## Unix a práce s genomickými daty Unix and genomic data

AACGTGTCTGCATAATAGTS TO ASSAA TGCCTTTCGCGGGTACGTTC	CCACTCCTTCCGTGATTGTTTCATATAGAATAGTTTCTGTCCGAAATTCCGAATCACATGCCACACAGAGTCGTCGTTGACGAGGGACTG
TA AGAGATACATTGG GATTACAGAAACTTCGCAGCTCTAC	ACTGACATATACTGCGTCGCTTTATTATTATACCTGATACGTACAGAGTAGCACGTTACTGACATTCCATCTGCCTTACACCTATCCGCTTAC
ACTAG CTCAAGCCATGGC CCTGCAATCGG GC GT AGCACCGC	CAGT AGTACAGGAA GT CT COGGAGGGAGTWIMMACTCGATTAGGCCCCCTCCTCTGCAGTCTTCATGTAACGATATAGTCTACGTGTCATGT
CT CG CT TT CATAGAT GTCCCTGA GG CT AA TC GC A	GTAGCA ATACGTACA AA AT CA CTACA TTTATGA GAGCTAGGTACAGCCCATCGTCTTATGAGGGAGGCACACAAGAGGATTACCGTTCGATCAC
AC CT CG TG AAGCAGATCGCT C CT TA AC GA CA	ATTATTTTCGC GC GG TA GG A MATGTGGACGACGACTGTGACGTTAGCAAGGAATCCGTATACATGACCCGACTAAACATACAGG
GT AC GC TG GC AAGACCAGO A GTO CA AA AC AC	AG TGCCAATT GO AA TC CG AA AG ATTATTACAACTAACCGAGGGAATATGCTCAAGCGGGACGCAGGAGGAACAGCCGCCGGTGGGGTC
AT GG TA TAAAGGTATGG C GC TC CG TA GA	AAGTTCACGCGC C GC GA TC AG TT TTACCTCTGCGG ATGTCTGCAGTCCAGACGTCCCGTCC
TO TO TA GG CATTCGACTGAATCTT CC CC AG AG GG	GTTGCG TGGGAC T AT AG GT TO AT ATTAACG AGAGGAACTAGTAATGCATACTCTCCCCGACCAATGCTGACCCAACCCTAGTCGCACCT
CT TA GACCGGACA ATCGTACGGCT TAGITC TG TATC	CCAATO TGTCCTTTOA GT TG CO ATCGAACGOMMGGTGCGTACGGGTCGAACACTGCAATCCGGGGCTTGAACGATCCTGGAACTCTCTGATT
GGCAATAGCGGGTT CCTATGGCTGGCCTGACTGCAACGG	GGACGGTCAAGTTATCGGATTTGCTC
CCCGCGTCTT	AGTAAGATTCTAAGGGTACT COMMON CONTROL CO

## A new advanced course

Lecturers: Václav Janoušek, Libor

Mořkovský

Date: January 8–10, 2016 (weekend)

Winter semester

Language: English or Czech\* Limited to 24 participants

Recommended for master's degree and

PhD students
SIS: 2 credits,
MB170C47,
link in the OR code:



The recent progress of Next Generation Sequencing (NGS) technologies led to a huge increase in the amount of data that biologists have to deal with. The usual amount of generated data is far beyond the capacity of common data analysis tools on the Microsoft Windows platform. The Unix environment provides efficient tools for handling large amounts of genomic data.

Participants of the course will gain sufficient skills and confidence in the Unix environment to use it for analysis of genomic data. We will explore the possibilities of the system using the examples of NGS data manipulation, analysis and visualization. The focus of the course is not one particular NGS analysis, but to teach the participants how to comfortably use any Unix tool to pursuit their scientific goals.

<sup>\*</sup> If all participants understand Czech, we will teach in Czech