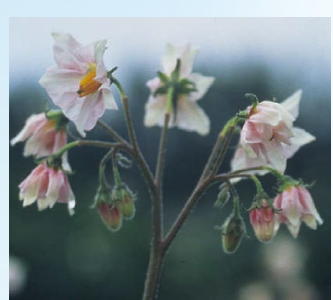


Kako razumemo, kaj se dogaja v rastlinski celici pod stresom?

- večnivojska integracija podatkov



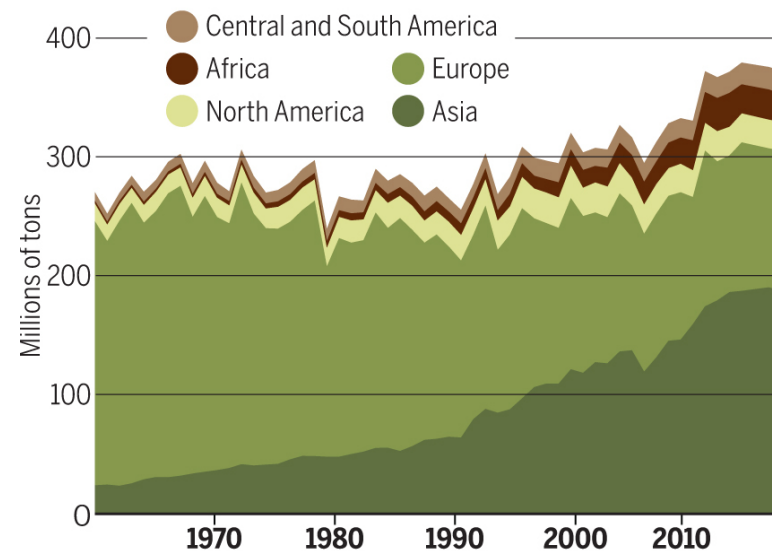
- Krompir je ena izmed rastlin, ki so jih v Stari svet prinesli po "odkritju" Amerike
- Spada v družino razhudnikovk, kamor prištevamo tudi paradižnik, tobak in volčjo češnjo



- Ko so v Franciji želeli krompir narediti bolj priljubljen, naj bi Marija Antoaneta v lase splela krompirjeve cvetove

Growing appetite

Potato production has grown in Asia, particularly in China and India, while falling in Europe.



- Danes je krompir osnovna poljščina v večini držav, Kitajska pa je vodilna država na svetu po pridelavi krompirja

“Smrtni sovražniki” krompirja

škodljivci



listne uši



koloradski hrošč



krompirjev bolhač

glive/glivične bolezni



črna listna pegavost



prašnata krastavost



ovelost krompirja



bela noga



krompirjeva plesen

virusi



virus zvijanja krompirjevih listov



virus Y



- bolezni, prenosljive z listnimi ušmi
- bolezni, prenosljive z dotikom
- bolezni, prenosljive z ogorčicami (*nematodes*)

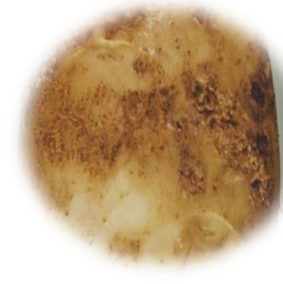
bakterije/bakterijske bolezni



obročasta gniloba

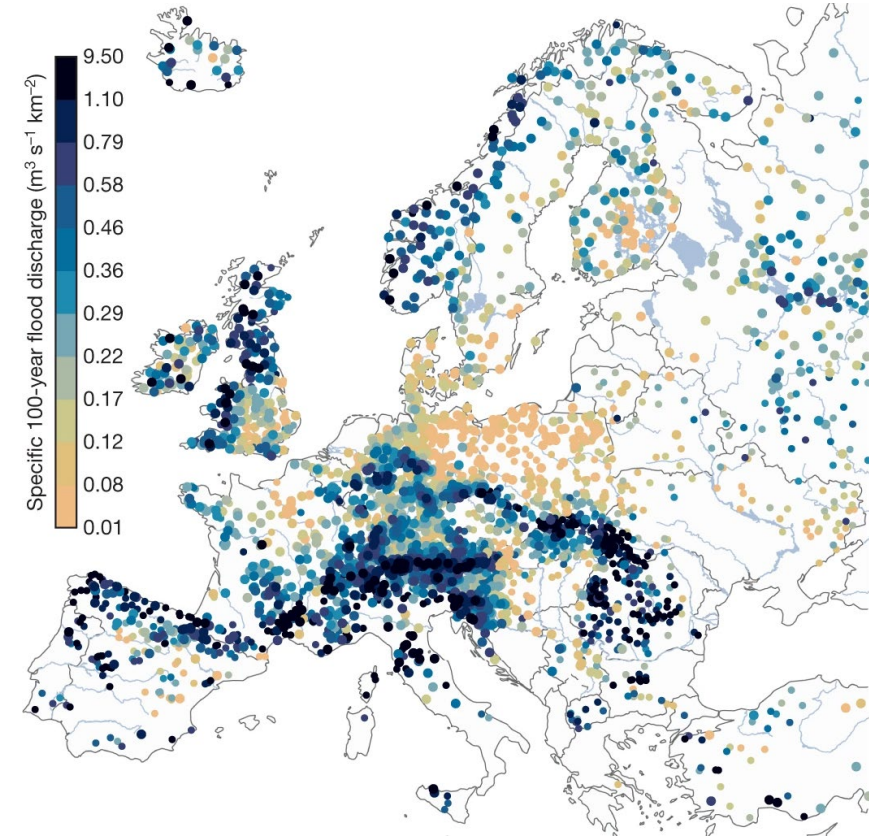
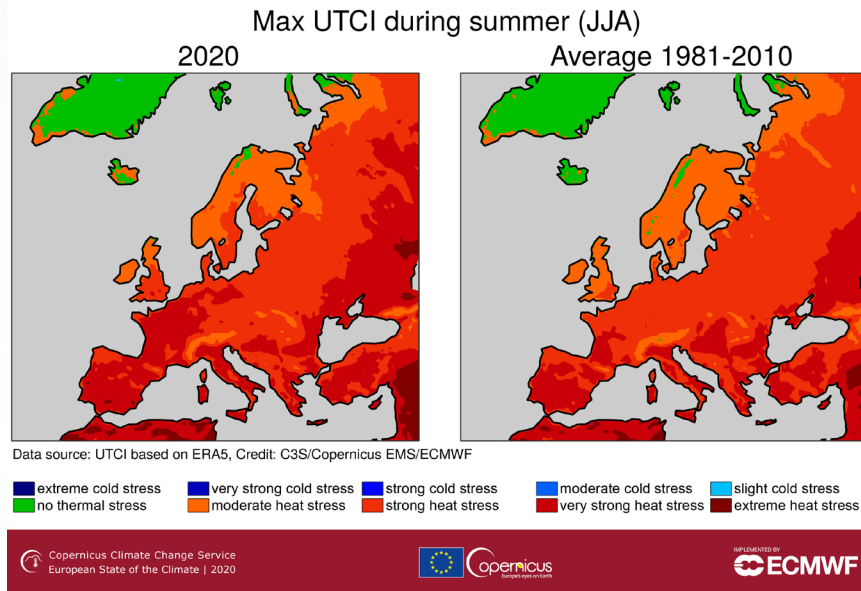
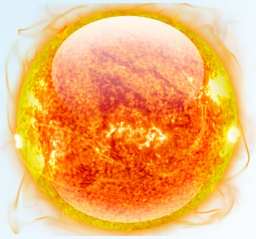


mehka bakterijska gniloba



navadna krastavost

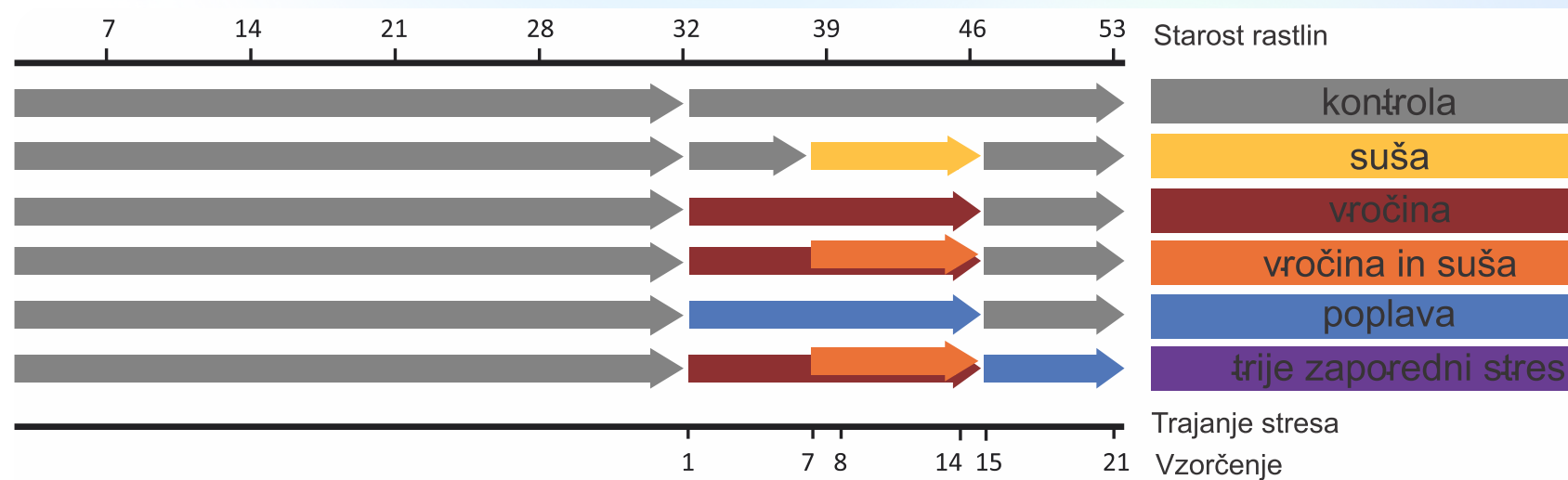
Novi izzivi v agronomiji: ekstremne vremenske razmere



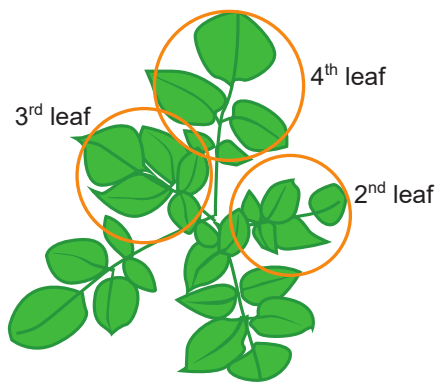
Eksperimentalni načrt



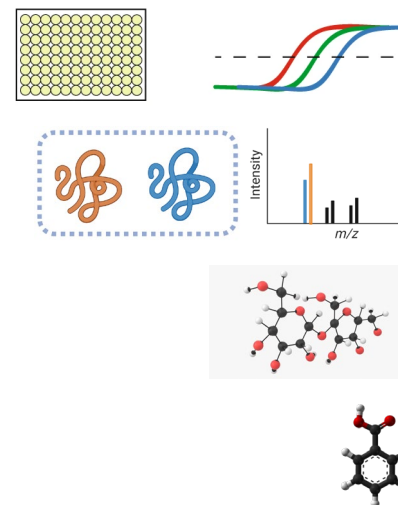
sorta Désirée, 320 rastlin



fenotipizacija



“omike”

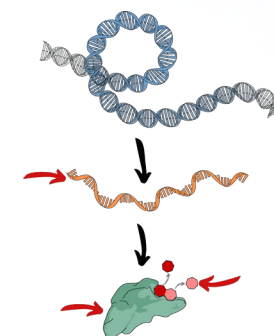


transkriptomika

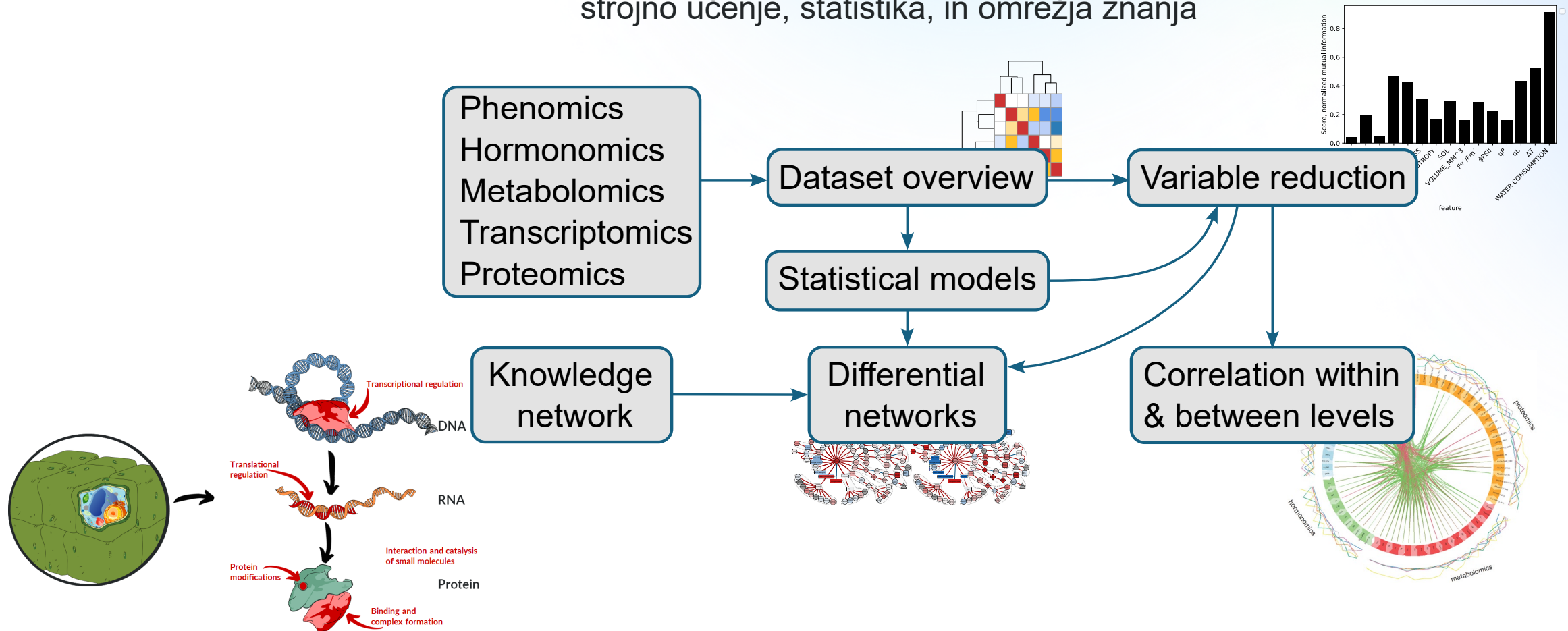
proteomika

metabolomika

hormonomika



strojno učenje, statistika, in omrežja znanja



<https://github.com/NIB-SI/multiOmics-integration>

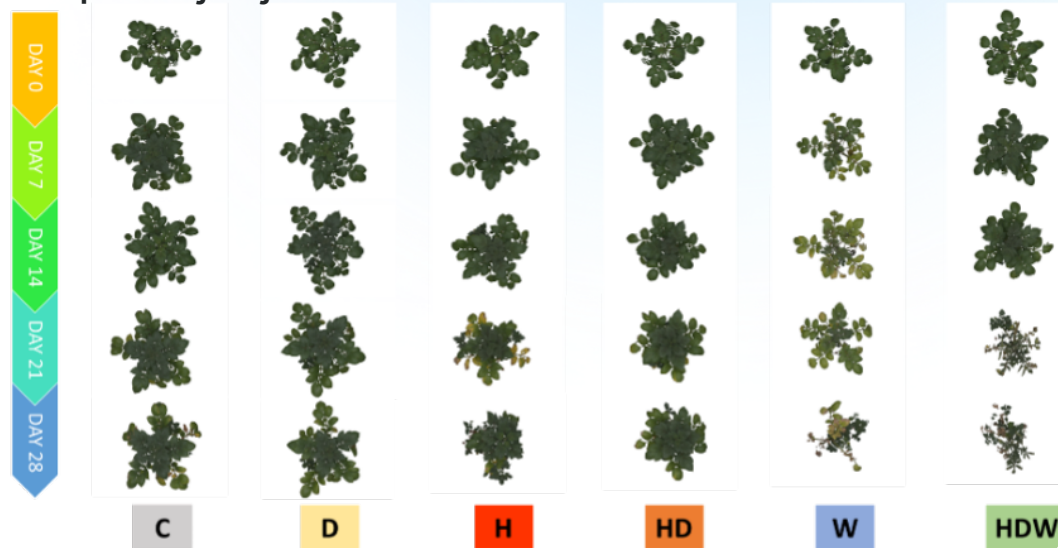


Fenotipizacija

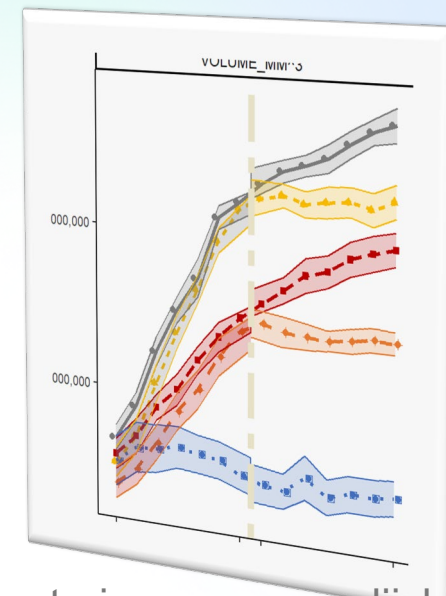
visoka raven avtomatizacije



spremljanje odziva na stress v realnem času



npr. RGB kamera: nadzemni del rastline



konstruirane spremenljivke,
npr. volumen rastline

gomolji ob koncu stresnega obdobja



kontrola



vročina



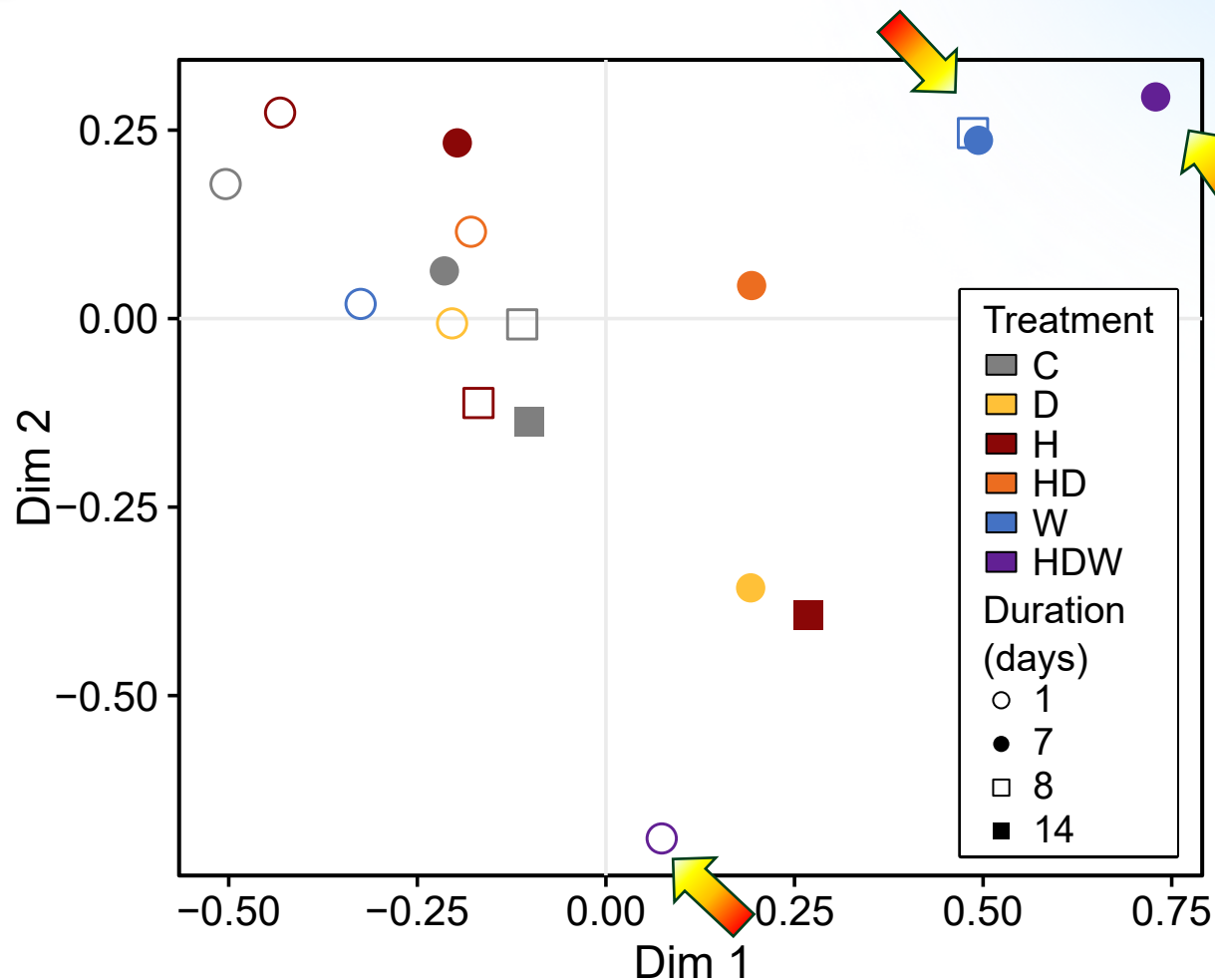
vročina+suša



poplava



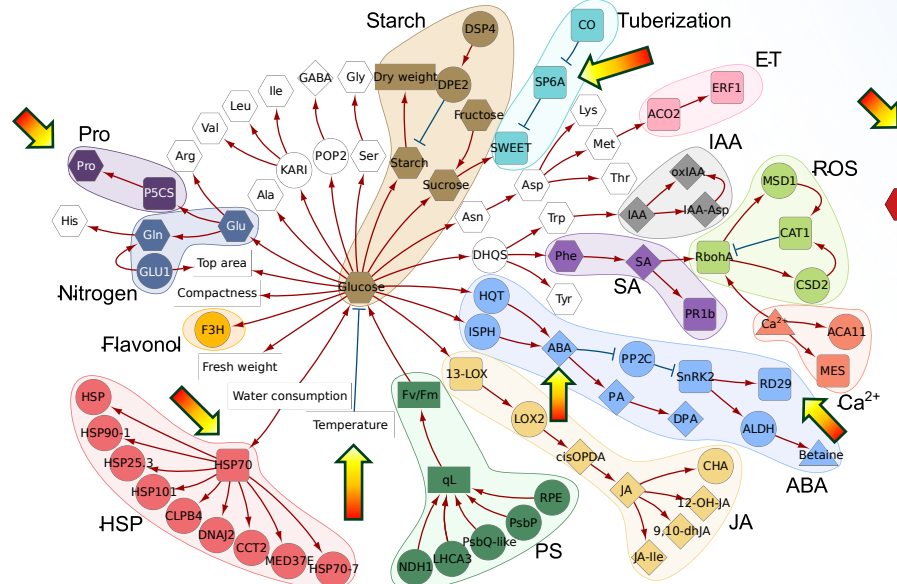
Integracija - osnovna vizualizacija *visoko-dimenzionalnih* podatkov



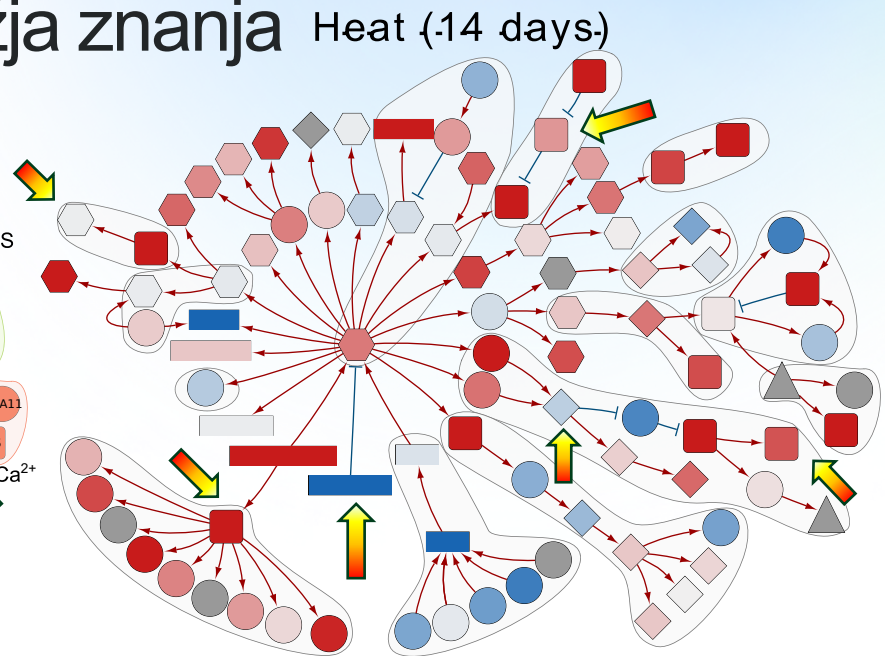
- redukcija dimenzij (meritve), projekcija več dimenzij v dve
- opazovanje relativnih razdalj med točkami
- trojni stress (HDW) se izkazal za zelo močnega, rastline so bile močno prizadete v rasti
- poplava povzroča najmočnejše spremembe



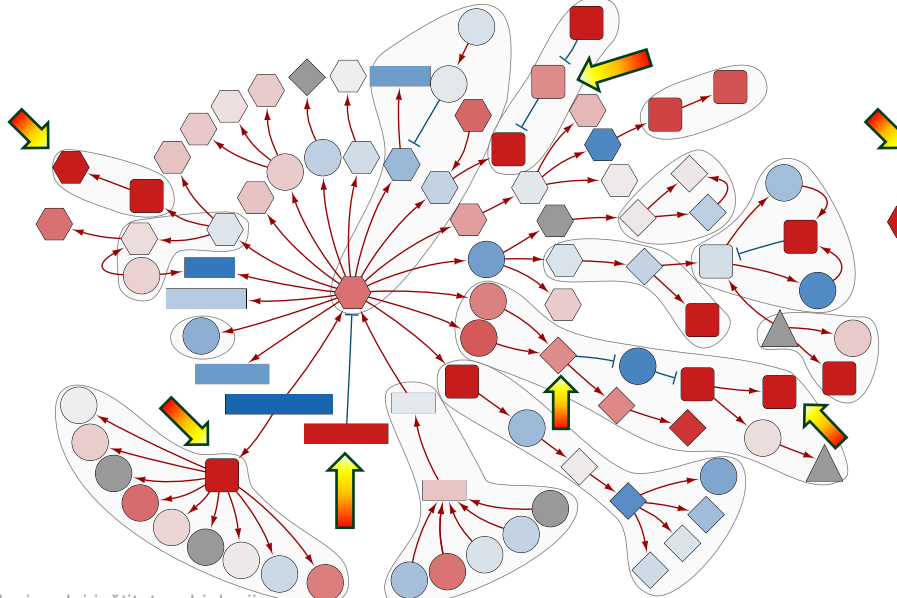
Integracija - uporaba omrežja znanja



Drought (-7 days)



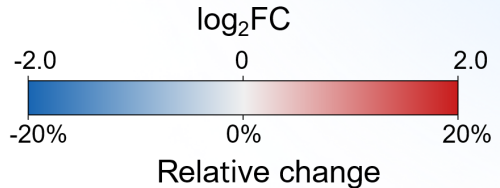
Heat (-14 days) + Drought (-7 days)



- Hormonomics
- Metabolomics
- Phenomics
- Proteomics
- Small molecule
- Transcriptomics

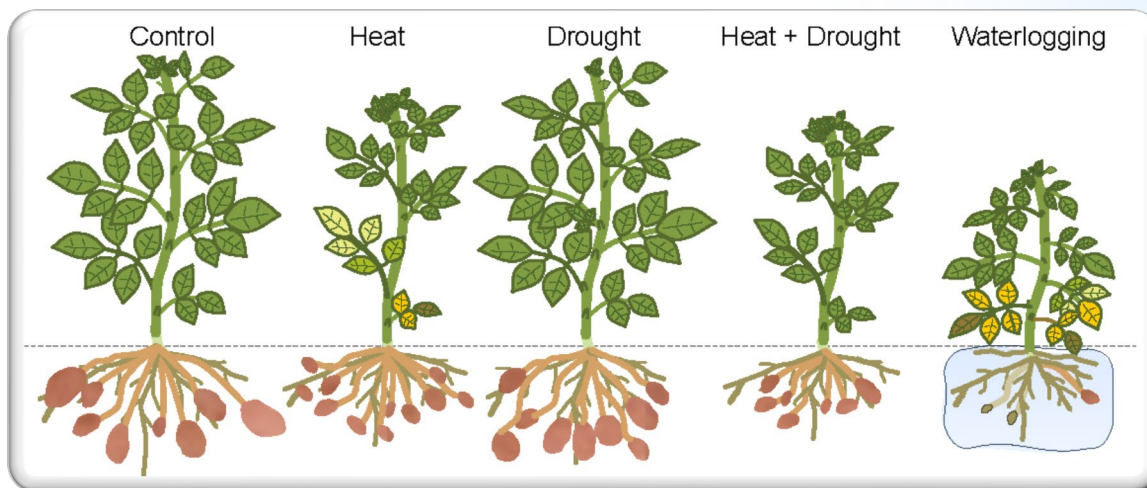
- Interaction (edge)
- Activation
 - Inhibition

- Associated pathway
- ABA
 - Ca²⁺
 - Flavonol
 - Nitrogen
 - ET
 - HSP
 - IAA
 - JA
 - ROS
 - PS
 - SA
 - Starch
 - Tuberization



- vsak stres povzroča različen odziv na molekularni ravni
- kombiniran stres ni zgolj seštevek učinkov posameznih stresov

Zaključki



- sorta Désirée
 - je zmerno odporna na sušo,
 - je pa zelo občutljiva na poplave

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JOURNAL ARTICLE

Integration of multi-omics data and deep phenotyping provides insights into responses to single and combined abiotic stress in potato

Maja Zagorščak, Lamis Abdelhakim, Natalia Yaneth Rodriguez-Granados, Jitka Široká, Arindam Ghatak, Carissa Bleker, Andrej Blejec, Jan Zrimec, Ondřej Novák, Aleš Pěnčík ... Show more

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Abstract

Potato (*Solanum tuberosum*) is highly water and space efficient but susceptible to abiotic stresses such as heat, drought, and flooding, which are severely exacerbated by climate change. Our understanding of crop acclimation to abiotic stress, however, remains limited. Here, we present a comprehensive molecular and physiological high-throughput profiling of potato (*Solanum tuberosum*, cv. Désirée) under heat, drought, and waterlogging applied as single stresses or in combinations designed to mimic realistic future scenarios. Stress responses were monitored via daily phenotyping and multi-omics analyses of leaf samples comprising proteomics, targeted transcriptomics, metabolomics, and hormonomics at several timepoints during and after stress treatments. Additionally, critical metabolites of tuber samples were analyzed at the end of the stress period. We performed integrative multi-omics data analysis using a bioinformatic pipeline that we

Zahvala



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