

## INSTRUCTING THE NEXT GENERATION OF BIOLOGISTS AT VBC

Recent advances in biomedical research have led to an unprecedented growth in the size and complexity of experimental datasets. In order to transform these observations into scientific knowledge, increasingly sophisticated data analysis methodologies are required. The VBCF Computational Biology Training unit, led by András Aszódi, provides practical courses in computational data analysis to researchers at all career stages at the Vienna BioCenter and beyond.

### OUR GOALS

The VBCF Computational Biology Training unit, developed by András Aszódi over more than 10 years, is part of the VBC Scientific Training curriculum. The program aims to:

- **Educate participants** in computational methodologies that are highly relevant to biomedical research, with a strong focus on applied statistics.
- **Improve communication** between experimental and computational biologists, enabling experimentalists to gain a better understanding of "what happens to their data" during analysis by computational experts.
- **Empower experimental researchers** to independently analyze their data as much as possible.
- **Support computational biologists** by providing advanced courses covering modern data analysis techniques.

### OUR PORTFOLIO

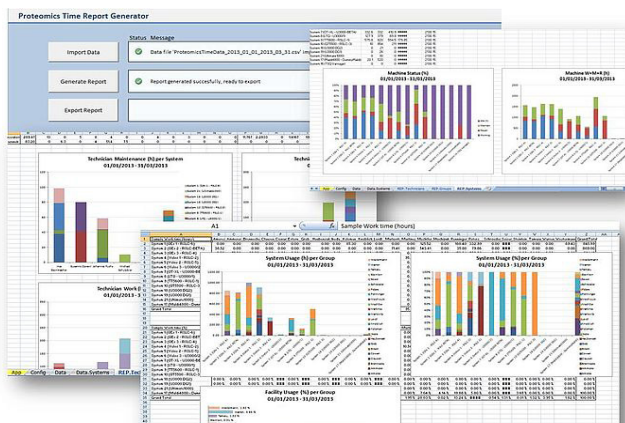
- **Programming skills:** These courses form the basis for computational data analyses by teaching programming languages such as R, Python, regular expressions, and UNIX shell scripting.
- **High Performance Computing:** We offer an introduction to the VBC computing cluster and software container technologies.
- **Data Analysis:** In addition to basic courses in biostatistics, we offer advanced training in machine learning, such as regression techniques and generalized linear methods. These courses are complemented by a course on scientific visualization.

We teach in a small seminar setting (max. 10 students) where the instructor can interact with the students individually. Students can try out their newly acquired knowledge through hands-on exercises. Detailed handouts and sample scripts are provided to help students apply the methods learned to their own research projects.

## OUR IMPACT

We usually hold more than 30 courses per year, with up to 400 participants. While the courses are primarily aimed at researchers at the VBC, we also welcome participants from other institutions in Vienna, such as research institutes of the Austrian Academy of Sciences and various Viennese universities. Our courses are registered in the training portal of the Global Organisation for Bioinformatics Learning, Education and Training [GOBLET] and in the TeSS learning resources of ELIXIR, an European life science infrastructure offering software tools and training material.

## OUR TRAININGS



```
9 import os
10 from config import INPUT_PATH, OUT
11
12 from Bio import SeqIO
13 from Bio.Seq import Seq
14 from Bio.Alphabet import IUPAC
15 from libs.IO.files import read_list
16 import csv
17
18 def find_primer_sequences(fasta_path,
19 # Load genes of interest into a
20 genes = read_list(genes_list_path)
21 # Initialize results
```



## CONTACT

Computational Biology Training  
Vienna BioCenter Core Facilities [VBCF]

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