the top, the header reads "Galaxy / Galaxy Docker Build" and includes navigation links for "Analyze Data", "Workflow", "Shared Data", "Visualization", "Help", and "User". The main content area features a large heading: "Hello, your Galaxy Docker container is running!". Below this, a message states: "To customize this page you can create a welcome.html page in your directory mounted to /export." Three buttons are provided: "Configuring Galaxy", "Installing Tools", and "Guided Tour". A cartoon whale carrying server racks is also visible. On the left, a "Tools" sidebar lists various bioinformatics tools under categories like "Get Data", "Text Manipulation", and "Convert Formats". On the right, a "History" sidebar shows a search for datasets and a list of recent jobs, including one titled "UCSC Main on Human, knownGene (genomes)" with a table of genomic coordinates.

Tools

search tools

Get Data

Collection Operations

Text Manipulation

Filter and Sort

Join, Subtract and Group

Convert Formats

AXT to concatenated FASTA
Converts an AXT formatted file to a concatenated FASTA alignment

AXT to FASTA Converts an AXT formatted file to FASTA format

AXT to LAV Converts an AXT formatted file to LAV format

BED-to-GEF converter

GEF-to-BED converter

LAV to BED Converts a LAV formatted file to BED format

MAF to BED Converts a MAF formatted file to the BED format

MAF to Interval Converts a MAF formatted file to the Interval format

MAF to FASTA Converts a MAF formatted file to FASTA format

Wiggle-to-Interval converter

Hello, your Galaxy Docker container is running!

To customize this page you can create a welcome.html page in your directory mounted to /export.

[Configuring Galaxy >](#) [Installing Tools >](#) [Guided Tour >](#)

Galaxy is an open platform for supporting data intensive research. Galaxy is developed by [The Galaxy Team](#) with the support of [many contributors](#). The Galaxy Docker project is supported by the University of Freiburg, part of de.NBI.

The [Galaxy Project](#) is supported in part by [IHGRI](#), [NSF](#), [The Huck Institutes of the Life Sciences](#), [The Institute for CyberScience at Penn State](#), and [Johns Hopkins University](#).

History

search datasets

Unnamed history
1 shown
22.3 MB

1: UCSC Main on Human, knownGene (genomes)
~190,000 regions
format: **bed**, database: **hg38**

display in IGB [View](#)
display with IGV [local](#) [human hg38](#)
display at UCSC [main](#)

1: Chrom	2: Start	3: End	4: Name	5
chr1	17368	17436	uc031t16.1	0
chr1	29903	31097	uc097t04.1	0
chr1	30266	31189	uc097t04.1	0
chr1	30365	30983	uc031t16.1	0
chr1	34553	36881	uc091t08.4	0

<https://galaxyproject.org>

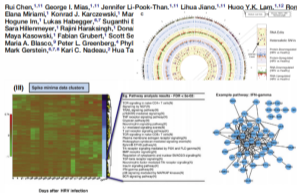
Visoko-zmogljivo računalništvo: realna potreba?

Resource

Cell

Personal Omics Profiling Reveals Dynamic Molecular and Medical Phenotypes

Rui Chen,^{1,11} George I. Mias,^{1,11} Jennifer Li-Pook-Than,^{1,11} Lihua Jiano,^{1,11} Huo Y.K. Lam,^{1,12} Ronq Chen,^{1,12} Elana Miriam,¹ Konrad J. Karczewski,¹ Mar Hogure Im,¹ Lukas Habegger,^{1,13} Suganthi E Sara Hillermeier,¹ Rajni Harakirah,¹ Dora Maya Kasowski,¹ Fabian Grubert,¹ Scott Se Maria A. Blasco,¹ Peter L. Greenberg,¹ Piyi Mark Gerstein,^{1,14} Kari C. Nadeau,² Hua Tu,¹ Eran E. Alizadeh,^{1,15} and J. Michael Cherry,^{1,16} et al.¹ Alan P. Boyle,¹ et al.¹ Ewan A. Ashley,¹



Large-scale prediction and testing of drug activity on side-effect targets

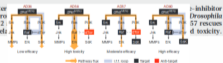
Eugen Loukinov,¹ Michael J. Keiser,^{1,2} Steven Whitebread,¹ Dmitri Mikhailov,¹ Jacques Hamon,¹ Jeremy L. Jenkins,¹ Paul Lavan,¹ Eckhard Weber,¹ Allison K. Doak,¹ Serge Gêlé,¹ Brian K. Shoicher,¹ & László Urban¹

Discovering the unintended 'off-targets' that predict adverse drug reactions is daunting by empirical methods. Here we use an unbiased, machine-learning approach to predict adverse drug reactions by computational molecular modeling.

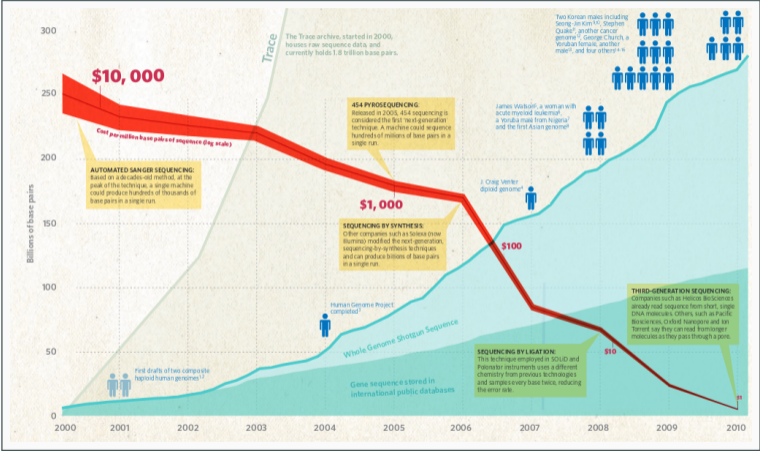
Chemical genetic discovery of targets and anti-targets for cancer polypharmacology

Arvin C. Dai¹, Tirrha K. Das^{1*}, Kevan M. Shokat¹ & Ross L. Cagan¹

The complexity of cancer has led to recent interest in drug repurposing; however, optimal kinase-inhibition models of multiple endocrine neoplasia type 2 (MEN2) oncogenic Ret-induced lethality, whereas re-



Podatkovna eksplozija v molekularni biologiji



English (en) ▾

ELIXIR-EXCELERATE HPC Train-the-Researcher course

Home ▸ My courses ▸ hpcmlg2017

NAVIGATION

- Home
 - Dashboard
 - Site pages
- My courses
 - GAAC2017_3
 - GAAC2017
 - hpcmlg2017
 - Participants
 - Badges
 - Competencies
 - Grades
 - Announcements and Communications Tools
 - Web Terminal
 - Day 1
 - Day 2
 - Feedback survey
 - ultb-2
 - RNA-seq
 - how-to-pathway

ADMINISTRATION

- Course administration

Announcements and Communications Tools

Dear participant,
welcome to the **ELIXIR-EXCELERATE HPC TIR course** in Malaga, Spain. Hope you will enjoy both days of the tutorial.

- News and Announcements Forum
- Discussion forum

Students can post questions to teachers and other students here.

- HPC Course chat room

Live chat for comments and questions during the course.

- The Survey
- Announcements

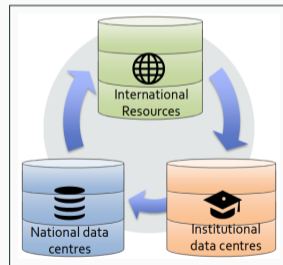
Web Terminal

- Web Terminal - Aleš Papič
 - Restricted** Not available unless: Your **Email address** is **ales.papic@mf.uni-lj.si** (hidden otherwise)
 - griduser001
- Web Terminal - Andrej Kastrin
 - Restricted** Not available unless: Your **Email address** is **andrej.kastrin@mf.uni-lj.si** (hidden otherwise)
 - griduser002

Neponovljivi raziskovalni izsledki za znanost niso pomembni.

— K. Popper, *The Logic of Scientific Discovery*

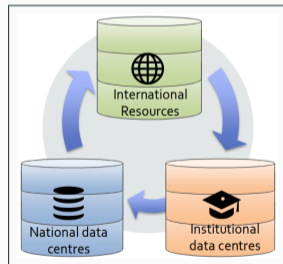
- Institucionalna podatkovna skladišča:
 - omejen doseg uporabnikov
 - pomanjkljivo označevanje
- Nacionalno podatkovno skladišče:
 - širši doseg
 - ustrezno označevanje
 - povezovanje z računskimi resursi



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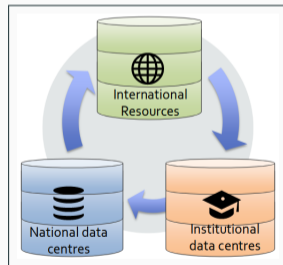
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Hvala za pozornost

`elixir@mf.uni-lj.si`