

# **Abordagens didáticas no ensino de bioinformática**

Professor: Dr. Luiz Marcelo Ribeiro Tomé

**Rio de Janeiro**

**2025**

- ❖ Conceito de Ensino;
- ❖ Conceito de Bioinformática;
- ❖ Evolução do Ensino de Bioinformática;
- ❖ Aula Expositiva em Bioinformática;
- ❖ Aula Prática (Hands-On);
- ❖ Aprendizagem Baseada em Problemas (PBL);
- ❖ Aprendizagem Baseada em Projetos;



## CONCEITO DE ENSINO

**“O ensino, basicamente, é todo o processo de construção do saber através da transferência de conhecimento, sendo este adquirido fora ou dentro da universidade, empírico ou científico.”**

Universidade Federal de Santa Maria (<https://ufsm.br/r-369-2318>)

**“Ensinar não é transferir conhecimento, mas criar as possibilidades para a sua própria produção ou a sua construção.”**

Paulo Freire, *Pedagogia da Autonomia: Saberes necessários à prática educativa* (1996, p. 75).

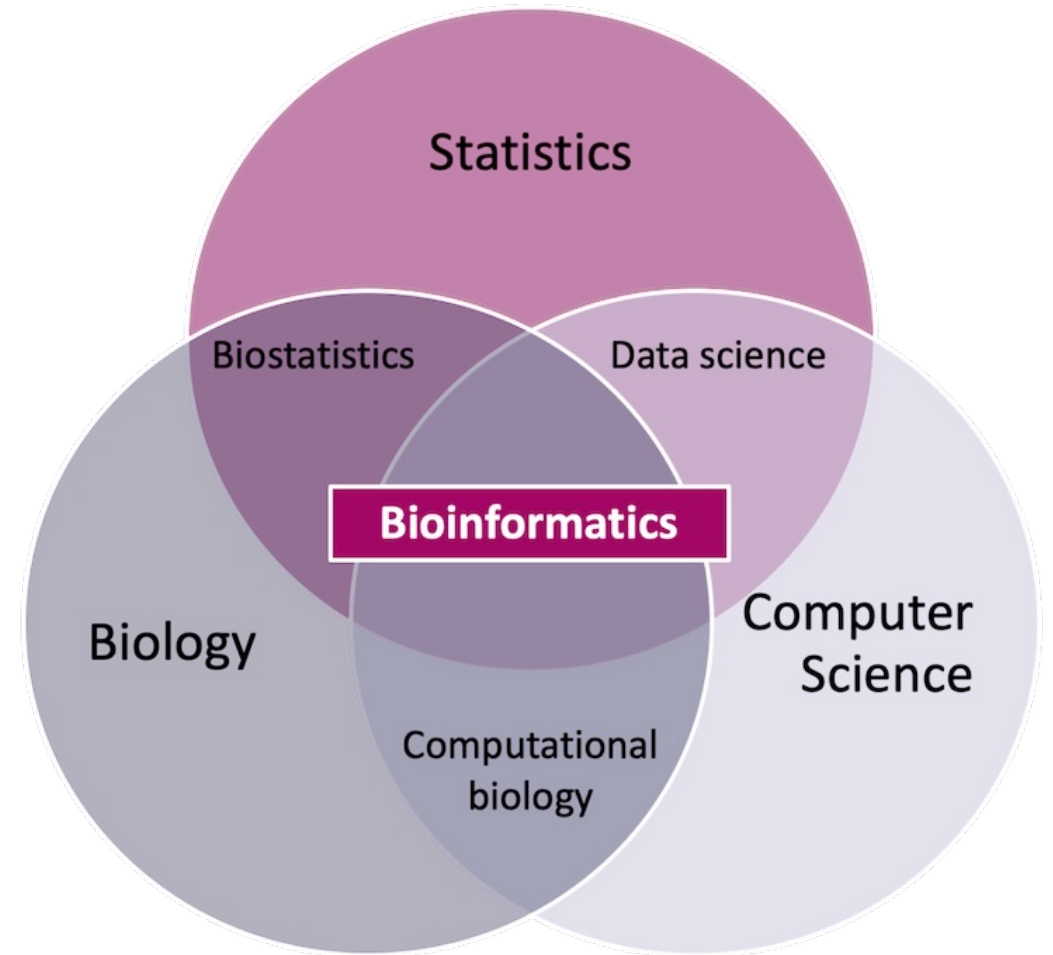
## ABORDAGENS DIDÁTICAS

- **Abordagens didáticas** referem-se aos métodos, estratégias e técnicas utilizadas pelos educadores para facilitar o aprendizado dos alunos.
- ❖ **Abordagem tradicional:** Focada em aulas expositivas e didáticas mais rígidas, com o professor como o centro do processo de ensino;
- ❖ **Abordagem colaborativa:** Valoriza o trabalho em grupo e a troca de experiências entre os alunos;
- ❖ **ABORDAGEM BASEADA EM PROBLEMAS E PROJETOS:** Propõe resolver questões ou desafios reais como forma de aprendizado;



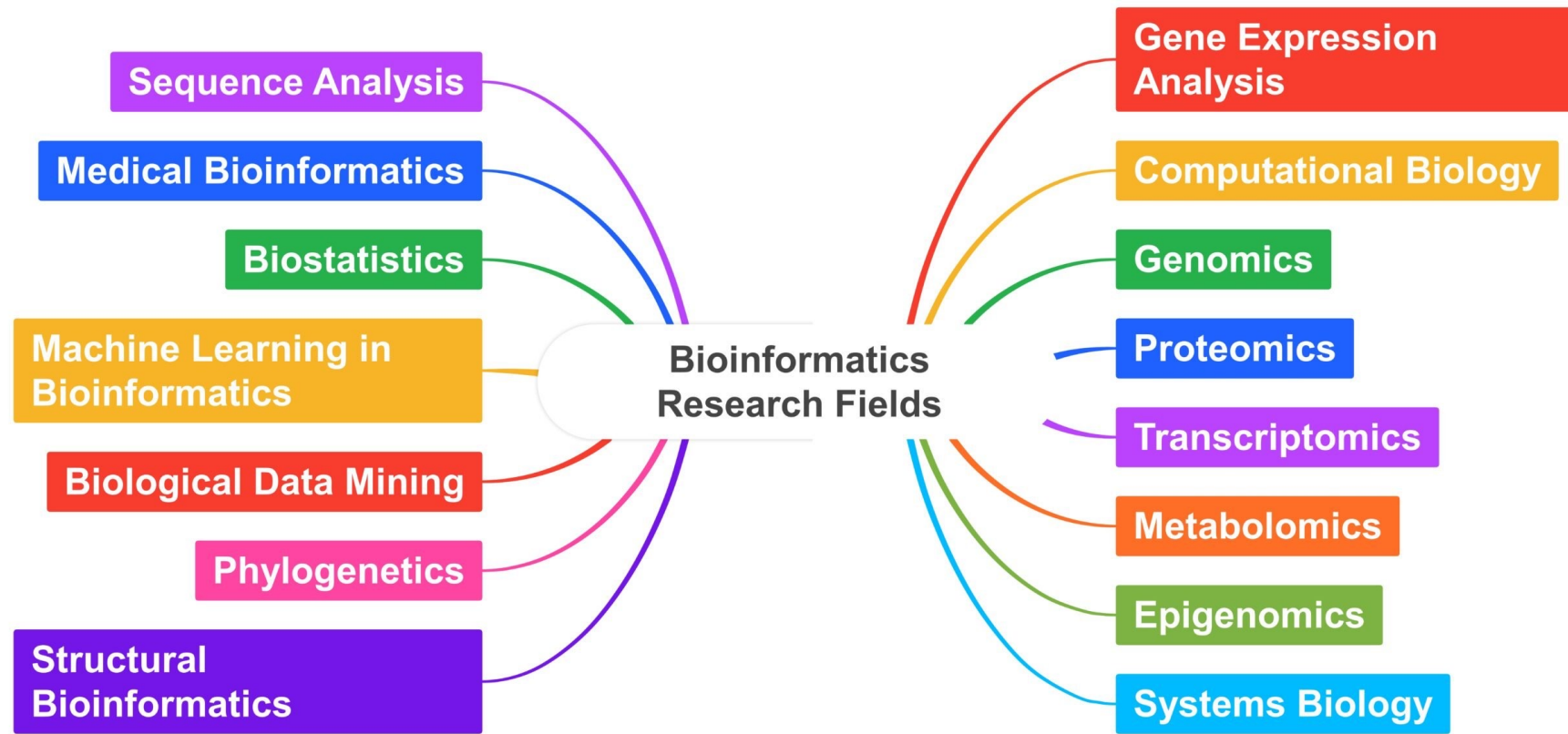
## CONCEITO DE BIOINFORMÁTICA

"A **Bioinformática** é uma **ciência interdisciplinar** que aplica métodos, conceitos e conhecimentos da **estatística, computação, matemática e biologia** para a **análise de dados biológicos.**"



## APLICAÇÕES DA BIOINFORMÁTICA

- Transformar dados brutos em informações significativas.



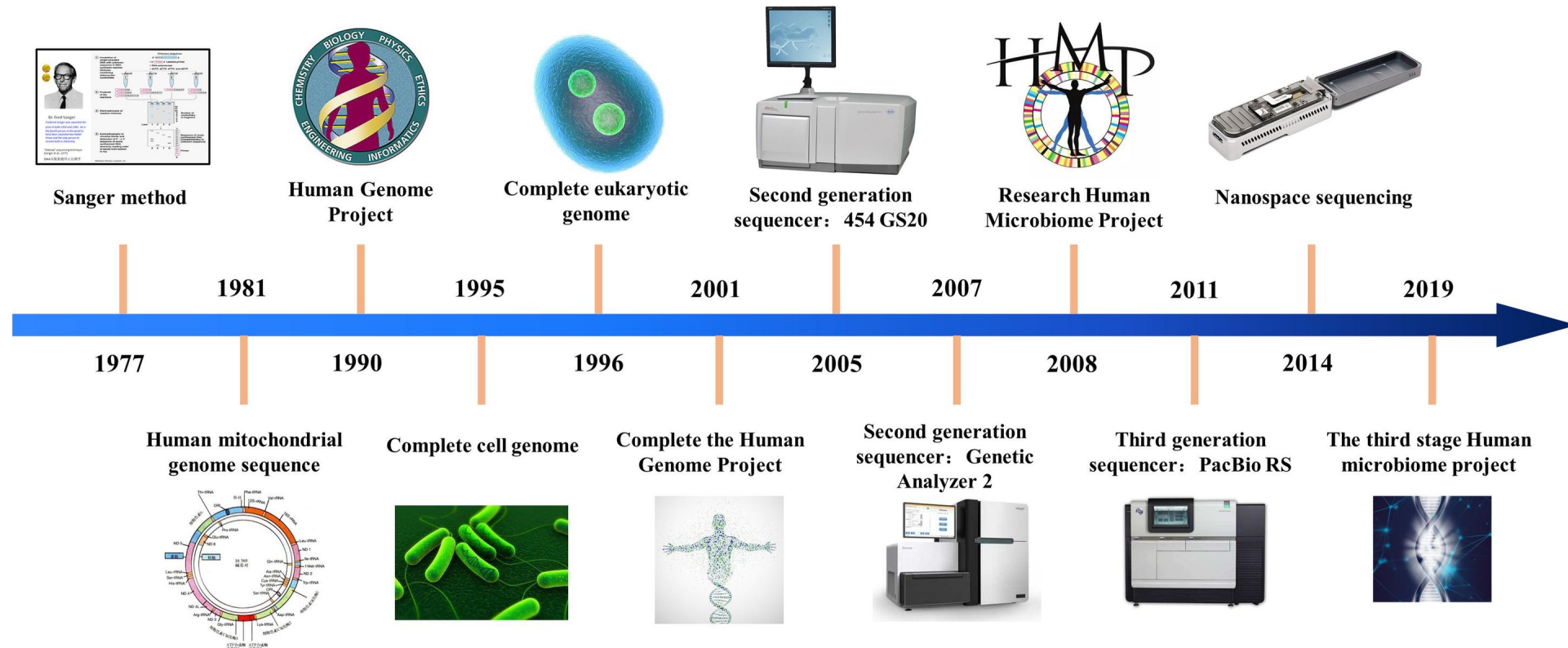
# APLICAÇÕES DA BIOINFORMÁTICA

A **bioinformática** é essencial para a análise e interpretação de grandes volumes de dados biológicos, desempenhando um papel fundamental em diversas áreas da ciência. Sua importância pode ser destacada em:

- **Genômica e Medicina de Precisão;**
- **Descoberta de Novos Fármacos e Desenvolvimento de terapias;**
- **Epidemiologia e Saúde Pública;**
- **Biotecnologia e Agricultura;**
- **Ecologia e Metagenômica;**

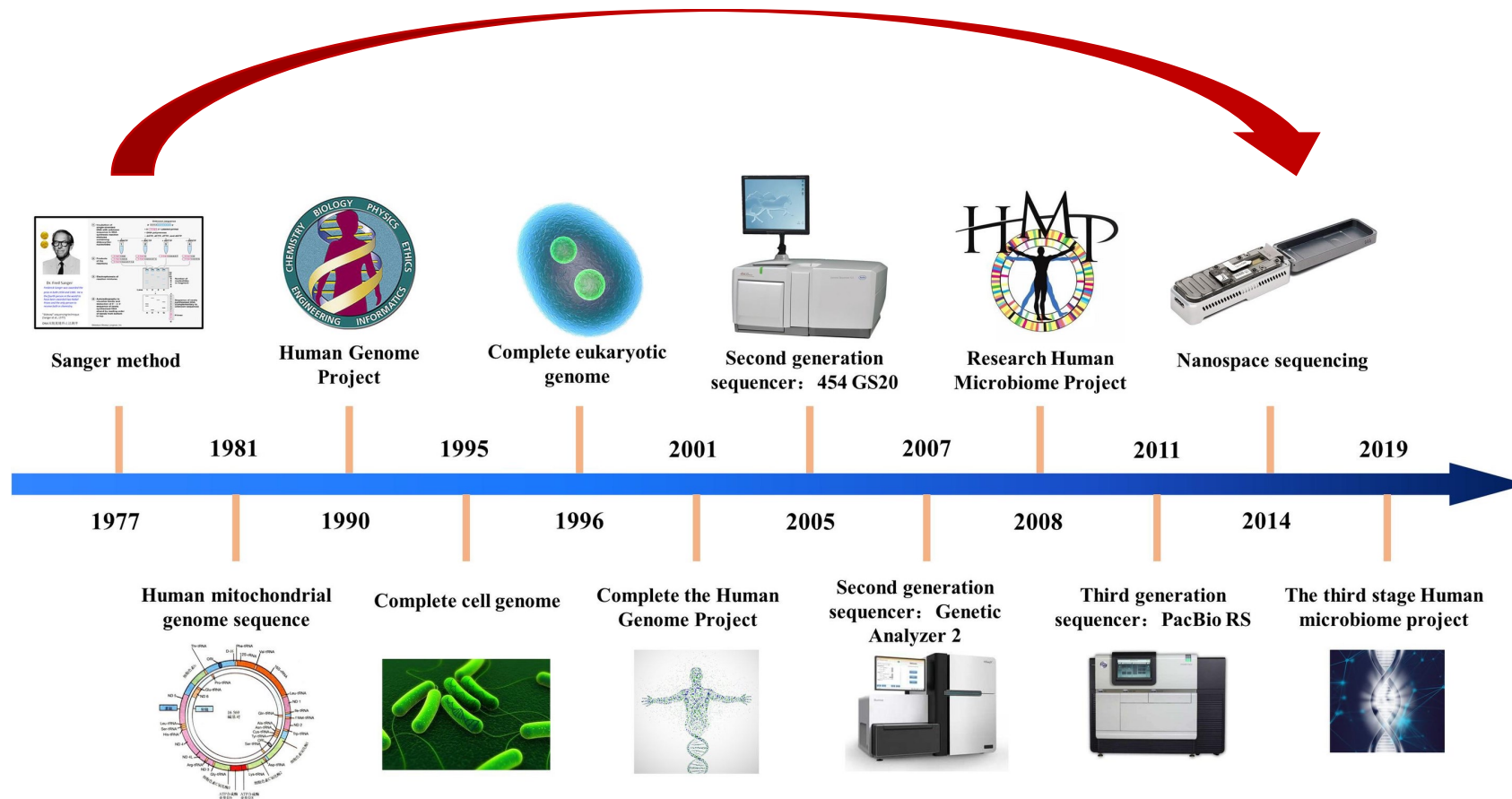
## EVOLUÇÃO DO ENSINO DE BIOINFORMÁTICA

- O avanço das tecnologias de sequenciamento impulsiona a evolução do ensino de bioinformática.



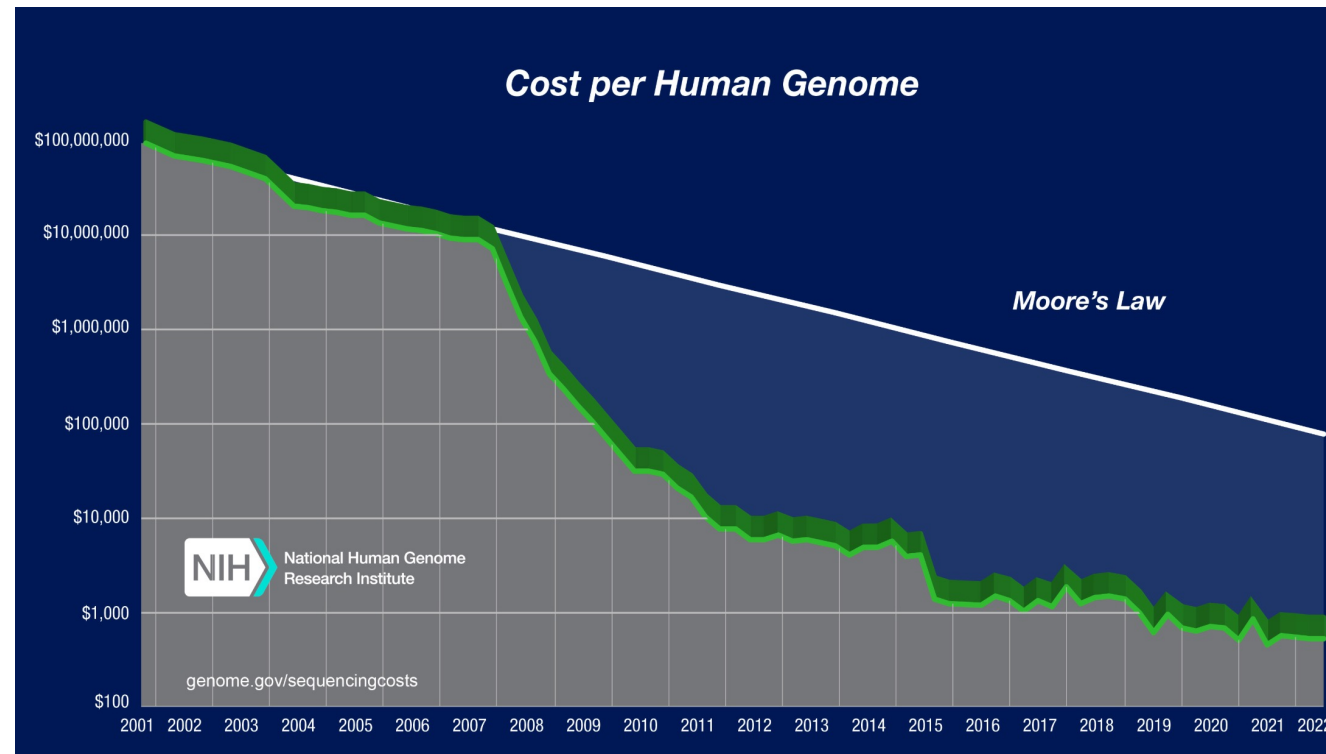
# EVOLUÇÃO DO ENSINO DE BIOINFORMÁTICA

- Aumento da complexidade na análise com o avanço das novas plataformas.



## EVOLUÇÃO DO ENSINO DE BIOINFORMÁTICA

- A redução do custo de sequenciamento e o aumento de dados disponíveis em bancos facilitam o ensino de bioinformática.



<https://www.genome.gov>

## **ETAPAS DO ENSINO DE BIOINFORMÁTICA**

## AULAS EXPOSITIVAS

### **Aulas expositivas são necessárias!**

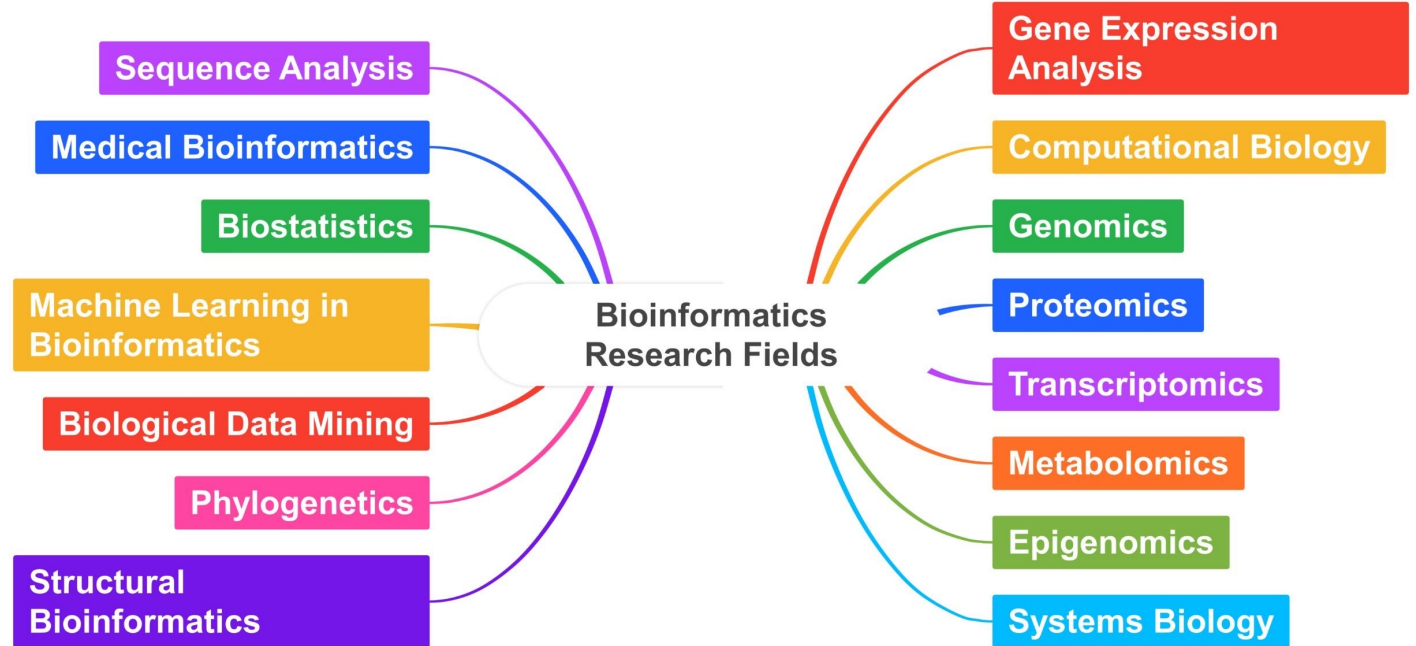
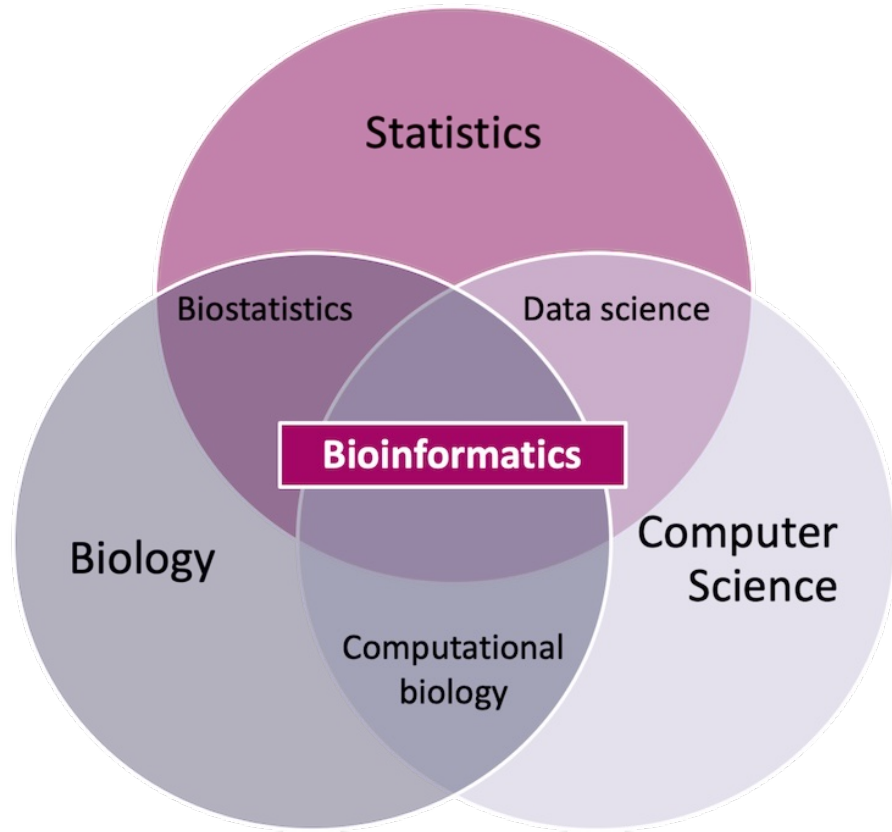
- Atendem estudantes e profissionais com diferentes formações.
- Permitem a apresentação clara de conceitos interdisciplinares.
- Facilitam a integração e a contextualização do conhecimento.
- Não devem ocupar a maior parte da carga horária.





## AULAS EXPOSITIVAS

### ❖ PRINCIPAIS CONCEITOS DA BIOINFORMÁTICA;



## AULA EXPOSITIVA

“No aprendizado, não existem perguntas bobas ou erradas. Toda dúvida é uma oportunidade de explorar novas ideias e construir conhecimento.”

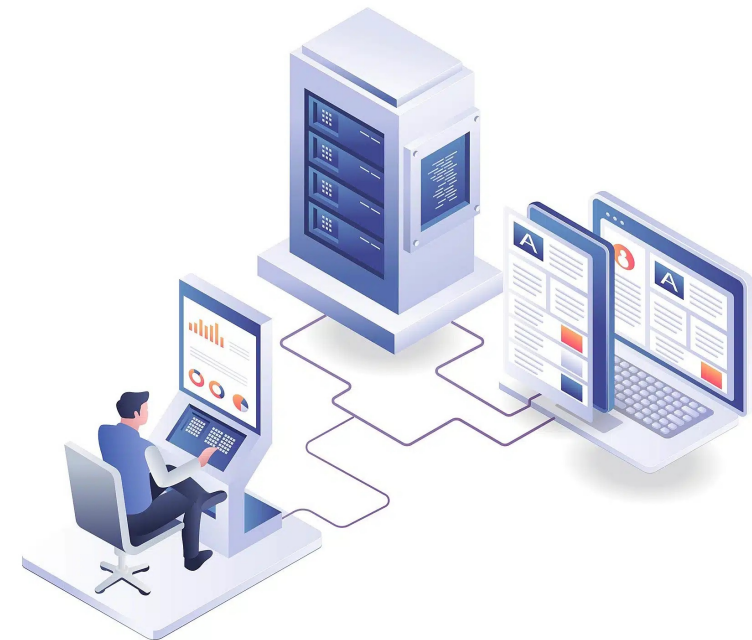
**AULA PRÁTICA (HANDS-ON)**

## PRIMEIRO GRANDE DESAFIO DE ENSINAR BIOINFORMÁTICA

- **Familiarização com o sistema operacional Linux** – Essencial para que os alunos desenvolvam habilidades na execução de ferramentas bioinformáticas.

```
Last login: Wed Jan 29 09:50:30 on console
(base) luizmarceloribeirato@MacBook-Air-de-Luiz ~ % ssh marcelo@150.164.26.10
marcelo@150.164.26.10's password:
=====
----- Welcome to LBMC@UFMG -----
----- Only authorized users can access this system -----
=====
LBMCF - SERVER I
=====
- Operating System....: AlmaLinux 8.10
- Kernel.....: 4.18.0-553.34.1.el8_10.x86_64
- Architecture.....: x86_64
- Hostname.....: j3-053-010
- CPU(s).....: 24
- Disk Space.....: 866G
- Memory used.....: 40269 MB
- Uptime.....: 4 days
=====
Web console: https://j3-053-010.icb.ufmg.br:9090/ or https://150.164.26.10:9090/

Last failed login: Mon Jan 27 12:44:30 -03 2025 from 134.17.16.19 on ssh:notty
There were 5 failed login attempts since the last successful login.
Last login: Sat Dec 28 15:20:29 2024 from 189.40.94.58
(base) [marcelo@j3-053-010 ~]$
```



# PRIMEIRO GRANDE DESAFIO DE ENSINAR BIOINFORMÁTICA

- **Familiarização com o sistema operacional Linux** – Essencial para que os alunos desenvolvam habilidades na execução de ferramentas bioinformáticas.



```
treinaweb@GABRIEL-PC: ~  
treinaweb@GABRIEL-PC:~$ ll /mnt/  
total 0  
drwxr-xr-x 1 root root 4096 Jul  2 21:44 ./  
drwxr-xr-x 1 root root 4096 Jul  2 21:44 ../  
drwxrwxrwx 1 root root 4096 Jun 28 22:30 /  
drwxrwxrwx 1 root root  512 Jul  2 11:25 /  
drwxrwxrwx 1 root root 4096 Jun 28 11:24 /  
drwxrwxrwx 1 root root  512 Jun 28 11:24 /  
treinaweb@GABRIEL-PC:~$
```



### SEGUNDO GRANDE DESAFIO DA BIOINFORMÁTICA

- **Instalação de softwares:** No ensino de bioinformática é uma barreira comum, mas que pode ser superada com estratégias adequadas.

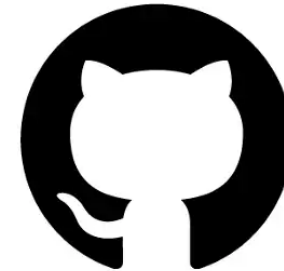


ANACONDA®

MINI CONDA®



git



GitHub



docker

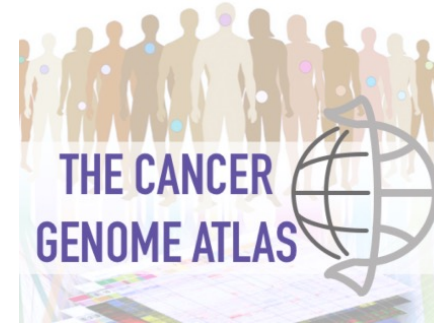
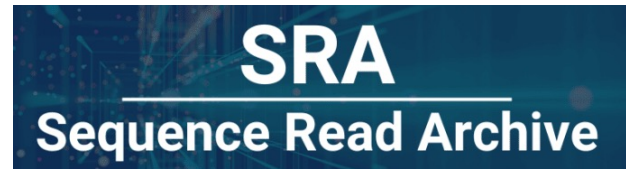
### SEGUNDO GRANDE DESAFIO DA BIOINFORMÁTICA

- **Incentivar a perseverança diante dos erros:** Erros na execução de softwares de bioinformática são comuns e fazem parte do processo de aprendizagem. É importante não desistir ao enfrentar o primeiro obstáculo. Com o tempo, as soluções se tornam mais fáceis de identificar.



### TRABALHAR COM OS DADOS

**Bancos de dados na bioinformática:** Disponibilização de dados biológicos é essencial para o ensino prático, permitindo que os alunos explorem, analisem e apliquem conceitos em cenários reais.

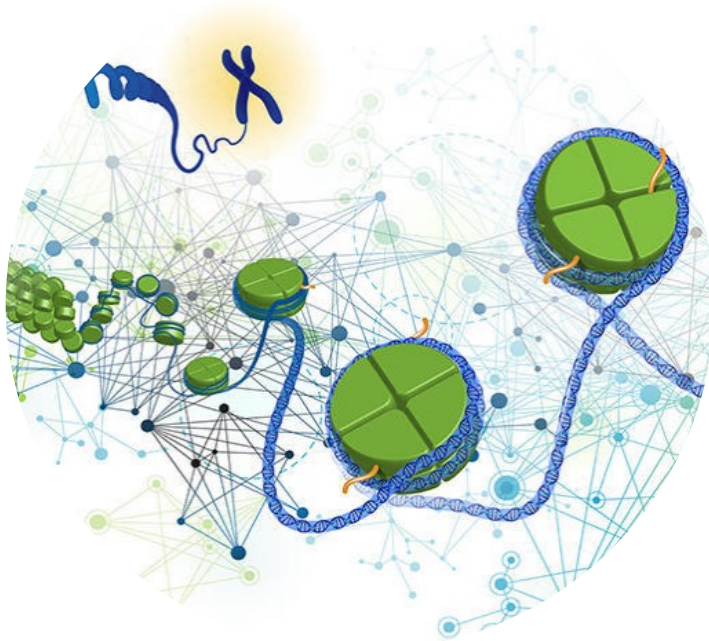




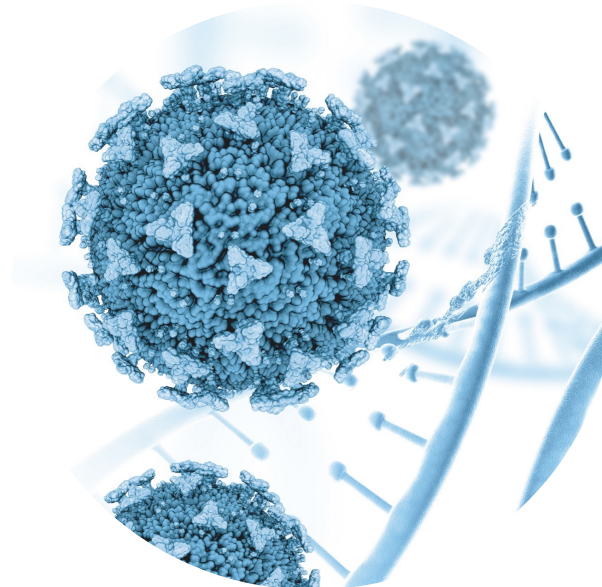
## CONTEXTUALIZAÇÃO DO ENSINO

**Utilizar problemas do mundo real!**

**Doenças Genéticas Humanas**



**Doenças Infecciosas**



**Agricultura**

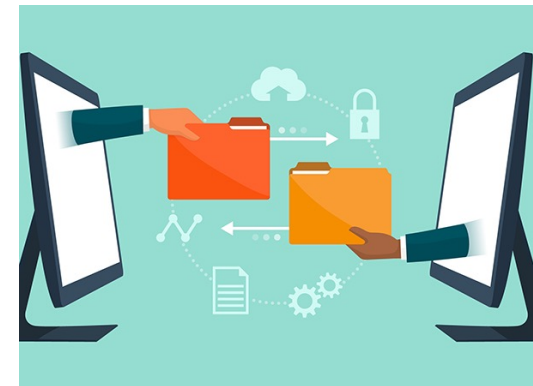


# FLUXO DE ANÁLISES EM BIOINFORMÁTICA

- **Obtenção de dados** – Coletar dados biológicos de bancos de dados públicos, experimentos laboratoriais ou sequenciamentos;
- **Organização dos dados** – Estruturar e armazenar os dados em formatos adequados para análise, garantindo acessibilidade e integridade;
- **Filtragem e limpeza** – Remover erros, duplicatas e dados irrelevantes para melhorar a qualidade da análise;
- **Análise dos dados** – Aplicar algoritmos estatísticos, modelagem computacional e aprendizado de máquina para identificar padrões e relações biológicas;

### FLUXO DE ANÁLISES EM BIOINFORMÁTICA

- **Interpretação e síntese** – Transformar os resultados brutos em informações compreensíveis, integrando diferentes fontes de dados;
- **Visualização de dados** – Criar gráficos, tabelas e representações visuais para facilitar a comunicação dos achados;
- **Armazenamento e compartilhamento** – Salvar os dados e resultados em repositórios públicos ou privados, permitindo acesso e reprodutibilidade.



### PRINCIPAL MENSAGEM SOBRE A AULA PRÁTICA (HANDS-ON)

A prática (hands-on) no ensino de bioinformática é fundamental para que os alunos resolvam problemas reais, como a análise de dados biológicos, aplicando ferramentas e técnicas essenciais.

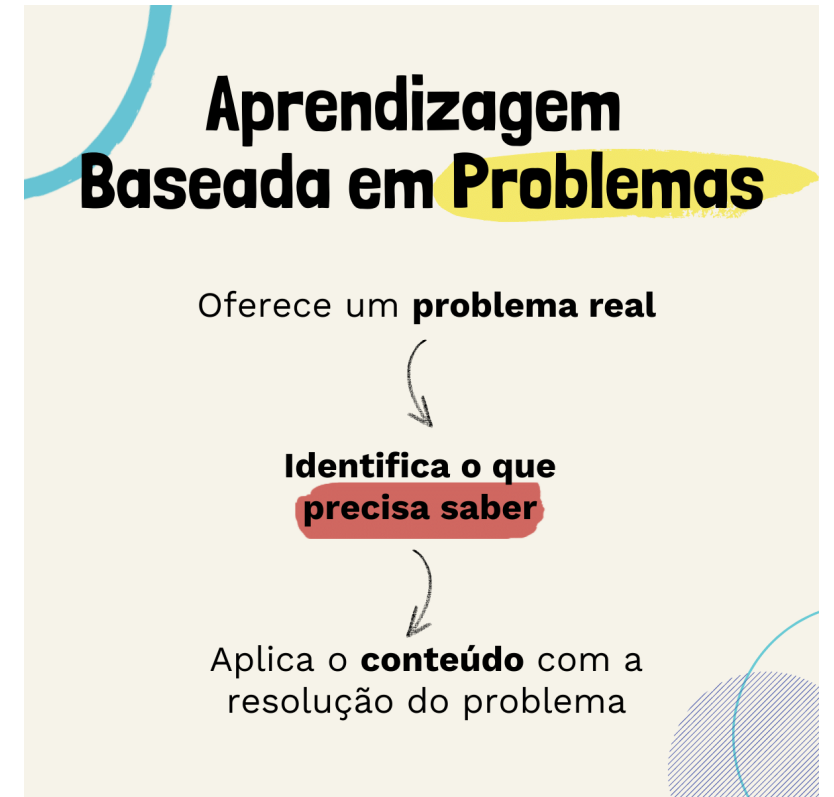
Isso fortalece habilidades técnicas e prepara para desafios profissionais.

### APRENDIZAGEM BASEADA EM PROBLEMAS (PBL);

- **PBL** coloca os estudantes no centro do processo de aprendizagem, incentivando a aplicação prática dos conhecimentos, o que não apenas facilita a compreensão, mas também estimula o interesse e a autonomia.

#### PBL na bioinformática:

Resolução de um caso real de análise de dados, assumindo agora o papel de tomadores de decisão.

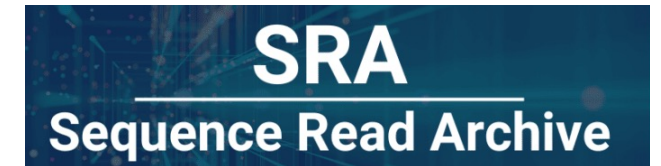


<https://tutormundi.com/>

## EXEMPLOS PRÁTICOS DE APLICAÇÃO DO PBL

### GENÔMICA:

**Problema:** Montagem do genoma de *Escherichia coli*, causadora de gastroenterite, a partir de dados de NGS provenientes de diferentes plataformas de sequenciamento.



**SRX20685116: Whole-genome-Seq of Escherichia coli bacteria**

1 ILLUMINA (Illumina NovaSeq 6000) run: 5.7M spots, 1.7G bases, 520.8Mb downloads

**Design:** Extract the genomic DNA of each individual and randomly break it, recover the required length of DNA fragments by electrophoresis, and add connectors for cluster preparation. Finally, machine sequencing was performed.

**Submitted by:** Xiamen University

**Study:** chromosome sequencing of tolerant mutants

[PRJNA974919](#) • [SRP438877](#) • [All experiments](#) • [All runs](#)  
[show Abstract](#)

**Sample:**

[SAMN35740992](#) • SRS17979155 • [All experiments](#) • [All runs](#)  
**Organism:** [Escherichia coli K-12](#)

**Library:**

**Name:** LYS3  
**Instrument:** Illumina NovaSeq 6000  
**Strategy:** WGS  
**Source:** GENOMIC  
**Selection:** size fractionation  
**Layout:** PAIRED

**Runs:** 1 run, 5.7M spots, 1.7G bases, [520.8Mb](#)

Run	# of Spots	# of Bases	Size	Published
<a href="#">SRR24925946</a>	5,650,389	1.7G	520.8Mb	2023-06-15

ID: 28114788

**SRX21874976: WGS of Enterobacterales: ONT RBKv14 validation**

1 OXFORD\_NANOPORE (MinION) run: 150,691 spots, 1.2G bases, 1Gb downloads

**Design:** Isolate genomic DNA was extracted and Oxford Nanopore MinION was used to generate single-end reads using the Rapid Barcoding Kit v14. Reads were filtered for Q-scores above 8 and lengths above 1000 bases.

**Submitted by:** Public Health Agency of Canada

**Study:** Evaluating Oxford Nanopore Technologies R10.4.1 flow cells and v14 library prep kits for Gram negative bacteria

[PRJNA1020811](#) • [SRP463007](#) • [All experiments](#) • [All runs](#)  
[show Abstract](#)

**Sample:**

[SAMN37529175](#) • SRS18966410 • [All experiments](#) • [All runs](#)  
**Organism:** [Escherichia coli](#)

**Library:**

**Name:** isolateD\_nanopore  
**Instrument:** MinION  
**Strategy:** WGS  
**Source:** GENOMIC  
**Selection:** RANDOM  
**Layout:** SINGLE

**Runs:** 1 run, 150,691 spots, 1.2G bases, [1Gb](#)

Run	# of Spots	# of Bases	Size	Published
<a href="#">SRR26162843</a>	150,691	1.2G	1Gb	2023-09-25

ID: 29767696

EXEMPLOS PRÁTICOS DE APLICAÇÃO DO PBL

GENÔMICA:



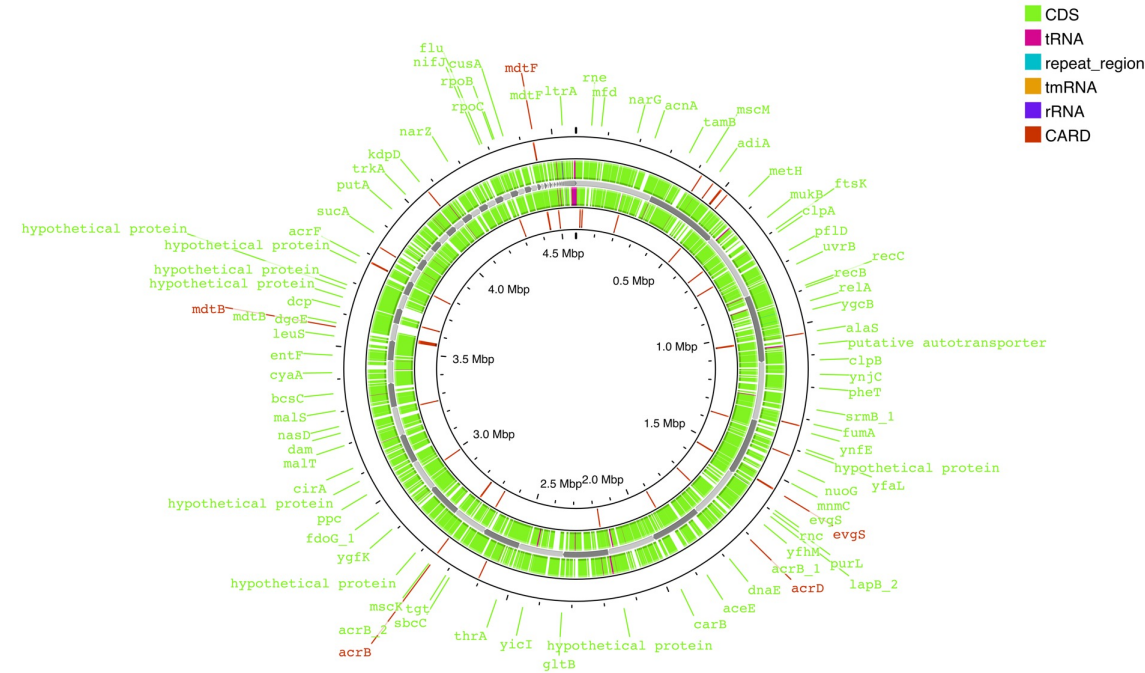
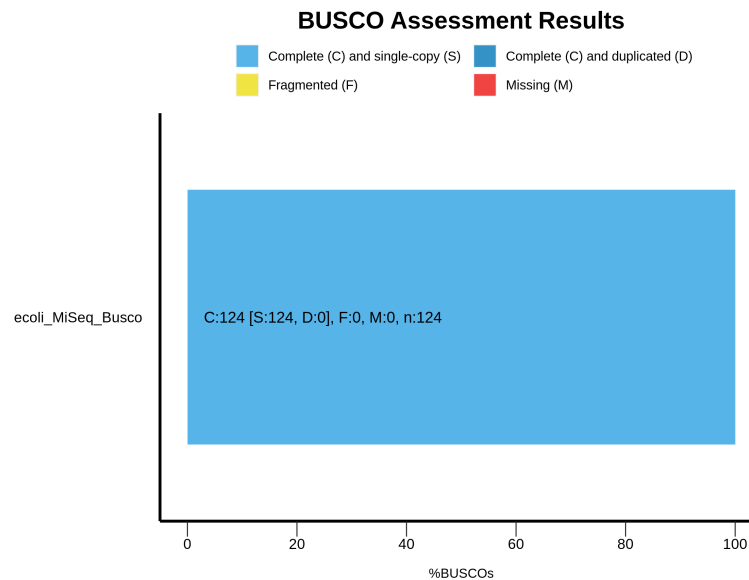


## EXEMPLOS PRÁTICOS DE APLICAÇÃO DO PBL

### GENÔMICA:

#### Report

	scaffolds
# contigs (>= 0 bp)	166
# contigs (>= 1000 bp)	68
# contigs (>= 5000 bp)	50
# contigs (>= 10000 bp)	44
# contigs (>= 25000 bp)	40
# contigs (>= 50000 bp)	25
Total length (>= 0 bp)	4574402
Total length (>= 1000 bp)	4547365
Total length (>= 5000 bp)	4506488
Total length (>= 10000 bp)	4461335
Total length (>= 25000 bp)	4398941
Total length (>= 50000 bp)	3842123
# contigs	82
Largest contig	299213
Total length	4556870
GC (%)	50.74
N50	178300
N75	88271
L50	10
L75	19
# N's per 100 kbp	32.92



All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).



## EXEMPLOS PRÁTICOS DE APLICAÇÃO DO PBL



### GENÔMICA:

**Problema:** Montagem do genoma de *Candida auris*, agente causador de doenças fúngicas invasivas, a partir de dados de NGS gerados por diferentes plataformas de sequenciamento.

SRA   [Create alert](#) [Advanced](#) [Help](#)

Full ▾ Send to: ▾

**SRX17010148: Cau\_B11220\_illumina**  
1 ILLUMINA (Illumina iSeq 100) run: 589,521 spots, 169.4M bases, 57.5Mb downloads

**Design:** Genomic DNA isolated using a modified version of Promega's Wizard Genomic DNA Purification Kit. Library created using Illumina's Nextera DNA Flex Library Prep Kit.

**Submitted by:** Worcester Polytechnic Institute

**Study:** *Candida auris* hybrid genome sequencing and assembly  
[PRJNA865346](#) • [SRP390732](#) • [All experiments](#) • [All runs](#)  
[show Abstract](#)

**Sample:** Pathogen: clinical or host-associated sample from [*Candida*] *auris*  
[SAMN30106616](#) • [SRS14595296](#) • [All experiments](#) • [All runs](#)  
**Organism:** [*Candida*] *auris*

**Library:**  
**Name:** cau1\_illumina  
**Instrument:** Illumina iSeq 100  
**Strategy:** WGS  
**Source:** GENOMIC  
**Selection:** RANDOM  
**Layout:** PAIRED

**Runs:** 1 run, 589,521 spots, 169.4M bases, [57.5Mb](#)

Run	# of Spots	# of Bases	Size	Published
<a href="#">SRR20993211</a>	589,521	169.4M	57.5Mb	2023-09-01

ID: 23789817  
<https://www.ncbi.nlm.nih.gov/sra>

**Related information**

BioProject

BioSample

Taxonomy

WGS

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**Search details**

SRR20993211[All Fields]

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[SRR20993211 \(1\)](#) SRA

[SRR20993210 \(1\)](#) SRA

[Haemophilus parainfluenzae strain EL1 chromosome, complete genome](#) Nucleotide

SRA   [Create alert](#) [Advanced](#) [Help](#)

Full ▾ Send to: ▾

**SRX17010149: Cau\_B11220\_nanopore**  
1 OXFORD\_NANOPORE (MinION) run: 24,080 spots, 298.4M bases, 257.4Mb downloads

**Design:** Genomic DNA isolated using a modified version of Promega's Wizard Genomic DNA Purification Kit. Library created using ONT's Rapid Barcoding Kit.

**Submitted by:** Worcester Polytechnic Institute

**Study:** *Candida auris* hybrid genome sequencing and assembly  
[PRJNA865346](#) • [SRP390732](#) • [All experiments](#) • [All runs](#)  
[show Abstract](#)

**Sample:** Pathogen: clinical or host-associated sample from [*Candida*] *auris*  
[SAMN30106616](#) • [SRS14595296](#) • [All experiments](#) • [All runs](#)  
**Organism:** [*Candida*] *auris*

**Library:**  
**Name:** cau1\_nanopore  
**Instrument:** MinION  
**Strategy:** WGS  
**Source:** GENOMIC  
**Selection:** RANDOM  
**Layout:** SINGLE

**Runs:** 1 run, 24,080 spots, 298.4M bases, [257.4Mb](#)

Run	# of Spots	# of Bases	Size	Published
<a href="#">SRR20993210</a>	24,080	298.4M	257.4Mb	2023-09-01

ID: 23789818

**Related information**

BioProject

BioSample

Taxonomy

WGS

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**Search details**

SRR20993210[All Fields]

[See more...](#)

---

**Recent activity**

[SRR20993210 \(1\)](#) SRA

[Haemophilus parainfluenzae strain EL1 chromosome, complete genome](#) Nucleotide

[Roseomonas mucosa strain AD1 chromosome, complete genome](#) Nucleotide

EXEMPLOS PRÁTICOS DE APLICAÇÃO DO PBL

GENÔMICA:



chopper



*BUSCO*

**Funannotate**



## EXEMPLOS PRÁTICOS DE APLICAÇÃO DO PBL

### GENÔMICA:

**Problema:** Montagem de genomas virais com potencial epidêmico e/ou pandêmico a partir de dados de NGS gerados por diferentes plataformas de sequenciamento.

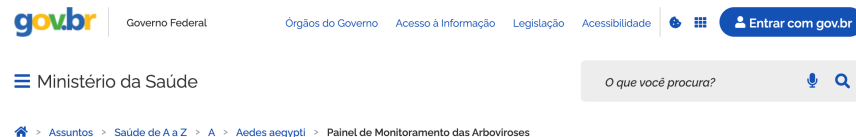


Início / Notícias / OMS afirma que COVID-19 é agora caracterizada como pandemia

### OMS afirma que COVID-19 é agora caracterizada como pandemia



11 Mar 2020



### Atualização de Casos de Arboviroses

Limpar Filtros

Casos prováveis

6.618.658

Óbitos em investigação

646

Óbitos por Dengue

6.161

Coefficiente de incidência

3113,4

Letalidade em casos prováveis

0,09

Letalidade em casos graves

5,84



Início / Alerta Epidemiológico - Mpox (MPXV clado I) - 8 de agosto de 2024

### Alerta Epidemiológico - Mpox (MPXV clado I) - 8 de agosto de 2024



DOWNLOAD

Em vista da circulação da variante do clado I do vírus da mpox (MPXV) na Região Africana, que está associada na Região Africana à transmissão sustentada e à ocorrência de casos em uma faixa etária mais ampla, incluindo crianças, a Organização Pan-Americana da Saúde/Organização Mundial da Saúde (OPAS/OMS) incentiva os Estados Membros a permanecerem vigilantes quanto à possibilidade de introdução dessa variante nas Américas e a continuarem seus esforços de vigilância, incluindo o sequenciamento genômico dos casos detectados, com ênfase especial nos grupos de maior risco.

EXEMPLOS PRÁTICOS DE APLICAÇÃO DO PBL

GENÔMICA:



Samtools

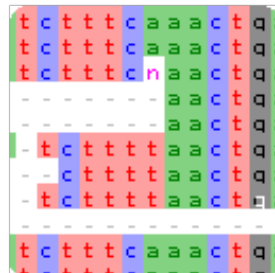
bcftools

VCFTools

iVar



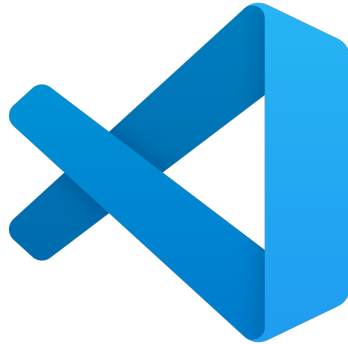
MAFFT



Nextclade

## EXEMPLOS PRÁTICOS DE APLICAÇÃO DO PBL

### GENÔMICA: Automação de tarefas



```
~/code/bash/helloworld.sh - Sublime Text (UNREGISTERED)
File Edit Selection Find View Goto Tools Project Preferences Help
helloworld.sh x
1 #!/bin/bash
2
3 message="Hello World!"
4 # this is a comment
5 echo $message
6
7 exit $?
8 |
```

```
146 echo
147 echo
148 fastqc "$R1" "$R2" -t "$threads"
149 echo
150 echo "-----"
151 echo "Trimagem das sequências (Trimmomatic)"
152 echo "-----"
153 echo
154 echo
155 trimmomatic PE -threads $threads -phred33 $R1 $R2 trim.$R1 trim_unpaired.$R1 trim.$R2 trim_unpaired.$R2 ILLUMINACLIP:$adaptador:2:3
156 echo
157 echo
158 echo "-----"
159 echo "Controle de qualidade das sequências após a trimagem (FastQC)"
160 echo "-----"
161 echo
162 echo
163 fastqc "trim.$R1" "trim.$R2" -t "$threads"
164 echo
165 echo
166 echo "-----"
167 echo "Mapeamento das reads na referência (minimap2)"
168 echo "-----"
169 echo
170 echo
171 minimap2 -ax sr "$referencia" "trim.$R1" "trim.$R2" > "$name.sam"
172
173 elif [ "$tech" == "iontorrent" ]; then
174 fq=$(ls *.fastq.gz | head -1)
175 name=$(echo "$fq" | sed -E 's/^\.*_(.*)\.fastq\.gz$/\1/')
176 echo
```

## EXEMPLOS PRÁTICOS DE APLICAÇÃO DO PBL

### TRANSCRIPTÔMICA:

**Problema:** Identificação de genes diferencialmente expressos no câncer de mama triplo negativo por meio da análise de dados de RNA-seq.



Series GSE264108		<a href="#">Query DataSets for GSE264108</a>
Status	Public on Jan 25, 2025	
Title	Triple-Negative Breast Cancer Shapes the Systemic Immune Landscape and Alters Neutrophil Functionality [bulkRNA-seq]	
Organism	<a href="#">Homo sapiens</a>	
Experiment type	Expression profiling by high throughput sequencing	
Summary	<p>Cancer dysregulates intratumoral innate-adaptive immune cell crosstalk, but it remains largely unknown how the systemic immune landscape is modified during breast cancer progression. Here, we comprehensively profiled the circulating immune profile of patients with stage I-III or stage IV triple-negative breast cancer (TNBC) and healthy donors (HDs). We showed that patients with metastatic TNBC (mTNBC) exhibited decreased numbers of circulating T cells, dendritic cell subsets and differentiated B cells compared to patients with stage I-III TNBC and HDs, which was partially associated with prior chemotherapy. Moreover, increased IL17 production by <math>\nu\delta 1</math> <math>\gamma\delta</math> T cells was observed in patients with mTNBC compared to HDs. Classical monocytes and neutrophils were increased in patients with mTNBC compared to HDs, irrespective of prior chemotherapy. Transcriptional and proteomic analysis, alongside ex vivo functionality assays, revealed increased migratory capacity, increased abundance of granule proteins, and elevated ROS production in circulating neutrophils from mTNBC patients. Some of these systemic immune alterations, including decreased levels of non-switched B cells and increased migratory capacity of neutrophils, were already evident in patients with stage I-III TNBC. Our data underscore the significant impact of TNBC disease stage on the systemic immune composition and function.</p>	
Overall design	Freshly isolated neutrophils from patients with mTNBC and age and BMI matched HDs were used for bulk RNA seq experiments.	
Contributor(s)	<a href="#">Bakker NA</a> , <a href="#">Garner H</a> , <a href="#">van Dyk E</a> , <a href="#">Champanhet E</a> , <a href="#">Klaver C</a> , <a href="#">Duijst M</a> , <a href="#">Voorwerk L</a> , <a href="#">Nederlof I</a> , <a href="#">Voorthuis R</a> , <a href="#">Liefwaard MC</a> , <a href="#">Nieuwland M</a> , <a href="#">de Rink I</a> , <a href="#">Bleijerveld O</a> , <a href="#">Oosterkamp HM</a> , <a href="#">Wessels LF</a> , <a href="#">Kok M</a> , <a href="#">de Visser KE</a>	
Citation(s)	Bakker NAM, Garner H, van Dyk E, Champanhet E et al. Triple-negative breast cancer modifies the systemic immune landscape and alters neutrophil functionality. <i>NPJ Breast Cancer</i> 2025 Jan 23;11(1):5. PMID: <a href="#">39843922</a>	

## EXEMPLOS PRÁTICOS DE APLICAÇÃO DO PBL

### TRANSCRIPTÔMICA:

npj | breast cancer

Article

Published in partnership with the Breast Cancer Research Foundation



<https://doi.org/10.1038/s41523-025-00721-2>

# Triple-negative breast cancer modifies the systemic immune landscape and alters neutrophil functionality

Check for updates

Noor A. M. Bakker <sup>1,2,3</sup>, Hannah Garner <sup>1,2,11</sup>, Ewald van Dyk <sup>1,2,4,11</sup>, Elisa Champanhet <sup>1</sup>, Chris Klaver <sup>1</sup>, Maxime Duijst <sup>1</sup>, Leonie Voorwerk <sup>1,10</sup>, Iris Nederlof <sup>1</sup>, Rosie Voorthuis <sup>5</sup>, Marte C. Liefwaard <sup>5</sup>, Marja Nieuwland <sup>6</sup>, Iris de Rink <sup>6</sup>, Onno B. Bleijerveld <sup>7</sup>, Hendrika M. Oosterkamp <sup>8</sup>, Lodewyk F. A. Wessels <sup>2,4</sup>, Marleen Kok <sup>1,9,12</sup> & Karin E. de Visser <sup>1,2,3,12</sup>



# EXEMPLOS PRÁTICOS DE APLICAÇÃO DO PBL

## TRANSCRIPTÔMICA:

Novos achados impulsionam análises e estimulam o desenvolvimento de habilidades.



### MALAT1 (ENSG00000251562)

<b>Symbol</b>	MALAT1
<b>Name</b>	metastasis associated lung adenocarcinoma transcript 1
<b>Synonyms</b>	HCN LINC00047 MALAT-1 mascRNA NCRNA00047 NEAT2 PRO1073
<b>Type</b>	lncRNA
<b>Location</b>	chr11:65497688-65506516 (GRCh38)
<b>Strand</b>	+
<b>Description</b>	This gene produces a precursor transcript from which a long non-coding RNA is derived by RNase P cleavage of a tRNA-like small ncRNA (known as mascRNA) from its 3' end. The resultant mature transcript lacks a canonical poly(A) tail but is instead sta... <span style="float: right;">▼ more</span>
<b>Annotation</b>	<a href="#">Cancer Gene Census</a>

The screenshot displays an R script in RStudio. The code performs the following steps:

- Identifies the top 20 genes (PADI) based on p-values.
- Creates a matrix of counts for the top 20 genes across different conditions.
- Normalizes the data using `as.data.frame(colData(rld)[c("condition")])`.
- Generates a heatmap for the gene `ENSG00000251562` (MALAT1) across conditions CA (Cyan) and HT (Red).
- The heatmap shows a clear difference in expression levels between the two conditions, with HT showing higher expression.



# EXEMPLOS PRÁTICOS DE APLICAÇÃO DO PBL

## TRANSCRIPTÔMICA:

Biochemistry and Biophysics Reports 37 (2024) 101592



ELSEVIER

Contents lists available at [ScienceDirect](https://www.sciencedirect.com)

Biochemistry and Biophysics Reports

journal homepage: [www.elsevier.com/locate/bbrep](https://www.elsevier.com/locate/bbrep)



### Downregulation of *MALAT1* in triple-negative breast cancer cells

Dagmara Kłopotowska, Janusz Matuszyk\*

*Hirsfeld Institute of Immunology and Experimental Therapy, Polish Academy of Sciences, Rudolfa Weigla 12, 53-114, Wrocław, Poland*

#### ARTICLE INFO

**Keywords:**

Breast cancer cell lines  
Non-coding RNA  
lncRNA  
Real-time PCR  
Reference gene

#### ABSTRACT

**Background:** *MALAT1* is one of the most abundant nuclear long non-coding RNAs, which has been found to be elevated in various types of cancers. However, conflicting reports on *MALAT1* in breast cancer cell lines challenge understanding of *MALAT1*'s involvement in breast cancer progression.

**Aim:** Measurement of normalized relative quantity (NRQ) of *MALAT1* transcripts in cell lines representing triple-negative breast cancer (TNBC) and luminal breast cancer.

**Materials and methods:** The studies were performed using cell lines representing luminal breast cancer (T47D, MCF-7), TNBC (MDA-MB-468, CAL-51, MDA-MB-231), and MCF-10A cell line of normal breast epithelial cells. Total RNA was isolated from six independent cell cultures of each line, treated with DNase I, and used to synthesize complementary DNA, which was used in quantitative real-time PCR (qPCR) assays. Four *MALAT1* fragments and reference genes *CCSER2*, *ANKRD17*, *PUM1*, *GAPDH* were amplified.

**Results:** Geometric means of the NRQ of *MALAT1* in breast cancer cell lines had the shortest 95% confidence intervals when *CCSER2* was used for normalization. *MALAT1* major transcript levels thus estimated in TNBC cell lines were found to be statistically significantly reduced compared to levels in both MCF-10A cells and luminal breast cancer cell lines, while *MALAT1* minority splice variants were found to be increased in almost all breast cancer cell lines.

**Conclusion:** *CCSER2*-normalized qPCR results indicate *MALAT1* downregulation in cell lines representing the more aggressive breast cancer subtype compared to both the normal breast epithelial cell line and the estrogen receptor-positive breast cancer cell lines.

## EXEMPLOS PRÁTICOS DE APLICAÇÃO DO PBL

### TRANSCRIPTÔMICA:



```
library(DESeq2)  
library(ggplot2)  
library(pheatmap)  
library(gplots)  
library(ggrepl)  
library(EnhancedVolcano)  
library(dplyr)
```

## EXEMPLOS PRÁTICOS DE APLICAÇÃO DO PBL

### TRANSCRIPTÔMICA:

**Problema:** Analisar, por meio de dados de RNA-seq, a resposta de *Escherichia coli* ao crescimento em concentrações subinibitórias de nove classes de antibióticos, no contexto da resistência aos antimicrobianos.

Advertisement End



RESEARCH ARTICLE  
March/April 2023 Volume 11 Issue 2 e00317-23  
<https://doi.org/10.1128/spectrum.00317-23>

### Comparative Analysis of Transcriptomic Response of *Escherichia coli* K-12 MG1655 to Nine Representative Classes of Antibiotics

Luyao Bie<sup>a,b</sup>, Mengge Zhang<sup>a</sup>, Juan Wang<sup>a,c</sup>, Meng Fang<sup>a</sup>, Ling Li<sup>a</sup>, Hai Xu <sup>a</sup>, Mingyu Wang <sup>a</sup>

<sup>a</sup>State Key Laboratory of Microbial Technology, Microbial Technology Research Institute, Shandong University, Qingdao, China

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<sup>c</sup>No.3 Middle School of Huimin, Binzhou, China

## EXEMPLOS PRÁTICOS DE APLICAÇÃO DO PBL



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<input checked="" type="checkbox"/>	Run	BioSample	Bases	Bytes	Experiment	Library Name	create_date	Sample Name	treatment	
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Scope: Self | Format: HTML | Amount: Quick | GEO accession: GSE220559

**Series GSE220559** [Query DataSets for GSE220559](#)

Status: Public on Jan 24, 2023

Title: Comparative transcriptomic response analysis of Escherichia coli K-12 MG1655 to nine antibiotics

Organism: [Escherichia coli](#)

Experiment type: Expression profiling by high throughput sequencing

Summary: To investigate and compare transcriptomic changes of Escherichia coli K-12 MG1655, the bacterium was exposed to nine antibiotics (tetracycline, mitomycin C, imipenem, ceftazidime, kanamycin, ciprofloxacin, polymyxin E, erythromycin, and chloramphenicol), and RNA-Seq was performed to determine comparative transcriptomic changes.

Overall design: Escherichia coli K-12 MG1655 was grown in MHB medium supplemented with antibiotics at concentrations that inhibit 50% growth (tetracycline 1.8 mg/L, mitomycin C 1.4 mg/L, imipenem 0.06 mg/L, ceftazidime 0.12 mg/L, kanamycin 1.6 mg/L, ciprofloxacin 0.012 mg/L, polymyxin E 0.4 mg/L, chloramphenicol 1.1 mg/L, erythromycin 7 mg/L). Cells were grown to mid-log phase, harvested, and subject to RNA-Seq analysis. Controls were performed (ethanol for erythromycin and chloramphenicol as they are dissolved in ethanol, and water for every other antibiotic). Triplicates were performed.

Contributor(s): [Bie L](#), [Zhang M](#), [Wang J](#), [Fang M](#), [Li L](#), [Xu H](#), [Wang M](#)

Citation(s): Bie L, Zhang M, Wang J, Fang M et al. Comparative Analysis of Transcriptomic Response of Escherichia coli K-12 MG1655 to Nine Representative Classes of Antibiotics. *Microbiol Spectr* 2023 Feb 28;:e0031723. PMID: [36853057](#)

Submission date: Dec 08, 2022

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Country: China

EXEMPLOS PRÁTICOS DE APLICAÇÃO DO PBL

TRANSCRIPTÔMICA:



Samtools

HTSeq



kallisto

3D RNA-seq App  
day RNA-seq analysis





## EXEMPLOS PRÁTICOS DE APLICAÇÃO DO PBL

### METAGENÔMICA:

**Problema:** Realizar análises de bioinformática de dados de sequenciamento de metagenômica ambiental no contexto da Saúde Única.

Chemosphere 258 (2020) 127271

Contents lists available at ScienceDirect

**Chemosphere**

journal homepage: [www.elsevier.com/locate/chemosphere](http://www.elsevier.com/locate/chemosphere)

### Temporal distribution of microbial community in an industrial wastewater treatment system following crash and during recovery periods

Hana Barak<sup>a</sup>, Asher Brenner<sup>a</sup>, Alex Sivan<sup>b</sup>, Ariel Kushmaro<sup>b, c, \*</sup>

<sup>a</sup> Unit of Environmental Engineering, Ben-Gurion University of the Negev, Beer-Sheva, Israel  
<sup>b</sup> Avram and Stella Goldstein-Goren, Department of Biotechnology Engineering, Ben-Gurion University of the Negev, Beer-Sheva, Israel  
<sup>c</sup> The Ilse Katz Center for Meso and Nanoscale Science and Technology, Ben-Gurion University of the Negev, Beer-Sheva, Israel

**HIGHLIGHTS**

- Microbial diversity and metabolism of an industrial wastewater MBR were analyzed.
- Microbial populations were changed due to failure/recovery of the treatment process.
- Different bacterial genera were correlated to TOC removal efficiency periods.

**ARTICLE INFO**

*Article history:*  
 Received 7 April 2020  
 Received in revised form 27 May 2020  
 Accepted 30 May 2020  
 Available online 5 June 2020

Handling Editor: Yongmei Li

**ABSTRACT**

Water and soil contamination by industrial wastes is a global concern. Biological treatment of industrial wastewater using bioreactors allows the removal of organic matter and nutrients and enables either reuse or safe discharge. Wastewater bioremediation depends in part on the microbial communities present in the bioreactor. To ascertain which communities may play a role in the remediation process, the present study investigates the microbial community structure and diversity of microorganisms found in a full-scale membrane bioreactor (MBR) for industrial wastewater treatment. The study was carried out using high-throughput data observations following a failure (crash) of the MBR and during the extended

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 National Center for Biotechnology Information

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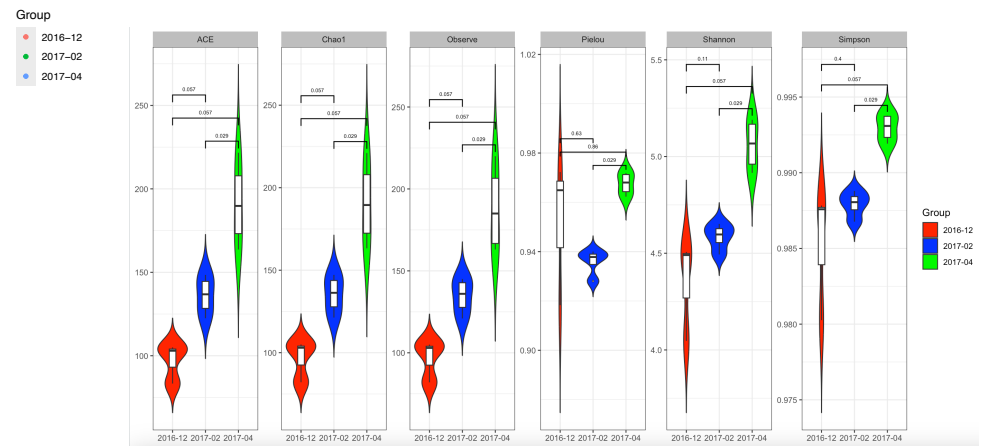
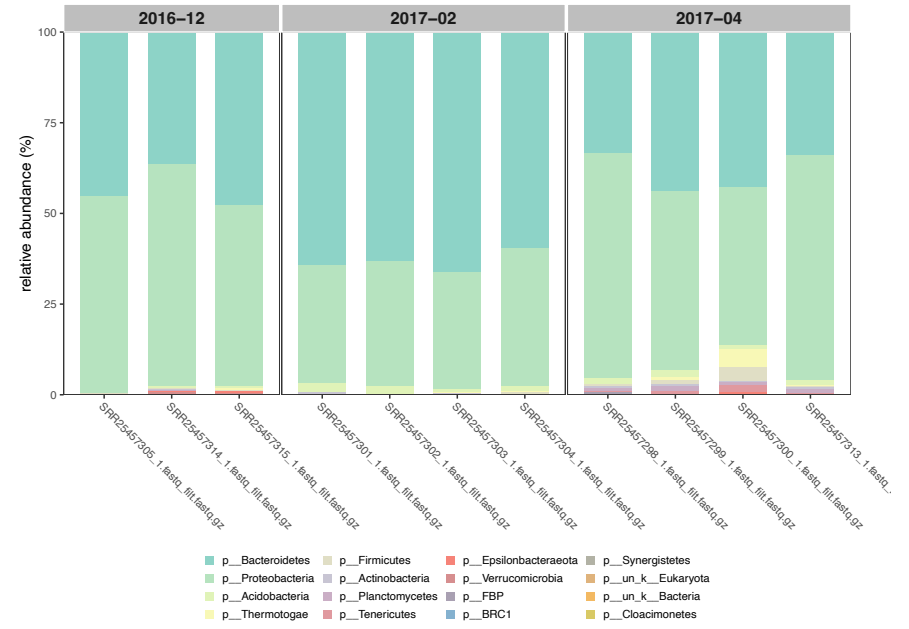
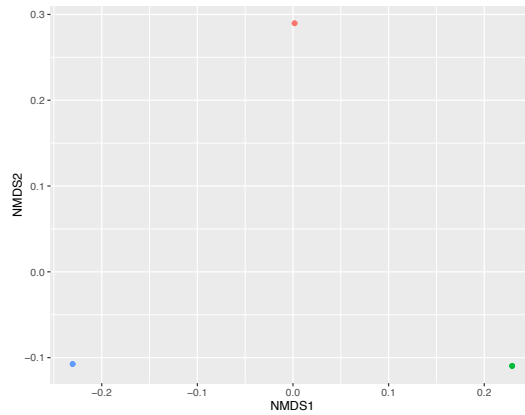
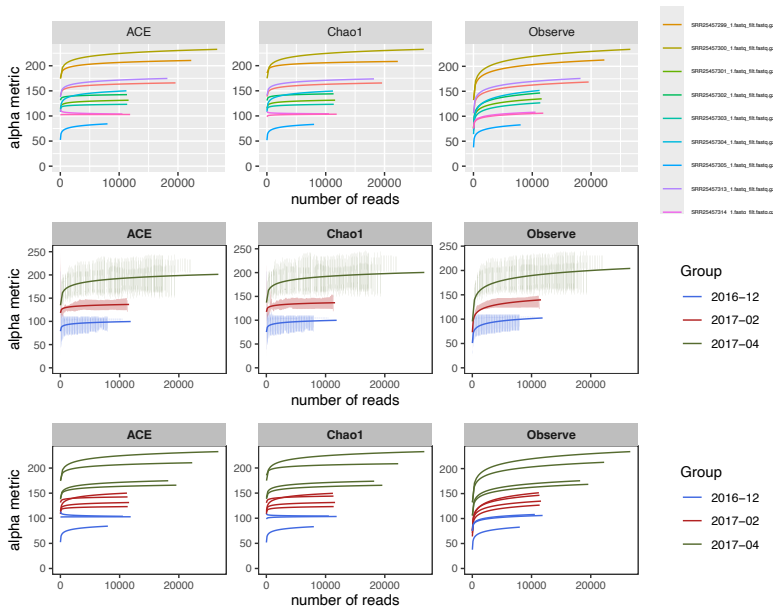
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## EXEMPLOS PRÁTICOS DE APLICAÇÃO DO PBL

### METAGENÔMICA:

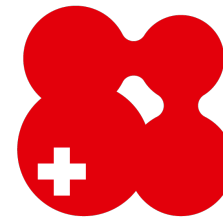





## EXEMPLOS PRÁTICOS DE APLICAÇÃO DO PBL

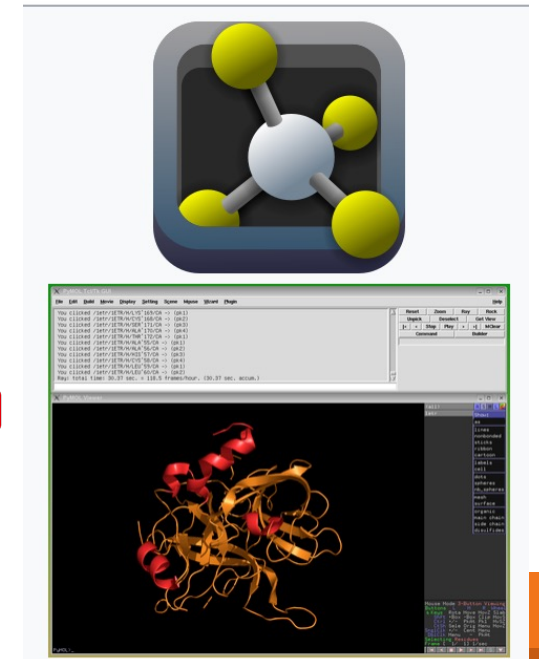
### MODELAGEM MOLECULAR:

**Problema:** Avaliação do impacto de mutações missense da proteína SPIKE do SARS-CoV na estrutura tridimensional de proteína.



SWISS-MODEL 

PyMOL



## APRENDIZAGEM BASEADA EM PROJETOS

- **Desenvolvimento de projetos com aplicação no mundo real**
- ❖ Formulação de perguntas e hipóteses;
- ❖ Desenho experimental;
- ❖ Aplicação prática do conhecimento em bioinformática;
- ❖ Resolução de problemas;
- ❖ Pensamento crítico;
- ❖ Método de aprendizado profundo.



### EVENTOS PARA RESOLVER DESAFIOS

**Maratonas científicas:** eventos intensivos, de curta duração, onde equipes de participantes se reúnem para resolver problemas específicos ou desenvolver projetos.



## ABORDAGENS DIDÁTICAS NO ENSINO DE BIOINFORMÁTICA

Integrando abordagens como aulas expositivas, práticas, PBL, aprendizagem baseada em projetos e maratonas científicas, buscamos não apenas transmitir conhecimento, mas também capacitar os alunos, no processo de ensino-aprendizagem, a resolver problemas reais em bioinformática.