CURRICULUM VITAE
Dariusz Plewczyński, PhD
www: https://plewczynski-lab.org
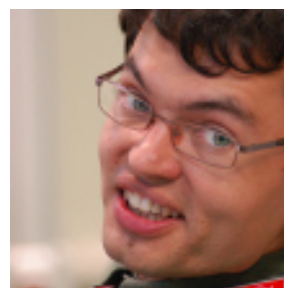
Affiliation

Professor of Exact and Natural Sciences; Principal Investigator
Laboratory of Bioinformatics and Computational Genomics,
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Education

MA: 1995, Faculty of Physics, Warsaw University, Poland. Major: theoretical physics. Thesis title: *"Statistical physics of phase transitions in thin magnetic layers"*;
PhD: 2001, Institute of Physical Chemistry, Poland. Major: physical chemistry. Dissertation title: *„Diffusion of curved surfaces"*;
PostDoc: 2001 – Warsaw, Poland, The International Molecular and Cell Biology Institute. Major: bioinformatics. Research project: „Structural Comparison of proteins";
2002 – San Diego, CA, The Sanford-Burnham Institute. Major: bioinformatics. Research project: „Improving the sequence alignment quality using predicted local 3D structure of a protein chain";
2003 – Helsinki, Finland, Helsinki University. Major: bioinformatics. Research project: "Structural alignment of proteins using DALI"
Habilitation: 2012, Institute of Computer Science Polish Academy of Sciences, Poland. Major: bioinformatics. Dissertation title: *„Applications of machine learning and data analysis techniques to biological function prediction of biomolecules"*

Positions held

Starting from October 2017 – Professor, DSc, PhD, the head of **Laboratory of Bioinformatics and Computational Genomics**, *Faculty of Mathematics and Information Science, Warsaw University of Technology*
Starting from December 2014 – Professor, DSc, PhD, Principal Investigator of **Laboratory of Functional and Structural Genomics**, *Center of New Technologies, University of Warsaw*
2013 till 2016 – Research consultant, Centre for Innovative Research, Faculty of Medicine, *Medical University of Bialystok*, Poland.
2002 till 2014 – Assistant Professor, Bioinformatics and Systems Biology Laboratory, Statistical Data Analysis & Systems Theory Unit, Interdisciplinary Centre for Mathematical and Computational Modelling, Warsaw University, Poland.
2011 till 2013 – Assistant Professor, Department of Physical Chemistry, Bioinformatics and Applied Mathematics Unit, Faculty of Pharmacy, Medical University of Warsaw, Poland.

Visiting Researcher

2004 – Rome, Italy, Merck Laboratories. Major: bioinformatics, chemoinformatics. Research project: "Applications of machine learning algorithms in virtual High-throughput screening"
2005 – Helsinki, Finland, Helsinki University. Major: bioinformatics. Research project: "Prediction of protein-protein interactions"
2003-2008 – Poznan, Poland, BioInfoBank Institute, Major: bioinformatics. Research project: „Prediction of protein function using sequence and structual information".
2011 – *Stanford University*, Centre of Professional Development, Top500 Innovators
2013/2014 – *The Jackson Laboratory & Yale University*, Farmington, CT, USA
2018 – *University of California*, Davis, CA, USA

Other professional activities and memberships

Member of the Polish Bioinformatics Society
Member of the Polish Physics Society
Member of the International Society for Computational Biology

Editorships & Reviewing boards

Main publications

<u>**Structural Genomics**</u>

1) **"3D-GNOME 2.0: a three-dimensional genome modeling engine for predicting structural variation-driven alterations of chromatin spatial structure in the human genome" by Wlasnowolski M, Sadowski M, Czarnota T, Jodkowska K, Szalaj P, Tang Z, Ruan Y, Plewczynski D. Nucleic Acids Res. 2020 May 22:gkaa388. doi: 10.1093/nar/gkaa388. PMID: 32442297**

2) "Spring Model - chromatin modeling tool based on OpenMM" by Kadlof M, Rozycka J, Plewczynski D. Methods. 2019 Nov 29. pii: S1046-2023(19)30053-2. doi: 10.1016/j.ymeth.2019.11.014. PMID: 31790732.

3) **"Spatial chromatin architecture alteration by structural variations in human genomes at the population scale" Sadowski M, Kraft A, Szalaj P, Wlasnowolski M, Tang Z, Ruan Y, Plewczynski D. Genome Biol. 2019 Jul 30;20(1):148. doi: 10.1186/s13059-019-1728-x. Erratum in: Genome Biol. 2019 Sep 3;20(1):188. PMID: 31362752.**

4) "Machine learning polymer models of three-dimensional chromatin organization in human lymphoblastoid cells" by Al Bkhetan Z, Kadlof M, Kraft A, Plewczynski D. Methods. 2019 Mar 7. pii: S1046-2023(18)30334-7. doi: 10.1016/j.ymeth.2019.03.002. PMID: 30853548.

5) "Intermingling of chromosome territories" by Szczepińska T, Rusek AM, Plewczynski D. Genes Chromosomes Cancer. 2019 Jul;58(7):500-506. doi: 10.1002/gcc.22736. Epub 2019 Mar 3. PMID: 30828902.

6) "*ShapeGTB: the role of local DNA shape in prioritization of functional variants in human promoters with machine learning*" by Malkowska M, Zubek J, <u>Plewczynski D</u>, Wyrwicz LS. *PEERJ* Volume: 6 Article Number: e5742 Pub: NOV 29 **2018**, *Impact Factor: 2.469*;

7) "*Three-dimensional Epigenome Statistical Model: Genome-wide Chromatin Looping Prediction*" by Al Bkhetan Z, <u>Plewczynski D</u>. *SCIENTIFIC REPORTS* Volume: 8 Article Number: 5217 Published: MAR 26 **2018**, *Impact Factor: 4.609*;

8) "*Three-dimensional organization and dynamics of the genome*" by Szalaj P, <u>Plewczynski D</u>. *CELL BIOLOGY AND TOXICOLOGY* Volume: 34 Issue: 5 Special Issue: SI Pages: 381-404 Published: OCT **2018**, *Times Cited: 3*, *Impact Factor: 3.390*;

9) "*The 4D nucleome project*" by Dekker J, Belmont AS, Guttman M, Leshyk VO, Lis JT, Lomvardas S, Mirny LA, O'Shea CC, Park PJ, Ren B, Politz JCR, Shendure J, Zhong S; <u>4D Nucleome Network</u>. *NATURE* Volume: 549 Issue: 7671 Pages: 219-226 Published: SEP 14 **2017,** *Times Cited:* 43, *Impact Factor:* 44.959;

10) "*An integrated 3-Dimensional Genome Modeling Engine for data-driven simulation of spatial genome organization*" by Szałaj P, Tang Z, Michalski P, Pietal MJ, Luo OJ, Sadowski M, Li X, Radew K, Ruan Y, <u>Plewczynski D.</u> *GENOME RESEARCH* Volume: 26 Issue: 12 Pages: 1697-1709 Published: DEC **2016**, *Times Cited: 7, Impact Factor: 13.796*;

11) "*3D-GNOME: an integrated web service for structural modeling of the 3D genome*" by Szalaj P, Michalski PJ, Wróblewski P, Tang Z, Kadlof M, Mazzocco G, Ruan Y,

Plewczynski D. ***NUCLEIC ACIDS RESEARCH*** Volume: 44 Issue: W1 Pages: W288-W293 Published: JUL 8 **2016**, *Times Cited: 7, Impact Factor: 10.235*;

12) "*CTCF-Mediated Human 3D Genome Architecture Reveals Chromatin Topology for Transcription*" Tang Z, Luo OJ, Li X, Zheng M, Zhu JJ, Szalaj P, Trzaskoma P, Magalska A, Wlodarczyk J, Ruszczycki B, Michalski P, Piecuch E, Wang P, Wang D, Tian SZ, Penrad-Mobayed M, Sachs LM, Ruan X, Wei CL, Liu ET, Wilczynski GM, Plewczynski D, Li G, Ruan Y. ***CELL*** Volume: 163 Issue: 7 Pages: 1611-1627 Published: DEC 17 **2015**, *Times Cited: 211, Impact Factor: 33.796*;

Genomics and Medical Genetics

8) ""**"Chromatin topology reorganization and transcription repression by PML-RARα in acute promyeloid leukemia" by Wang P, Tang Z, Lee B, Zhu JJ, Cai L, Szalaj P, Tian SZ, Zheng M, Plewczynski D, Ruan X, Liu ET, Wei CL, Ruan Y. Genome Biol. 2020 May 11;21(1):110. doi: 10.1186/s13059-020-02030-2. PMID: 32393309**

9) "Exploring 3D chromatin contacts in gene regulation: The evolution of approaches for the identification of functional enhancer-promoter interaction" Xu H, Zhang S, Yi X, Plewczynski D, Li MJ. Comput Struct Biotechnol J. 2020 Feb 28;18:558-570. doi: 10.1016/j.csbj.2020.02.013. eCollection 2020. PMID: 32226593

10) "Identification of Breast Cancer Subtype Specific MicroRNAs Using Survival Analysis to Find Their Role in Transcriptomic Regulation" by Denkiewicz M, Saha I, Rakshit S, Sarkar JP, Plewczynski D. Front Genet. 2019 Oct 31;10:1047. doi: 10.3389/fgene.2019.01047. eCollection 2019. PMID: 31798622.

11) "Upregulation of MLK4 promotes migratory and invasive potential of breast cancer cells" by Marusiak AA, Prelowska MK, Mehlich D, Lazniewski M, Kaminska K, Gorczynski A, Korwat A, Sokolowska O, Kedzierska H, Golab J, Biernat W, Plewczynski D, Brognard J, Nowis D. Oncogene. 2019 Apr;38(15):2860-2875. doi: 10.1038/s41388-018-0618-0. Epub 2018 Dec 14. PMID: 30552384.

12) "*Oncogenes expand during evolution to withstand somatic amplification*" by Wang X, Li X, Zhang L, Wong SH, Wang MHT, Tse G, Dai RZW, Nakatsu G, Coker OO, Chen Z, Ko H, Chan JYK, Liu T, Cheng CHK, Cheng ASL, To KF, Plewczynski D, Sung JJY, Yu J, Gin T, Chan MTV, Wu WKK. ***Annals of oncology*** Volume 29, Issue 11, 1 November **2018**, Pages 2254-2260, *Impact Factor: 13.930*;

13) "*Inhibition of protein disulfide isomerase induces differentiation of acute myeloid leukemia cells*" by Chlebowska-Tuz J, Sokolowska O, Gaj P, Lazniewski M, Firczuk M, Borowiec K, Sas-Nowosielska H, Bajor M, Malinowska A, Muchowicz A, Ramji K, Stawinski P, Sobczak M, Pilch Z, Rodziewicz-Lurzynska A, Zajac M, Giannopoulos K, Juszczynski P, Basak GW, Plewczynski D, Ploski R, Golab J, Nowis D. ***HAEMATOLOGICA*** Volume: 103 Issue: 11 Pages: 1843-1852 Published: OCT 31 **2018**, *Impact Factor: 7.012*;

14) "*A global reference for human genetic variation*" by 1000 Genomes Project Consortium, Auton A, Brooks LD, Durbin RM, Garrison EP, Kang HM, Korbel JO, Marchini JL, McCarthy S, McVean GA, Abecasis GR. ***NATURE*** Volume: 526 Issue: 7571 Pages: 68+ Published: OCT **2015**, *Times Cited: 2252, Impact Factor: 44.959*;

Bioimaging data analysis

11) **"Ultrastructural visualization of 3D chromatin folding using volume electron microscopy and DNA in situ hybridization" by Trzaskoma P, Ruszczycki B, Lee B, Pels KK, Krawczyk K, Bokota G, Szczepankiewicz AA, Aaron J,**

Walczak A, Śliwińska MA, Magalska A, Kadlof M, Wolny A, Parteka Z, Arabasz S, Kiss-Arabasz M, Plewczyński D, Ruan Y, Wilczyński GM. Nat Commun. 2020 May 1;11(1):2120. doi: 10.1038/s41467-020-15987-2. PMID: 32358536

12) "Three-Dimensional Segmentation and Reconstruction of Neuronal Nuclei in Confocal Microscopic Images" by Ruszczycki B, Pels KK, Walczak A, Zamłyńska K, Such M, Szczepankiewicz AA, Hall MH, Magalska A, Magnowska M, Wolny A, Bokota G, Basu S, Pal A, Plewczynski D, Wilczyński GM. Front Neuroanat. 2019 Aug 20;13:81. doi: 10.3389/fnana.2019.00081. eCollection 2019. PMID: 31481881.

13) "*Quantitative 3-D morphometric analysis of individual dendritic spines*" by Basu S, Saha PK, Roszkowska M, Magnowska M, Baczynska E, Das N, Plewczynski D, Wlodarczyk J. **SCIENTIFIC REPORTS**   Volume: 8   Article Number: 3545   Published: FEB 23 **2018**, *Impact Factor: 4.609*;

14) "*2dSpAn: semiautomated 2-d segmentation, classification and analysis of hippocampal dendritic spine plasticity*" by Basu S, Plewczynski D, Saha S, Roszkowska M, Magnowska M, Baczynska E and Wlodarczyk J. **BIOINFORMATICS**   Volume: 32   Issue: 16   Pages: 2490-2498   Published: AUG 15 2016, *Times Cited: 3, Impact Factor: 8.561*;

15) "*Computational Approach to Dendritic Spine Taxonomy and Shape Transition Analysis*" by Bokota G, Magnowska M, Kuśmierczyk T, Łukasik M, Roszkowska M and Plewczynski D. **FRONTIERS IN COMPUTATIONAL NEUROSCIENCE**   Volume: 10   Article Number: 140   Published: DEC 23 **2016**, *Impact Factor: 2.073*;

Functional Genomics and Bioinformatics

14) "Novel COL12A1 variant as a cause of mild familial extracellular matrix-related myopathy" by Jezela-Stanek A, Walczak A, Łaźniewski M, Kosińska J, Stawiński P, Murcia Pienkowski V, Biernacka A, Rydzanicz M, Kostrzewa G, Krajewski P, Plewczyński D, Płoski R. Clin Genet. 2019 Jun;95(6):736-738. doi: 10.1111/cge.13534. Epub 2019 Mar 28. PMID: 30920656.

15) "Disentangling the complexity of low complexity proteins" by Mier P, Paladin L, Tamana S, Petrosian S, Hajdu-Soltész B, Urbanek A, Gruca A, Plewczynski D, Grynberg M, Bernadó P, Gáspári Z, Ouzounis CA, Promponas VJ, Kajava AV, Hancock JM, Tosatto SCE, Dosztanyi Z, Andrade-Navarro MA. Brief Bioinform. 2019 Jan 30. doi: 10.1093/bib/bbz007. PMID: 30698641.

16) "*The structural variability of the influenza A hemagglutinin receptor-binding site*" by Lazniewski M, Dawson WK, Szczepinska T, Plewczynski D. **Briefings in functional genomics** Volume 17, Issue 6, 26 November **2018**, Pages 415-427, *Impact Factor: 3.416*;

17) "*Predicting Post-Translational Modifications from Local Sequence Fragments Using Machine Learning Algorithms: Overview and Best Practices*" by Tatjewski M, Kierczak M, Plewczynski D. Prediction of protein secondary structure Book Series: **Methods in Molecular Biology**   Volume: 1484   Pages: 275-300   Published: **2017**, *Times Cited: 2*;

18) "*3DFlu: database of sequence and structural variability of the influenza hemagglutinin at population scale*" by Mazzocco G, Lazniewski M, Migdał P, Szczepińska T, Radomski JP, Plewczynski D. **DATABASE** (Oxford)   Article Number: baw130   Published: OCT 2 **2016**, *Impact Factor: 3.755*;

19) "*Binding Activity Prediction of Cyclin-Dependent Inhibitors*" by Saha I, Rak B, Bhowmick SS, Maulik U, Bhattacharjee D, Koch U, Lazniewski M, Plewczynski D.

JOURNAL OF CHEMICAL INFORMATION AND MODELING Volume: 55 Issue: 7 Pages: 1469-1482 Published: JUL **2015**, *Times Cited: 8, Impact Factor: 4.112*;

20) "*Consensus classification of Human Leukocyte Antigens class II proteins*" by I. Saha, G. Mazzocco and D. Plewczynski. **IMMUNOGENETICS** Volume: 65 Issue: 2 Pages: 97-105 Published: FEB **2013**, *Times Cited: 8, Impact Factor: 2.094*;

21) „*AMS 4.0: consensus prediction of post-translational modifications in protein sequences*" by D. Plewczynski, S. Basu and I. Saha. ***AMINO ACIDS*** Volume: 43 Issue: 2 Pages: 573-582 Published: AUG **2012**, *Times Cited: 26, Impact Factor: 2.946*;

22) "*Fuzzy Clustering of Physicochemical and Biochemical Properties of Amino Acids*" by I. Saha, U. Maulik, S. Bandyopadhyay and D. Plewczynski**. *AMINO ACIDS*** Volume: 43 Issue: 2 Pages: 583-594 Published: AUG **2012**, *Times Cited: 37, Impact Factor: 2.946*;

Network and Computational Modelling of Biological Data

21) "Aggregated Network Centrality Shows Non-Random Structure of Genomic and Proteomic Networks" by Halder AK, Denkiewicz M, Sengupta K, Basu S, Plewczynski D. Methods. 2019 Nov 15. pii: S1046-2023(19)30050-7. doi: 10.1016/j.ymeth.2019.11.006. PMID: 31740366.

22) "FunPred 3.0: improved protein function prediction using protein interaction network" by Saha S, Chatterjee P, Basu S, Nasipuri M, Plewczynski D. PeerJ. 2019 May 22;7:e6830. doi: 10.7717/peerj.6830. eCollection 2019. PMID: 31198622.

23) "*3gClust: Human Protein Cluster Analysis*" by Halder AK, Chatterjee P, Nasipuri M, Plewczynski D, Basu S. ***IEEE/ACM Transactions on Computational Biology and Bioinformatics*** 30 May **2018**, *Impact Factor: 2.428*;

24) "*Social adaptation in multi-agent model of linguistic categorization is affected by network information flow*" by Zubek J, Denkiewicz M, Barański J, Wróblewski P, Rączaszek-Leonardi J, Plewczynski D. **PLOS ONE** Volume: 12 Issue: 8 Article Number: e0182490 Published: AUG 15 **2017**, *Impact Factor: 3.352*;

25) "*Detecting reliable non interacting proteins (NIPs) significantly enhancing the computational prediction of protein-protein interactions using machine learning methods*" Srivastava A, Mazzocco G, Kel A, Wyrwicz LS, Plewczynski D. **MOLECULAR BIOSYSTEMS** Volume: 12 Issue: 3 Pages: 778-785 Published: **2016**, *Impact Factor: 2.838*;

26) "*A combined systems and structural modeling approach repositions antibiotics for Mycoplasma genitalium*" by Kazakiewicz D, Karr JR, Langner KM, Plewczynski D. **COMPUTATIONAL BIOLOGY AND CHEMISTRY** Volume: 59 Special Issue: SI Pages: 91-97 Part: B Published: DEC **2015**, *Times Cited: 4, Impact Factor: 1.345*;

27) "*Ensemble learning prediction of protein-protein interactions using proteins functional annotations*" by Saha I, Zubek J, Klingström T, Forsberg S, Wikander J, Kierczak M, Maulik U, Plewczynski D. **MOLECULAR BIOSYSTEMS** Volume: 10 Issue: 4 Pages: 820-830 Published: **2014**, *Times Cited: 19, Impact Factor: 2.838*;

28) "*Information-sharing and aggregation models for interacting minds*" by Migdał P, Rączaszek-Leonardi J, Denkiewicz M and Plewczynski D**. *JOURNAL OF MATHEMATICAL PSYCHOLOGY*** Volume: 56 Issue: 6 Pages: 417-426 Published: DEC **2012**, *Times Cited: 5, Impact Factor: 3.0*;

Research projects

- 2021-2025 NCN Grant **OPUS** "*Multiscale spatial reorganization of chromatin in response to replication stress and its role in cellular protection against genomic instability*" to D. Plewczynski, PI;
- 2020-2024 NCN Grant **PRELUDIUM BIS** "*Spatial network model of Sequence and Structure diversity of Human genome at a population scale*" to D. Plewczynski, PI;
- 2020-2023 EU Grant **ITN** "*Molecular Basis of Human Enhanceropathies*" to D. Plewczynski, Polish co-PI;
- 2017-2021 FNP Grant **TEAM** "T*hree-dimensional Human Genome structure at the population scale: computational algorithm and experimental validation for lymphoblastoid cell lines of selected families from 1000 Genomes Project*" to D. Plewczynski, PI;
- 2015-2019 NCN Grant **OPUS** "*iCell: information processing in living organisms. The role of three-dimensional structure and multi-scale properties in controlling the biological processes in a cell*" to D. Plewczynski, PI;
- 2016-2017 NCN Grant **PRELUDIUM** "*Analysis of mechanisms of drug resistance to trastuzumab in HER2 overexpressing breast cancer based on gene expression changes in selected cell lines*" to Anna Rusek (PhD student), D. Plewczynski – scientific advisor;
- 2015-2016 NCN Grant **ETIUDA** "*Integration of information in biological and synthetic systems*" to J. Zubek (PhD student), D. Plewczynski – scientific advisor;
- 2014-2017 NCN Grant **OPUS** "*Virtual High Throughput Screening (vHTS) derivation of a cross-immunity model for the Influenza-A Virus Infections*" to D. Plewczynski, PI;
- 2008-2011 **KBN** Grant "*Application of machine learning methods to prediction of protein-protein interactions*" - Polish Ministry of Science grant to dr D. Plewczynski, PI;
- Grant LSHG-CT-2003-503265 **BIOSAPIENS**, a large-scale effort to annotate human genome using both informatics tools and input from experimentalists. The Network will create a European Virtual Institute for Genome Annotation, bringing together many of the best laboratories in Europe. This institute will help to improve bioinformatics research in Europe and encourage cooperation between various laboratories The BioSapiens network tries also to integrate experimentalists and bioinformaticians, through a directed programme of genome analysis, focused on specific biological problems. The annotations generated by the Institute will be available in the public domain and easily accessible on the web. This will be achieved initially through a distributed annotation system (DAS), which will evolve to take advantage of new developments in the GRID. The Institute will establish a permanent European School of Bioinformatics, to train bioinformaticians and to encourage best practise in the exploitation of genome annotation data for biologists. The courses and meetings will be open to all scientists throughout Europe, and available at all levels, from basic courses for experimentalists to more advanced training for experts. The BioSapiens NoE will increase European competitiveness, by new discoveries, increased integration, expert training and improved tools and services, and enhance Europe's role in the academic and industrial exploitation of genomics. 6th Framework EC Project to dr L. Rychlewski, participant;
- Grant SP22-CT-2004-003831 **SEPSDA**, Combatting and eventually eradicating the new coronavirus causing Severe Acute Respiratory Syndrome (SARS) requires specific and efficient antiviral drugs and improved diagnostics. The Sino-European Project on SARS Diagnostics and Antivirals (SEPSDA) is an integrated project that applies modern biotechnical technology for the generation of improved diagnostics and of lead compounds for antiviral drugs. SEPSDA brings together leading SARS researchers from

Germany, Denmark, Poland, and China, who together have an excellent publication record on the molecular biology of SARS coronavirus (SARS-CoV). Several of the existing anti-SARS drug leads as well as the first antibody-based diagnostic kit were created by members of SEPSDA. Participation of four leading laboratories in China brings SEPSDA in the unique position of having access to samples from Chinese patients at various stages of disease. Serological studies will lead to improved SARS diagnostics, 6th Framework EC Project to dr L. Rychlewski, participant;

- Grant QLRT-CT2000-00127 **ELM**, The four principal objectives of the ELM consortium are to (1) design, (2) develop, (3) maintain and (4) apply, a novel infrastructure resource devoted to the prediction of functional motifs in protein sequences. ELM (short for Eukaryotic Linear Motif) will be both "virtual" - provided electronically - and "distributed" - provided by a network of sites. Effective prediction of short motifs will require the implementation of hitherto unique context-dependent filtering software, 6th Framework EC Project to dr L. Rychlewski, participant;

- *Searching and characterization of new protein domains responsible for important biological processes in RNA metabolism in eukaryotic cells* – Polish Ministry of Science grant to dr K. Ginalski, participant;

- *Mathematical modeling of activity and metabolism of human neuronal cells* – Polish Ministry of Science grant to dr J. Karbowski, participant;

- *The role of noncoding RNA during resting time of seeds in plants* – Polish Ministry of Science grant to dr S. Swiezewski, participant;

- *Proteomic analysis of molecular machinery responsible for degradation of RNA in mammals* – Polish Ministry of Science grant to dr hab. A. Dziembowski, participant;

- Grant ESF-FT039 DRUST, "*Digging for the roots of understanding*" collaborative research project (CRP) brings together eminent European research groups that cover the full breadth of Cognitive Science (cognitive anthropology, cognitive neuroscience, cognitive psychiatry, artificial intelligence, linguistics, philosophy, and psychology) in an interdisciplinary examination of how different types of common ground support interpersonal and intercultural understanding. Communication plays a key role for such an understanding but only to the extent that dialog partners have sufficient common ground. Misunderstandings occur because most dimensions on which common ground can exist are not universally shared and not a priori present. ESF EuroUnderstanding Project to dr Joanna Rączaszek-Leonardii, polish co-PI;

Teaching experience

<u>Lectures</u>: Bioinformatics (UW, WUT); Drug Design (WUM); Machine Learning (UW); statistical data analysis (UW).
<u>Seminars and labs</u>: Bioinformatics; Systems Biology; Machine Learning; Statistical Physics; Cognitive Systems; Computational Intelligence.

Awards

2013 – Senior Fulbright Fellowship to visit Harvard University, MA, USA;
2011 – Top500 Innovators: Science, Management and Commercialization Award; Polish Ministry of Science and Higher Education
1994 – Sosnowski Award (for outstanding physicists); Polish Physical Society
1993 – 1994 Polish Ministry of Education and Science Award
1986 – 1987 Polish Ministry of Education

Languages:

Polish (native), English (fluent), Germany (basic)

Hobby

Photography, History, Traveling, Robotics and Artificial Intelligence.