Bartosz Czech, PhD, Eng.

Curriculum vitae

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Experience

Assistant Professor, Department of Genetics, Wrocław University of Environmental and Life Sciences
May 2026 – present · Wrocław, Poland

- Research in bioinformatics and computational biology; teaching bioinformatics and biostatistics.

Senior Bioinformatician, 7N, contracted to a global pharmaceutical company
July 2019 – present · Warsaw, Poland

- Processing and modelling of high-throughput drug response screens; co-author of the open-source gDR suite (Bioconductor).
- NGS data analysis: bulk and single-cell RNA-seq, whole-genome sequencing, 16S rRNA.
- Mass spectrometry phosphoproteomics.
- R/Shiny applications and production WDL pipelines; product owner role in an agile team.

Founder and owner, GeneStat
2019 – present · Wrocław, Poland

- Bioinformatics and statistics services for research groups and companies: sequencing and spatial transcriptomics data analysis, statistical analysis of experiments, written reports.

NGS data analysis internship, Center for Quantitative Genetics and Genomics, Aarhus University
July – August 2018 · Foulum, Denmark

Statistical analysis internship, Biostat sp. z o.o.
July – August 2016 · Rybnik, Poland

Education

MBA in Healthcare Management with elements of clinical research, Poznan University of Medical Sciences
2025 – present

PhD in Biological Sciences, Wrocław University of Environmental and Life Sciences
2019 – 2024

MSc in Bioinformatics (biostatistics and bioinformatics programming), Wrocław University of Environmental and Life Sciences
2017 – 2019

BSc in Bioinformatics, Wrocław University of Environmental and Life Sciences
2014 – 2017

Publications

Peer-reviewed articles

1. Zieliński P, Frąszczak M, **Czech B**, Dobosz P, Adamiak K, Mierzejewski P, Stępień R, Mielczarek M (2026). A proof-of-concept study: reference transcriptome choice as a hidden analytical variable in breast cancer RNA-seq analysis. *International Journal of Molecular Sciences*, 27(21):9398. doi:10.3390/ijms27219398
2. Prochowska S, **Czech B**, Eberhardt M, Niżański W (2026). Motile sperm head morphometry in relation to sperm kinematics and freezability in cats. *Theriogenology*, 255:117839. doi:10.1016/j.theriogenology.2026.117839
3. Paul S, Hagenbeek TJ, Tremblay J, Kameswaran V, Ong C, Liu C, Guarnaccia AD, Mondo JA, Hsu PL, Kljavin NM, **Czech B**, Smola J, Nguyen DAH, Lacap JA, Pham TH, Liang Y, Blake RA, Gerosa L, Grimmer M, Xie S, Daniel B, Yao X, Dey A (2025). Cooperation between the Hippo and MAPK pathway activation drives acquired resistance to TEAD inhibition. *Nature Communications*, 16:1743. doi:10.1038/s41467-025-56634-y

4. Rozek W, Kwasnik M, Socha W, **Czech B**, Rola J (2024). Profiling of snoRNAs in exosomes secreted from cells infected with influenza A virus. *International Journal of Molecular Sciences*, 26(1):12. doi:10.3390/ijms26010012
5. Goetz A, Shanahan F, Brooks L, Lin E, Mroue R, Dela Cruz D, Hunsaker T, **Czech B**, Dixit P, Segal U, Martin S, Foster SA, Gerosa L (2024). Computational modeling of drug response identifies mutant-specific constraints for dosing panRAF and MEK inhibitors in melanoma. *Cancers*, 16(16):2914. doi:10.3390/cancers16162914
6. Prochowska S, Napierkowska S, **Czech B**, Niżański W (2023). Feline sperm head morphometry in relation to male pedigree and fertility. *Theriogenology*, 208:119–125. doi:10.1016/j.theriogenology.2023.06.006
7. Kwasnik M, Socha W, **Czech B**, Wasiak M, Rola J, Rozek W (2023). Protein-coding region derived small RNA in exosomes from influenza A virus–infected cells. *International Journal of Molecular Sciences*, 24(1):867. doi:10.3390/ijms24010867
8. **Czech B**, Wang Y, Wang K, Luo H, Hu L, Szyda J (2022). Host transcriptome and microbiome interactions in Holstein cattle under heat stress condition. *Frontiers in Microbiology*, 13:998093. doi:10.3389/fmicb.2022.998093
9. **Czech B**, Szyda J, Wang K, Luo H, Wang Y (2022). Fecal microbiota and their association with heat stress in Bos taurus. *BMC Microbiology*, 22:171. doi:10.1186/s12866-022-02576-0
10. Suchocki T, **Czech B**, Dunislawska A, Slawinska A, Derebecka N, Wesoly J, Siwek M, Szyda J (2021). SNP prioritization in targeted sequencing data associated with humoral immune responses in chicken. *Poultry Science*, 100(11):101433. doi:10.1016/j.psj.2021.101433
11. Mielczarek M, **Czech B**, Stańczyk J, Szyda J, Guldbrandtsen B (2020). Extraordinary command line: basic data editing tools for biologists dealing with sequence data. *The Open Bioinformatics Journal*, 13(1):137–145. doi:10.2174/1875036202013010137
12. Kotlarz K, Mielczarek M, Suchocki T, **Czech B**, Guldbrandtsen B, Szyda J (2020). The application of deep learning for the classification of correct and incorrect SNP genotypes from whole-genome DNA sequencing pipelines. *Journal of Applied Genetics*, 61(4):607–616. doi:10.1007/s13353-020-00586-0
13. **Czech B**, Guldbrandtsen B, Szyda J (2020). Patterns of DNA variation between the autosomes, the X chromosome and the Y chromosome in Bos taurus genome. *Scientific Reports*, 10:13641. doi:10.1038/s41598-020-70380-9
14. **Czech B**, Frąszczak M, Mielczarek M, Szyda J (2018). Identification and annotation of breed-specific single nucleotide polymorphisms in Bos taurus genomes. *PLOS ONE*, 13(6):e0198419. doi:10.1371/journal.pone.0198419

Preprints

1. **Czech B**, Wang Y (2023). Genome-wide association study of heat stress response in Bos taurus. *bioRxiv*. doi:10.1101/2023.06.05.543663

Software

- **ggwas**: ggplot2 plots for GWAS summary statistics (R; under review at Bioconductor). github.com/bczech/ggwas
- **BRASSVis**: plots of gene fusions and structural variants from BRASS (R). github.com/bczech/BRASSVis
- **gDR**: co-author of the R suite for drug response screens (Bioconductor). github.com/gdrplatform

Teaching

I teach bioinformatics and biostatistics at Wrocław University of Environmental and Life Sciences. Courses in 2026/27: Biostatistics; Data Analysis (machine learning in R and Python); Computer Lab (Unix command line for bioinformatics); Coding Lab for Erasmus+ students (in English). Materials: bczech.github.io/teaching.

Conference presentations

Talks

- Czech B, Szyda J (2024). Gut microbiota composition and gene expression in Holstein cattle under heat stress. Invited talk (in Polish), XXIX Winter School of Cattle Breeders, Zakopane, Poland.
- Jaśkowski B, Czech B, Niżański W (2023). Evaluation of the size of the recipient's corpus luteum after synchronization as an additional criterion for increasing the pregnancy rate after an embryo transfer in cattle. Japan–Poland Joint Seminar, Morioka, Japan.
- Czech B, Szyda J, Wang Y (2022). Host transcriptome and microbiome data integration in Chinese Holstein cattle under heat stress. 73rd Annual Meeting of the European Federation of Animal Science (EAAP), Porto, Portugal.
- Czech B, Wang K, Chen S, Wang Y, Szyda J (2021). Faecal microbiota and their association with heat stress in *Bos taurus*. 72nd EAAP Annual Meeting, Davos, Switzerland.

- Czech B, Suchocki T, Szyda J (2019). SNP prioritisation in GWAS with dense marker sets. 70th EAAP Annual Meeting, Ghent, Belgium.
- Suchocki T, Czech B, Siwek M, Szyda J (2019). Breed specific reference genomes in cattle. 70th EAAP Annual Meeting, Ghent, Belgium.
- Czech B, Zając M, Wasyl D, Mielczarek M, Sztromwasser P (2019). Optimization of de novo genome assembly based on second and third generation sequencing data. XXIV International Conference of Student Scientific Circles, Wrocław, Poland.
- Czech B, Mielczarek M, Frąszczak M, Szyda J (2018). Breed specific reference genomes in cattle. 69th EAAP Annual Meeting, Dubrovnik, Croatia.
- Czech B (2018). Construction of *Bos taurus* breed specific reference genomes. XXIII International Conference of Student Scientific Circles, Wrocław, Poland.
- Czech B, Dobkowski E, Mielczarek M, Frąszczak M, Szyda J (2017). Construction of *Bos taurus* breed specific reference genomes for Fleckvieh, Simmental, Guernsey and Brown Swiss. Vortragstagung der DGfZ und GfT, University of Hohenheim, Stuttgart, Germany.
- Czech B, Dobkowski E, Barski P, Odziemczyk M (2017). Creating the Brown Swiss breed specific reference genome. XXII International Conference of Student Scientific Circles, Wrocław, Poland.

Posters

- Jaśkowski B, Czech B, Jaśkowski J (2024). Corpus luteum in embryo recipient heifers: practical aspects. 32nd World Buiatrics Congress.
- Mielczarek M, Czech B, Stępień R, et al. (2024). The effect of transcriptomic annotations in breast cancer DGE study. European Human Genetics Conference (ESHG). *European Journal of Human Genetics* 32(Suppl 2):915.
- Stępień R, Szyda J, Czech B, Mielczarek M (2023). The effect of transcriptomic annotations in breast cancer differential gene expression study. 17th International Symposium on Integrative Bioinformatics, Wrocław, Poland.
- Czech B, Szyda J, Wang Y (2022). Host transcriptome and microbiome data integration in Chinese Holstein cattle under heat stress. 73rd EAAP Annual Meeting, Porto, Portugal.
- Czech B, Wang K, Chen S, Wang Y, Szyda J (2021). Challenges of 16S rRNA gene analysis in Chinese Holstein cows under heat stress condition. 72nd EAAP Annual Meeting, Davos, Switzerland.
- Czech B, Szyda J, Wang K, Chen S, Wang Y (2020). The effect of pipelines and databases on the analysis of the fecal microbiota of dairy cattle. 71st EAAP Annual Meeting (online).
- Szyda J, Czech B, Wang K, Chen S, Wang Y (2020). The application of mixed linear models for the analysis of microbiome influence on heat stress in Chinese Holstein cows. 71st EAAP Annual Meeting (online).
- Kotlarz K, Mielczarek M, Suchocki T, Czech B, Guldbrandtsen B, Szyda J (2020). Don't play too much! Deep learning to classify true and false positive SNPs in whole genome sequence. 71st EAAP Annual Meeting (online).
- Czech B, Guldbrandtsen B, Szyda J (2020). Patterns of DNA variation between the autosomes, the X chromosome and the Y chromosome in *Bos taurus* genome. Autumn Workshop of the Polish Bioinformatics Society (PTBI).
- Kotlarz K, Mielczarek M, Suchocki T, Czech B, Guldbrandtsen B, Szyda J (2020). Dig (deep)er: deep learning algorithms for the imbalanced classification of correct and incorrect SNP genotypes from WGS pipelines. Autumn Workshop of the Polish Bioinformatics Society (PTBI).
- Czech B, Guldbrandtsen B, Szyda J (2019). Pattern of genetic variation between autosomes and sex chromosomes in *Bos taurus* genome. 70th EAAP Annual Meeting, Ghent, Belgium.

Skills

- **Sequencing and omics data:** WGS and WES, Variant calling, Structural variants and gene fusions, Bulk RNA-seq, Single-cell RNA-seq, Spatial transcriptomics (Visium HD), Small RNA-seq, ChIP-seq, ATAC-seq and scATAC-seq, Epigenomics, 16S rRNA and metagenomics, Genome annotation, Comparative and population genomics.
- **Drug discovery and proteomics:** Dose-response modelling, Drug combinations and synergy, High-throughput screens, CRISPR screens, MS phosphoproteomics, Kinase activity (KSEA), Pathway and enrichment analysis, Network biology, Structural biology.
- **Statistics and machine learning:** Linear and mixed models, GWAS and statistical genetics, Study design and power analysis, Multi-omics integration, Exploratory data analysis, Supervised and unsupervised learning, Deep learning, Feature engineering, scikit-learn, caret, TensorFlow and Keras, PyTorch.
- **Programming and visualisation:** R, R packages (Bioconductor), Shiny, Python, Bash, sed, AWK, SQL, Git, GitHub, GitLab, ggplot2, Plotly, Seaborn, Dash, R Markdown and Quarto, Jupyter, LaTeX, REST APIs.
- **Pipelines, infrastructure and data:** WDL pipelines, HPC and Slurm, Linux, AWS, Docker, Kubernetes, Conda, Snowflake, MySQL and SQLite, Database design, FAIR data, Metadata management.

- **Collaboration and delivery:** Scrum, Product ownership, Jira, Trello, Reports for non-specialists, Scientific writing, Technical documentation, Teaching and training.

Memberships

European Federation of Animal Science (since 2018) · Polish Bioinformatics Society (since 2018)

Languages

Polish (native) · English (upper-intermediate) · Spanish (basic)