Signed by / Podpisano przez:
UNIWERSYTET MEDYCZNY W ŁODZI Damian Kołat
Date / Data:
2026-07-19 23:09

EDUCATIONAL GUIDE FOR THE SUBJECT (SYLLABUS)

NAME OF DEPARTMENT PROVIDING THE COURSE: Department of Functional Genomics

FIELD OF STUDY: International Doctoral School / Doctoral School of Molecular Medicine

EDUCATIONAL PROFILE: general academic

SPECIALTY: -

LEVEL OF EDUCATION: 3rd degree

Course unit title: *In silico* analyzes of transcriptome in cancer diseases.

Course unit code: -

Type of course unit: elective

Course aims: This course is intended to familiarize PhD students with bioinformatics repositories containing information about the expression profile in cancer samples. Clinical data of oncological patients used in the assessment of survival, histopathological subtypes and genetic classification will also be presented. The presentation of *in silico* analyzes will be preceded by a discussion of selected repositories in terms of the information they contain. The course also includes a practical part in which doctoral students will try to solve exemplary research problems.

Form of study: stationary or on-line

Year and semester of study: summer semester (all years)

Types of educational activities and number of hours allocated:

Subject	Language course	Self-study	Lecture	Exercises	Laboratory	Seminar	Practical	e-learning	Profession practice	Other (what?)	ECTS points
						20					

Number of ECTS credits allocated and their structure according to students' form of learning: -

Names of course unit's faculty: Faculty of Medicine (Faculty of Biomedical Sciences)
Prerequisites: status of a doctoral student in the Doctoral School of Medical University of Lodz
Learning activities and teaching methods: seminars – verbal presentation, multimedia presentation, analysis of selected bioinformatics repositories, discussion, demonstration, project – solving example research problems.

Course unit content:

Lectures (12 hours): The topics of the lectures will be related to the following issues:

Utilization of Broad GDAC Firehose, cBioPortal, Genomic Data Commons, Gene Expression Omnibus, and GEOExplorer as repositories containing clinical and molecular data from oncological patients.
Functionality of OncoDB, TNMplot, GEPIA2, GENT2, and Oncopression as repositories enabling the automation of transcriptomic analyses.
Use of UALCAN, Coexpedia, GECO, and CorrelationAnalyzeR repositories for gene expression correlation.
Usefulness of KMPlotter, OncoLnc, PrognoScan, cSurvival, and SurvivalGenie as repositories used in survival analysis.
Description of the FABRIC, TANRIC, and ENCORI repositories in terms of their use for, among others: assessment of the mutation frequency of genes, protein domains, as well as analyzes of non-coding RNA.

Practical part (8 hours, individual work):

Individual assessment of the functionality of the discussed repositories in order to use them to solve exemplary scientific issues (the tasks will be discussed in detail during the seminars).
Preparation of short responses with proposed solutions for specific research problems.

Educational effects:

Knowledge:

After completing the course, doctoral student knows and understands:
global achievements, including theoretical foundations as well as general issues and selected detailed issues appropriate for a given scientific discipline (P8S_WG); scientific research methodology (P8S_WG); fundamental dilemmas of modern civilization (P8S_WK), principles of disseminating the results of scientific activities (P8S_WG); basic issues related to the use of bioinformatics repositories for *in silico* analyzes in the assessment of the transcriptome of particular cancer diseases.

Skills:

After completing the course, doctoral student is able to:
use knowledge from various fields of science to creatively identify, formulate and innovatively solve complex problems or perform research tasks (P8S_UW); critically analyze and evaluate the results of scientific research, expert activity and other creative work and their contribution to the development of knowledge (P8S_UW); communicate on specialist topics to an extent that enables active participation in the international scientific community (P8S_UK); speak a foreign language at level B2 of the Common European Framework of Reference for Languages, to an extent that enables participation in an international scientific and professional environment (P8S_UK); independently plan and act for their own development and inspire and organize the development of other people (P8S_UU); as well as communicate, analyze and evaluate the possibilities of using the acquired knowledge.

Attitudes and transferrable (generic) competencies:

Doctoral student is ready to:
critically assess the achievements within a given scientific discipline (P8S_KK); critically assess one's own contribution to the development of a given scientific discipline (P8S_KK); recognize the importance of knowledge in solving cognitive and practical problems (P8S_KK); conducting scientific activities independently (P8S_KR).

Learning resources:

Basic literature:

1. Tomczak K, Czerwińska P, Wiznerowicz M. The Cancer Genome Atlas (TCGA): an immeasurable source of knowledge. Contemp Oncol (Pozn). 2015;19(1A):A68-77. doi: 10.5114/wo.2014.47136. PMID: 25691825; PMCID: PMC4322527.
2. Cerami E, Gao J, Dogrusoz U, Gross BE, Sumer SO, Aksoy BA, Jacobsen A, Byrne CJ, Heuer ML, Larsson E, Antipin Y, Reva B, Goldberg AP, Sander C, Schultz N. The cBio cancer genomics portal: an open platform for exploring multidimensional cancer genomics data. Cancer Discov. 2012 May;2(5):401-4. doi: 10.1158/2159-8290.CD-12-0095. Erratum in: Cancer Discov. 2012 Oct;2(10):960. PMID: 22588877; PMCID: PMC3956037.
3. Kelman G, Brandes N, Linial M. The FABRIC Cancer Portal: A Ranked Catalogue of Gene Selection in Tumors Over the Human Coding Genome. Cancer Res. 2021 Feb 15;81(4):1178-1185. doi: 10.1158/0008-5472.CAN-20-3147. Epub 2020 Dec 4. PMID: 33277365.
4. Park SJ, Yoon BH, Kim SK, Kim SY. GENT2: an updated gene expression database for normal and tumor tissues. BMC Med Genomics. 2019 Jul 11;12(Suppl 5):101. doi: 10.1186/s12920-019-0514-7. PMID: 31296229; PMCID: PMC6624177.
5. Bartha Á, Győrffy B. TNMplot.com: A Web Tool for the Comparison of Gene Expression in Normal, Tumor and Metastatic Tissues. Int J Mol Sci. 2021 Mar 5;22(5):2622. doi: 10.3390/ijms22052622. PMID: 33807717; PMCID: PMC7961455.
6. Tang Z, Kang B, Li C, Chen T, Zhang Z. GEPIA2: an enhanced web server for large-scale expression profiling and interactive analysis. Nucleic Acids Res. 2019 Jul 2;47(W1):W556-W560. doi: 10.1093/nar/gkz430. PMID: 31114875; PMCID: PMC6602440.
7. Lánczky A, Győrffy B. Web-Based Survival Analysis Tool Tailored for Medical Research (KMplot): Development and Implementation. J Med Internet Res. 2021 Jul 26;23(7):e27633. doi: 10.2196/27633. PMID: 34309564; PMCID: PMC8367126.
8. Tang G, Cho M, Wang X. OncoDB: an interactive online database for analysis of gene expression and viral infection in cancer. Nucleic Acids Res. 2022 Jan 7;50(D1):D1334-D1339. doi: 10.1093/nar/gkab970. PMID: 34718715; PMCID: PMC8728272.
9. Chandrashekar DS, Karthikeyan SK, Korla PK, Patel H, Shovon AR, Athar M, Netto GJ, Qin ZS, Kumar S, Manne U, Creighton CJ, Varambally S. UALCAN: An update to the integrated cancer data analysis platform. Neoplasia. 2022 Mar;25:18-27. doi: 10.1016/j.neo.2022.01.001. Epub 2022 Jan 22. PMID: 35078134; PMCID: PMC8788199.

10. Yang S, Kim CY, Hwang S, Kim E, Kim H, Shim H, Lee I. COEXPEDIA: exploring biomedical hypotheses via co-expressions associated with medical subject headings (MeSH). Nucleic Acids Res. 2017 Jan 4;45(D1):D389-D396. doi: 10.1093/nar/gkw868. Epub 2016 Sep 26. PMID: 27679477; PMCID: PMC5210615.
11. Li J, Han L, Roebuck P, Diao L, Liu L, Yuan Y, Weinstein JN, Liang H. TANRIC: An Interactive Open Platform to Explore the Function of lncRNAs in Cancer. Cancer Res. 2015 Sep 15;75(18):3728-37. doi: 10.1158/0008-5472.CAN-15-0273. Epub 2015 Jul 24. PMID: 26208906; PMCID: PMC4573884.
12. Barrett T, Wilhite SE, Ledoux P, Evangelista C, Kim IF, Tomashevsky M, Marshall KA, Phillippy KH, Sherman PM, Holko M, Yefanov A, Lee H, Zhang N, Robertson CL, Serova N, Davis S, Soboleva A. NCBI GEO: archive for functional genomics data sets--update. Nucleic Acids Res. 2013 Jan;41(Database issue):D991-5. doi: 10.1093/nar/gks1193. Epub 2012 Nov 27. PMID: 23193258; PMCID: PMC3531084.
13. Hunt GP, Grassi L, Henkin R, Smeraldi F, Spargo TP, Kabiljo R, Koks S, Ibrahim Z, Dobson RJB, Al-Chalabi A, Barnes MR, Iacoangeli A. GEOexplorer: a webserver for gene expression analysis and visualisation. Nucleic Acids Res. 2022 Jul 5;50(W1):W367-W374. doi: 10.1093/nar/gkac364. PMID: 35609980; PMCID: PMC9252785.
14. Heath, A. P., Ferretti, V., Agrawal, S., An, M., Angelakos, J. C., Arya, R., Bajari, R., Baqar, B., Barnowski, J. H. B., Burt, J., Catton, A., Chan, B. F., Chu, F., Cullion, K., Davidsen, T., Do, P. M., Dompierre, C., Ferguson, M. L., Fitzsimons, M. S., Ford, M., … Grossman, R. L. (2021). The NCI Genomic Data Commons. Nature genetics, 53(3), 257–262. https://doi.org/10.1038/s41588-021-00791-5.
15. Lee J, Choi C. Oncopression: gene expression compendium for cancer with matched normal tissues. Bioinformatics. 2017 Jul 1;33(13):2068-2070. doi: 10.1093/bioinformatics/btx121. PMID: 28881874.
16. Najafov J, Najafov A. GECO: gene expression correlation analysis after genetic algorithm-driven deconvolution. Bioinformatics. 2019 Jan 1;35(1):156-159. doi: 10.1093/bioinformatics/bty623. PMID: 30010797.
17. Miller HE, Bishop AJR. Correlation AnalyzeR: functional predictions from gene co-expression correlations. BMC Bioinformatics. 2021 Apr 20;22(1):206. doi: 10.1186/s12859-021-04130-7. PMID: 33879054; PMCID: PMC8056587.
18. Mizuno H, Kitada K, Nakai K, Sarai A. PrognoScan: a new database for meta-analysis of the prognostic value of genes. BMC Med Genomics. 2009 Apr 24;2:18. doi: 10.1186/1755-8794-2-18. PMID: 19393097; PMCID: PMC2689870.
19. Cheng X, Liu Y, Wang J, Chen Y, Robertson AG, Zhang X, Jones SJM, Taubert S. cSurvival: a web resource for biomarker interactions in cancer outcomes and in cell lines. Brief Bioinform. 2022 May 13;23(3):bbac090. doi: 10.1093/bib/bbac090. PMID: 35368077; PMCID: PMC9116376.
20. Dwivedi B, Mumme H, Satpathy S, Bhasin SS, Bhasin M. Survival Genie, a web platform for survival analysis across pediatric and adult cancers. Sci Rep. 2022 Feb 23;12(1):3069. doi: 10.1038/s41598-022-06841-0. PMID: 35197510; PMCID: PMC8866543.
21. Li JH, Liu S, Zhou H, Qu LH, Yang JH. starBase v2.0: decoding miRNA-ceRNA, miRNA-ncRNA and protein-RNA interaction networks from large-scale CLIP-Seq data. Nucleic Acids Res. 2014 Jan;42(Database issue):D92-7. doi: 10.1093/nar/gkt1248. Epub 2013 Dec 1. PMID: 24297251; PMCID: PMC3964941.

Additional literature:

1. Edelman LB, Eddy JA, Price ND. In silico models of cancer. Wiley Interdiscip Rev Syst Biol Med. 2010 Jul-Aug;2(4):438-459. doi: 10.1002/wsbm.75. PMID: 20836040; PMCID: PMC3157287.
2. Dhall A, Jain S, Sharma N, Naorem LD, Kaur D, Patiyal S, Raghava GPS. In silico tools and databases for designing cancer immunotherapy. Adv Protein Chem Struct Biol. 2022;129:1-50. doi: 10.1016/bs.apcsb.2021.11.008. Epub 2021 Dec 23. PMID: 35305716.

Methods and methods of verifying learning outcomes, including the form and conditions for passing the subject: Attendance at the seminar, active participation and completion of planned tasks during classes.

Additional information:

The seminar is carried out by the Department of Functional Genomics, Medical University of Lodz. Person responsible for the course: Damian Kołat, PhD (e-mail: damian.kolat@umed.lodz.pl).

Potential instructors: Damian Kołat PhD; Żaneta Kałuzińska-Kołat, PhD.

Statement and signature of the course leader:

I hereby state that the content of the curriculum included in the syllabus below is the result of my individual work completed as part of a work contract/cooperation resulting from a civil law contract and that author rights to this title are not the property of a third party.