English Syllabus
Course Title: Practical use of NCBI databases and allied web resources in biomedical sciences: from gene to functional analysis
Profile: Molecular; Interdisciplinary
Discipline: Medical Sciences
Coordinator: Prof. Tomasz Popławski
Responsible Unit: Department of Microbiology and Pharmaceutical Biochemistry (Zakład Mikrobiologii i Biochemii Farmaceutycznej)
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Format: ONLINE (synchronous, live)
Druga połowa semestru letniego - 09:00 - 12:45
Duration / Workload: 5 didactic hours (5×45 min); single session
Participant Limit: Minimum 10 (to open); Maximum 25
Course Objectives
Enable PhD students to find, extract, and interpret gene- and variant-level evidence using the NCBI ecosystem (PubMed, Gene, ClinVar, dbSNP; optionally GEO) and to translate curated gene lists into functional insights via established web enrichment tools.
Learning Outcomes (students will be able to…)

1. Build reproducible PubMed strategies using MeSH, filters, and field tags for a defined gene/pathway.
2. Navigate NCBI Gene, ClinVar, and dbSNP to capture identifiers, metadata, and clinical significance with transparent citation.
3. Link literature evidence to gene/variant interpretation and summarize evidence in a concise, auditable format.
4. Perform basic pathway/GO enrichment on NCBI-derived gene lists using widely used web tools (e.g., DAVID, Metascape) and report limitations.
5. Produce a brief end-to-end workflow (inputs → queries/IDs → outputs) suitable for lab documentation and replication.
Prerequisites (recommended)
Basic molecular biology; familiarity with literature searching (no coding required).
Course Content

NCBI Ecosystem Overview: How PubMed Connects to Gene, ClinVar, dbSNP (and Optionally GEO)
Advanced PubMed: MeSH, filters, fielded queries, saving/rerunning strategies.
Gene & variant evidence: extracting gene summaries, transcripts, variation IDs, pathogenicity/clinical significance.
From gene list to insight: functional annotation and enrichment using external, widely used web tools (e.g., DAVID, Metascape); interpretation caveats.
Case study: Integrating multi-database evidence to form a testable hypothesis.
Teaching Methods

Interactive online seminar with live demonstrations, guided hands-on tasks, short team exercise, and Q\&A.
Assessment (Pass/Fail)
Mandatory submission of a short case worksheet the same day, containing:
(i) a PubMed strategy (final query + rationale + 3 key references),
(ii) one gene and one variant summary (NCBI links/IDs; evidence note),
(iii) an enrichment snapshot (tool, date/version, input list, top terms + one limitation).
Active participation in hands-on segments is required.

5-Hour Session Plan (timeline)

0:00–0:30 — Orientation; outcomes; NCBI ecosystem map.
0:30–1:45 — PubMed advanced search (live demos + mini-tasks).
1:55–2:45 — NCBI Gene / ClinVar / dbSNP: targeted retrieval & interpretation.
2:55–3:40 — From gene list to insight: enrichment demo (DAVID/Metascape) + reporting.
3:50–5:00 — Case study (team exercise) + wrap-up; assignment brief.

Materials & Platforms: NCBI (PubMed, Gene, ClinVar, dbSNP; optional GEO); external enrichment tools (DAVID, Metascape). Browser-based; no local installation required.
Academic Integrity & Reproducibility: All submissions must be original and document exact queries, IDs, tool names, and dates/versions to ensure reproducibility.