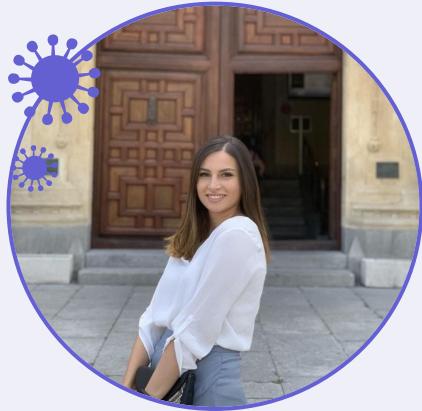


How to destroy the world using Python and a synthetic virus

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Health biologist
Pharmaceutical Regulation Specialist
PyConES 2024 organizer



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Biomedical Engineer
PhD Student in Biophysics and Bioengineering
Python Spain Association Secretary

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**IMPORTANT
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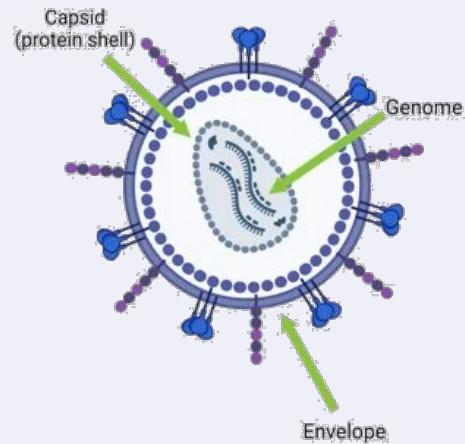
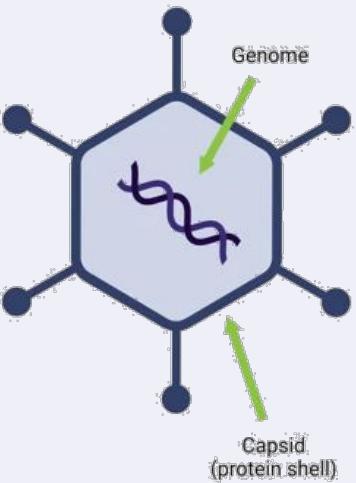
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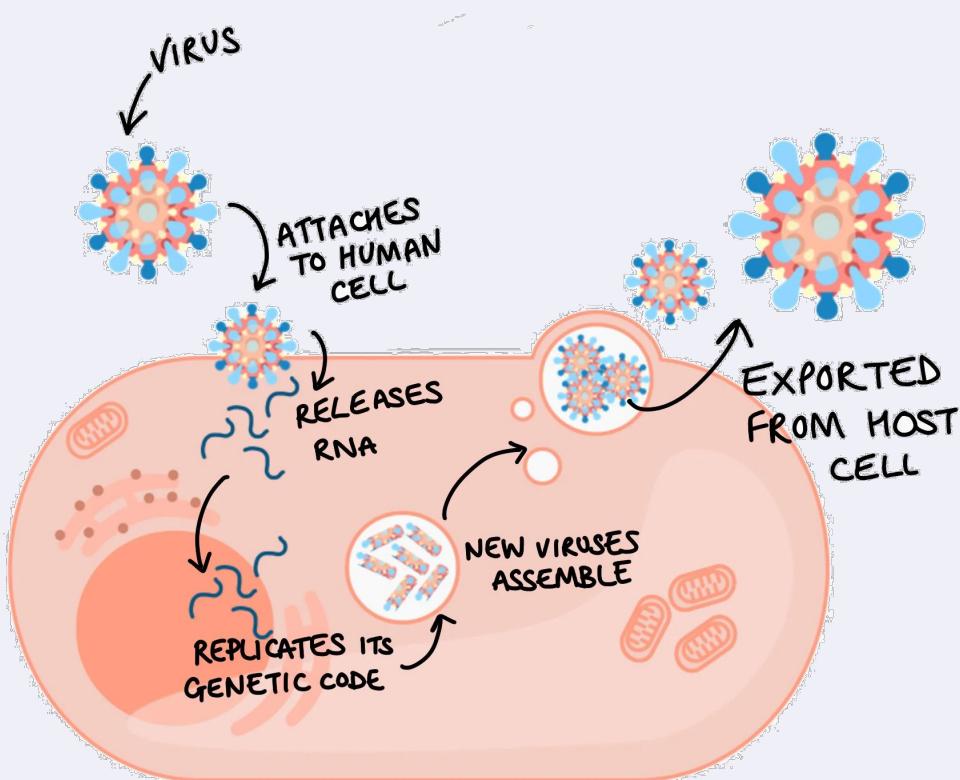
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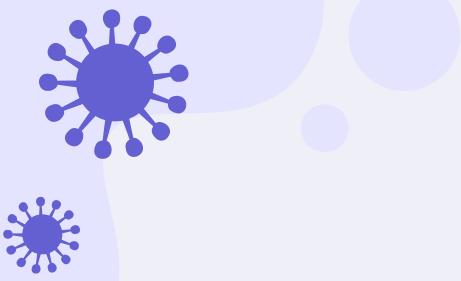
INTRODUCTION

A virus is an infectious agent that can replicate only within a host organism



VIRUS PROPAGATION





Synthetic biology

Design and construction of new biological entities or modification of the existing ones to achieve new functionalities



Medicine

Drugs and vaccines design



Agriculture

Engineered plants and foods



Industry

Sustainably-produced fuels, materials and medicines



Environment

Bioremediation

2

BASIC GENETICS

BASIC CONCEPTS

Gene: segment of DNA that determines a trait

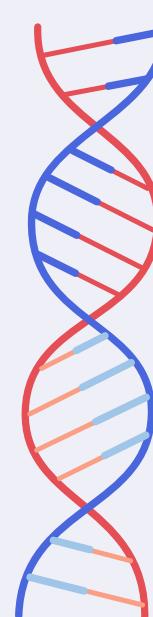
DNA: double helix of bases (letters)

RNA: single helix complementary to the parent DNA

Mutation: letter(s) change



DNA



RNA

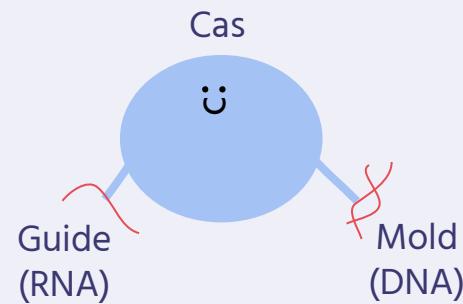


GENE EDITING

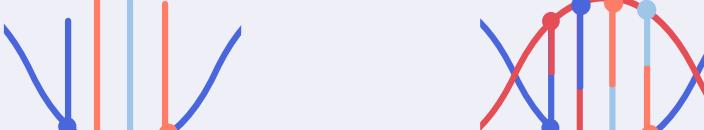
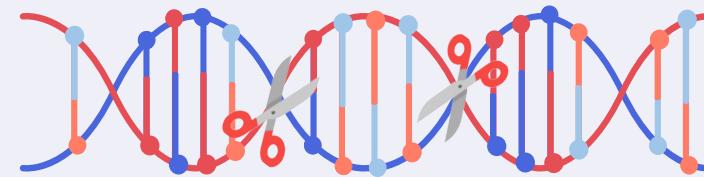
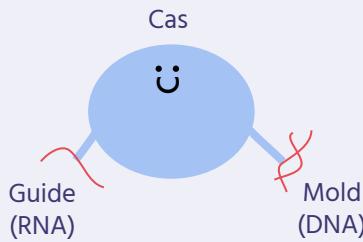


CRISPR-Cas

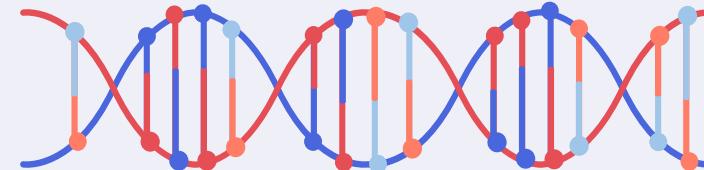
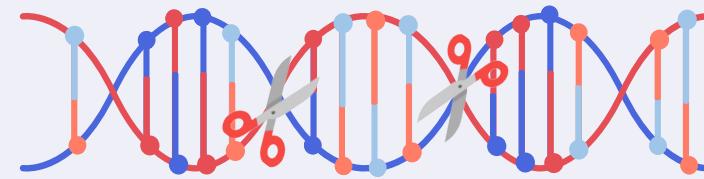
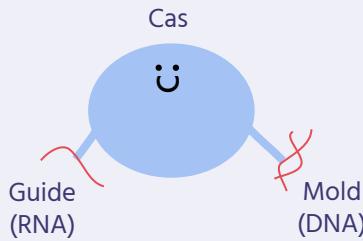
Cut and paste of
DNA and RNA



GENE EDITING



GENE EDITING

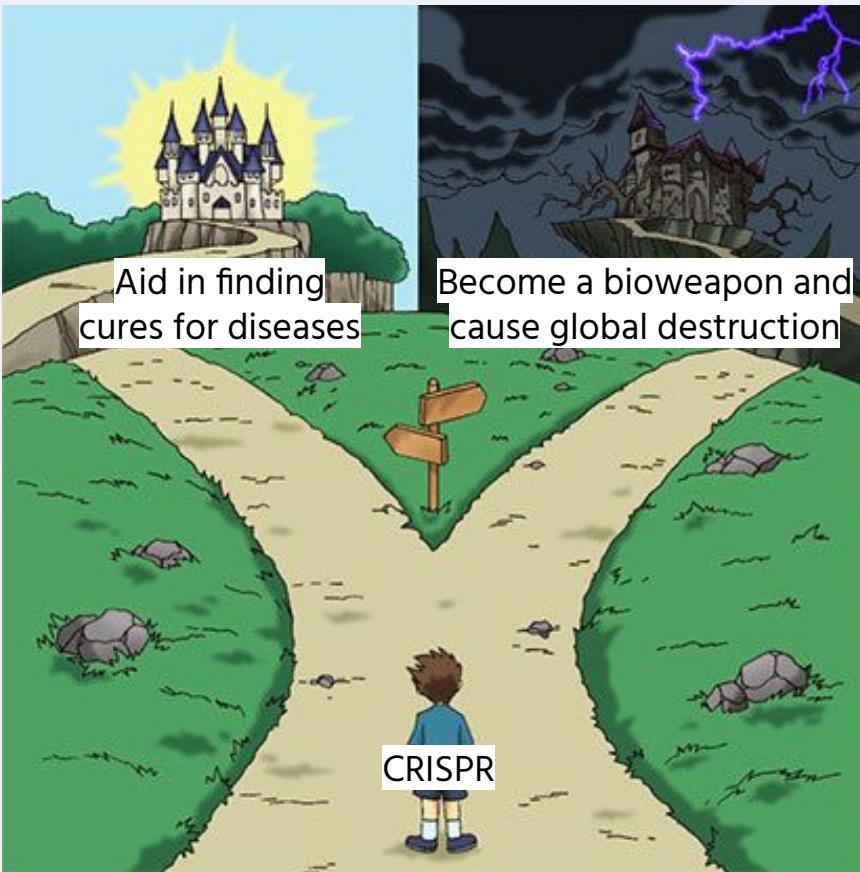


ME WHEN LEARNING ABOUT
CRISPR

3

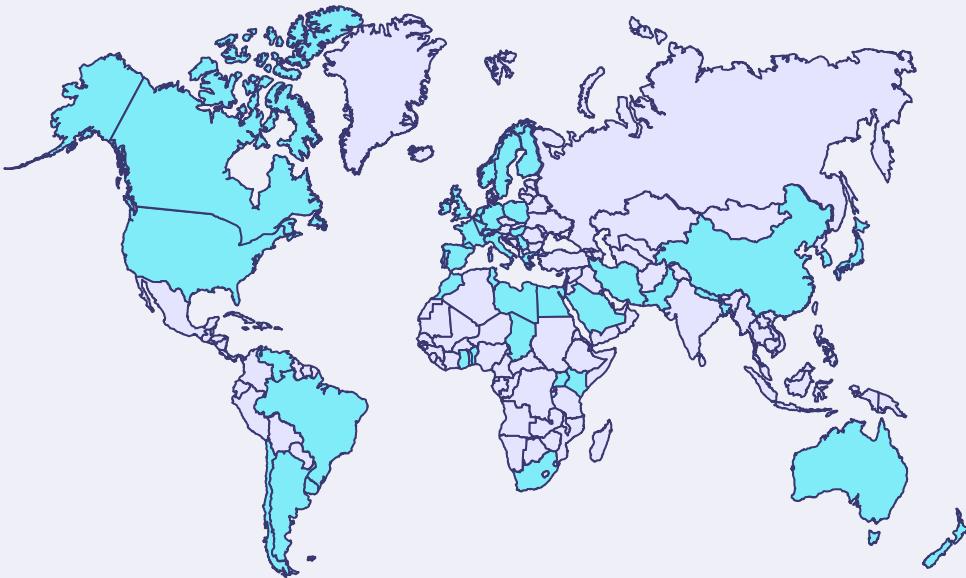
PRACTICAL CASE

PRACTICAL CASE





SPREAD OF THE DISEASE



Start with an **adenovirus serotype 41**
(acute gastroenteritis)

1. Add **lipid membrane** for **adverse weathers**: add VP24, GP and VP40 genes from ebola virus
2. Add ability to **infect vectors** for areas with **heat and humidity**: add NS1, NS4B and NS5 genes from dengue virus
3. Add **virulence**: add VP35, VP30 and L genes from ebola virus

ncbi.nlm.nih.gov/nuccore/AB728839.1

An official website of the United States government [Here's how you know](#)

National Library of Medicine

National Center for Biotechnology Information

Log in

Nucleotide adenovirus 41 Advanced

GenBank

Human adenovirus 41 DNA, complete genome, strain: SaP3-3F

GenBank: AB728839.1

[FASTA](#) [Graphics](#)

Go to:

LOCUS AB728839 34179 bp DNA linear VRL 18-DEC-2013

DEFINITION Human adenovirus 41 DNA, complete genome, strain: SaP3-3F.

ACCESSION AB728839

VERSION AB728839.1

KEYWORDS .

SOURCE Human adenovirus 41

ORGANISM [Human adenovirus 41](#)

Viruses; Varidnaviria; Bamfordvirae; Preplasmiviricota;
Tectiliviricetes; Rowavirales; Adenoviridae; Mastadenovirus; Human
mastadenovirus F.

REFERENCE 1

AUTHORS Kinumaki,A., Sekizuka,T., Takamizawa,M., Igarashi,T. and Kuroda,M.

TITLE Detection of abundant Human Adenovirus 41 sequences in the feces of

Send to:

Complete Record
Coding Sequences

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 Collections Analysis Tool

Download 1 item.

Format

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Create File

Sequence Features
Sequence
Annotation
Assembly
Protein
Taxonomy

[Log in](#)

Nucleotide

Nucleotide

ebola virus

Advanced

[Search](#)[Help](#)

GenBank ▾

Send to: ▾

[Change region shown](#)[Customize view](#)**Analyze this sequence**[Run BLAST](#)[Pick Primers](#)[Highlight Sequence Features](#)[Find in this Sequence](#)**Articles about the VP30 gene**

Ebola virus VP30 and nucleoprotein interactions modulate viral RNA synthesis [Nat Commun. 2017]

Detection of links between Ebola nucleocapsid and virulence using disorder α [Mol Biosyst. 2015]

Zaire ebolavirus strain Ebola_virus/DRC/Likati/Human/2017/1, complete genome

GenBank: MH481611.2

[FASTA](#) [Graphics](#)

Go to: ▾

LOCUS MH481611 18898 bp cRNA linear VRL 13-JUL-2018

DEFINITION Zaire ebolavirus strain Ebola_virus/DRC/Likati/Human/2017/1, complete genome.

ACCESSION MH481611

VERSION MH481611.2

KEYWORDS .

SOURCE Zaire ebolavirus

ORGANISM [Zaire ebolavirus](#)

Viruses; Riboviria; Orthornavirae; Negarnaviricota;
Haploviricotina; Monjiviricetes; Mononegavirales; Filoviridae;
Orthoebolavirus; Orthoebolavirus zairensis.

REFERENCE 1 (bases 1 to 18898)

AUTHORS Wawina-Bokalanga,T., Vanmechelen,B., Vergote,V., Marti-Carreras,J.,



Nucleotide

Nucleotide

ebola virus

Advanced

GenBank ▾

Zaire ebolavirus strain Ebola_virus/DRC/Likati/Human/

GenBank: MH481611.2

[FASTA](#) [Graphics](#)Go to:

LOCUS MH481611 18898 bp cRNA linear VRL 13-JUL-2018
DEFINITION Zaire ebolavirus strain Ebola_virus/DRC/Likati/Human/2017/1, complete genome.
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ORGANISM [Zaire ebolavirus](#)
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 Haploviricotina; Monjiviricetes; Mononegavirales; Filoviridae;
 Orthoebolavirus; Orthoebolavirus zairensis.
REFERENCE 1 (bases 1 to 18898)
AUTHORS Wawina-Bokalanga,T., Vanmechelen,B., Vergote,V., Marti-Carreras,J.,

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Detection of links between Ebola nucleocapsid and virulence using disorder α [Mol Biosyst. 2015]

9721 atttttctg cttcaagggtt tgaggaggt gtttgttatt ggctattgtt atattacaat
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10311..11066
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Details

Display: FASTA

GenBank

Help

```
from tkinter.filedialog import askopenfile

def main():

    print('Please select the file with the virus you want to modify')
    virus_file = askopenfile(mode='r')
    virus_seq = virus_file.readlines()[1:]
    virus_seq = ''.join(virus_seq).replace('\n', '')

    DNA_guide_mutated_virus_seq_mold = knock_in(virus_seq)

    mutated_virus_file.write(mutated_virus_seq)
    mutated_virus_file.close()

    guide_file = open('GUIDE.txt', 'w')
    guide_file.write(DNA_to_RNA(DNA_guide))
    guide_file.close()

    mold_file = open('MOLD.txt', 'w')
    mold_file.write(mold)
    mold_file.close()
```



marinamoropez / synvirus-europython24

```
from tkinter.filedialog import askopenfile

def main():

    print('Please select the file with the virus you want to modify')
    virus_file = askopenfile(mode='r')
    virus_seq = virus_file.readlines()[1:]
    virus_seq = ''.join(virus_seq).replace('\n', '')

    DNA_guide, mutated_virus_seq, mold = knock_in(virus_seq)

    mutated_virus_file = open('MUTATED_SEQUENCE.txt', 'w')
    mutated_virus_file.write(mutated_virus_seq)
    mutated_virus_file.close()

    guide_file = open('GUIDE.txt', 'w')
    guide_file.write(DNA_to_RNA(DNA_guide))
    guide_file.close()

    mold_file = open('MOLD.txt', 'w')
    mold_file.write(mold)
    mold_file.close()
```

```
from tkinter.filedialog import askopenfile

def main():

    print('Please select the file with the virus you want to modify')
    virus_file = askopenfile(mode='r')
    virus_seq = virus_file.readlines()[1:]
    virus_seq = ''.join(virus_seq).replace('\n', '')

    DNA_guide, mutated_virus_seq, mold = knock_in(virus_seq)

    mutated_virus_file = open('MUTATED_SEQUENCE.txt', 'w')
    mutated_virus_file.write(mutated_virus_seq)
    mutated_virus_file.close()

    guide_file = open('GUIDE.txt', 'w')
    guide_file.write(DNA_to_RNA(DNA_guide))
    guide_file.close()

    mold_file = open('MOLD.txt', 'w')
    mold_file.write(mold)
    mold_file.close()

def DNA_to_RNA(DNA_guide):

    RNA_guide = ""
    for base in DNA_guide:
        if base == "T":
            RNA_guide += "A"
        elif base == "A":
            RNA_guide += "U"
        elif base == "C":
            RNA_guide += "G"
        elif base == "G":
            RNA_guide += "C"
```

```
def knock_in(virus_seq):

    print('Please select the file with the gene you want to add to the virus')
    added_gene_file = askopenfile(mode='r')
    added_gene_seq = added_gene_file.readlines()[1:]
    added_gene_seq = ''.join(added_gene_seq).replace('\n', '')

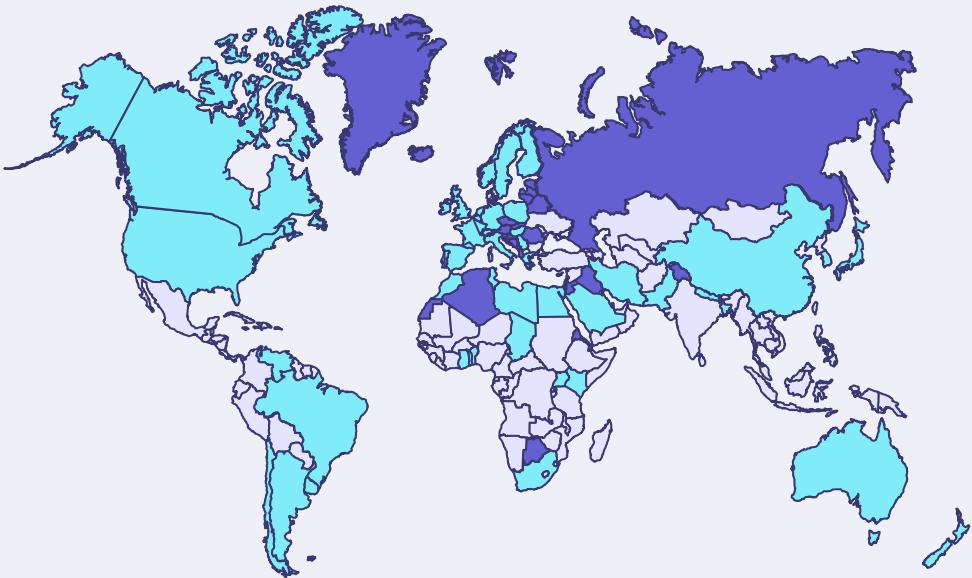
    mutation_position = int(input("Introduce the numeric position where you want to enter the new gene (e.g. 1, 25, 203): "))
    while mutation_position <= 0:
        print('Invalid input. Introduce positive number. ')
        mutation_position = int(input("Introduce the numeric position where you want to enter the new gene (e.g. 1, 25, 203): "))

    DNA_guide = virus_seq[mutation_position-25:mutation_position+25]
    mutated_virus_seq = virus_seq[:mutation_position] + added_gene_seq + virus_seq[mutation_position:]
    mold = virus_seq[mutation_position-25:mutation_position] + added_gene_seq + virus_seq[mutation_position:mutation_position+25]

    return DNA_guide, mutated_virus_seq, mold
```



SPREAD OF THE DISEASE



Start with an **adenovirus serotype 41** (acute gastroenteritis)

1. Add **lipid membrane for adverse weathers**: add VP24, GP and VP40 genes from ebola virus
2. Add ability to **infect vectors** for areas with **heat and humidity**: add NS1, NS4B and NS5 genes from dengue virus
3. Add **virulence**: add VP35, VP30 and L genes from ebola virus

Fragment of
the original
adenovirus 41

VP24 gene
from ebola
virus

Example with Python: add VP24 gene from ebola virus
to have a **lipid membrane for adverse weathers**
(add in the position 29.937 of av41)

TCATCCAAATCTGCCAACATCACCTCAGTGTGCTACAAACGAGATAAACAGTGGGTATG
CTTTTACTTTAAATGGTCAGCGAACCGGGAAAACCTTTCACCCACCCACCGCTGTATTT
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CAAGGATCCTGACACGAATGCAAAGTTGATTCTGAAATTAAAGCTCTTGCTATCTAA

Example with Python: add VP24 gene from ebola virus
to have a **lipid membrane** for **adverse weathers**
(add in the position 29.937 of av41)

Fragment of
the original
adenovirus 41

TCATCCAAATCTGCCAACATCACCTCAGTGTGCTACAACGAGATAAACAGTGGGTATG
CTTTTACTTTAAATGGTCAGCGAACCGGGAAAACCTTTACCCACCCACCGCTGTATTT
GCTACATAACTGAACAATAAAATCATTGCAGGCACAATCTTCGCATTTCTTTCCAGATG
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GACATCCCATTATTACACCCCCGTTGCCTCCAACGGCTTGCAAGAAAAACCTCCGGGA
GTCCTCAGCCTGAAATACACTGATCCACTTACAACCAAAAACGGGGCTTAACCTTAAACTG

Guide (RNA)

UAGAAGCGUAAAGAAAAAAAGGUUCUACUUUGCUCGGUCUGAACUUCUACU

Fragment of the original adenovirus 41

VP24 gene
from ebola
virus

Mold (DNA)

TCATCCAAATCTGCCTAACATCACCTCAGTGTGCTACAACGAGATAAACAGTGGGTATG
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Fragment of the original adenovirus 41

VP24 gene from ebola virus

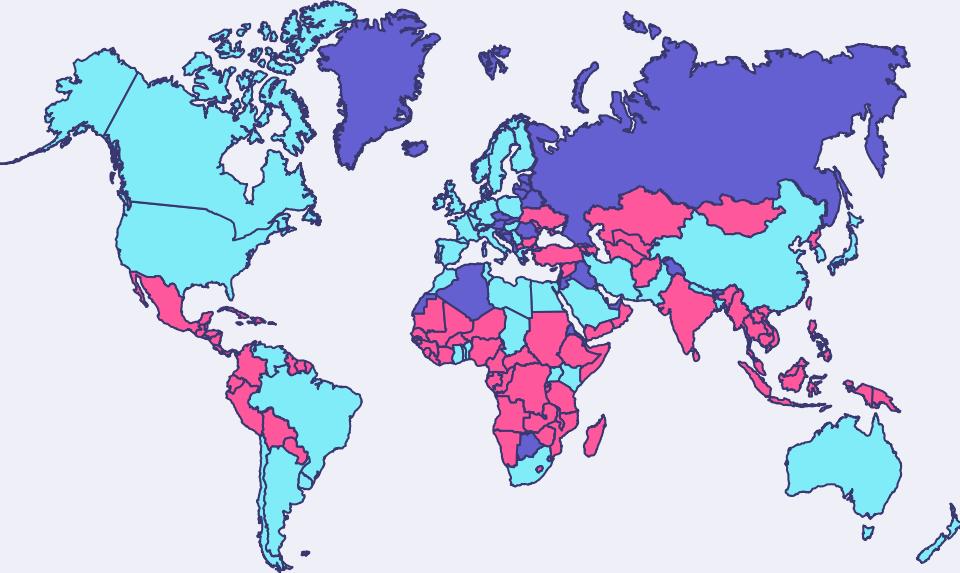
Mutated adenovirus 41

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SPREAD OF THE DISEASE



Start with an **adenovirus serotype 41** (acute gastroenteritis)

1. Add **lipid membrane** for **adverse weathers**: add VP24, GP and VP40 genes from ebola virus
2. Add ability to **infect vectors** for areas with **heat and humidity**: add NS1, NS4B and NS5 genes from dengue virus
3. Add **virulence**: add VP35, VP30 and L genes from ebola virus

SPREAD OF THE DISEASE



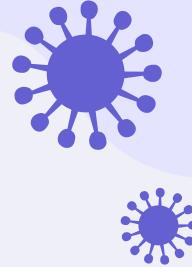
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4

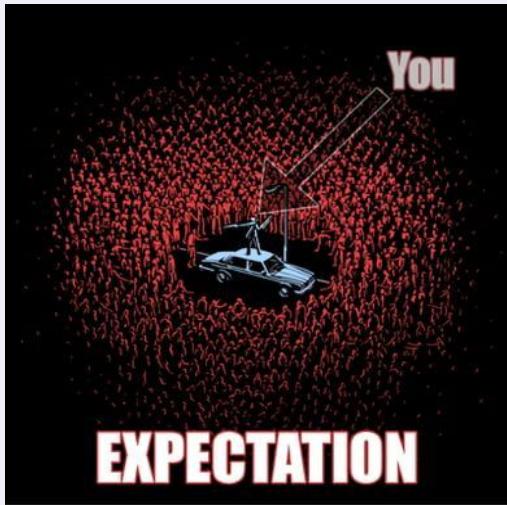
IMPORTANT CONSIDERATIONS



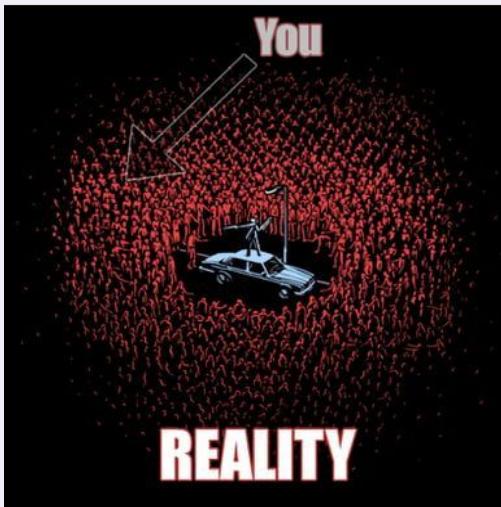
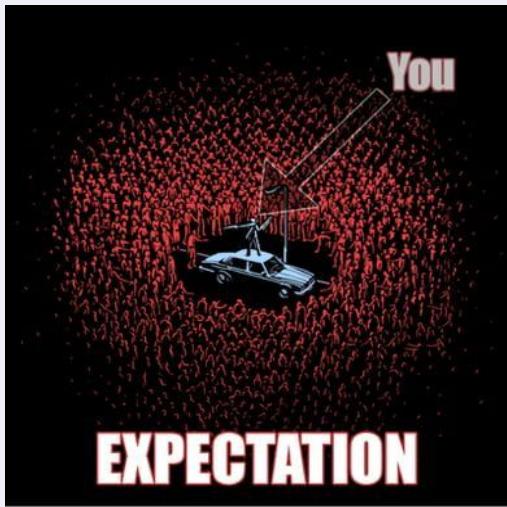
THE HARSH REALITY



THE HARSH REALITY

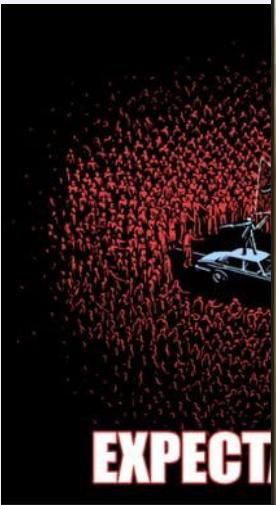


THE HARSH REALITY



THE HARSH REALITY

NOT FUNNY



EXPECT



CRYED



ALITY



THE HARSH REALITY



THE HARSH REALITY



ACKNOWLEDGE

Not everything is what it seems

There are still things to be discover

THE HARSH REALITY



LACK OF KNOWLEDGE

Not everything is what it seems

Complex systems that are not compartmentalized

There are still things to be discover



UNPREDICTABILITY

Biology has its own ways



WARNING

DANGER



WARNING

DANGER

WARNING

THE HARSH REALITY



LACK OF KNOWLEDGE

Not everything is what it seems

There are still things to be discovered

Complex systems that are not compartmentalized



LEGALITY

Maybe... don't...

UNPREDICTABILITY

Biology has its own ways



Geneva protocol and UN are watching



SOME EXAMPLES

SO WHAT CAN WE DO?



SO WHAT CAN WE DO?

GENE
CORRECTION



SO WHAT CAN WE DO?

GENE
CORRECTION



CAR-T
CELLS



SO WHAT CAN WE DO?

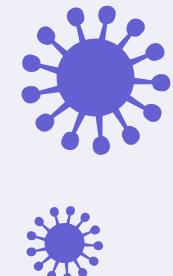
GENE
CORRECTION



VIRUS
TREATMENTS



CAR-T
CELLS



SO WHAT CAN WE DO?

GENE
CORRECTION



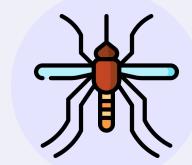
VIRUS
TREATMENTS



CAR-T
CELLS



INFECTIOUS
DISEASES



SO WHAT CAN WE DO?



“Designing cancer vaccines with Python”



SO WHAT CAN WE DO?



"Designing cancer vaccines with Python"



5

FINAL CONCLUSIONS

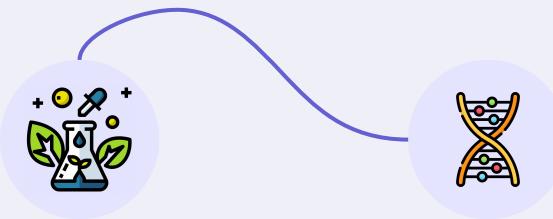
FINAL CONCLUSIONS



SYNTHETIC BIOLOGY

Different
applications

FINAL CONCLUSIONS



SYNTHETIC BIOLOGY

Different applications

GENETIC EDITING

CRISPR-Cas can be used to create and modify the genome

FINAL CONCLUSIONS



SYNTHETIC BIOLOGY

Different applications



GENETIC EDITING

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UNLEASHING CHAOS

We can create "a living being on demand"

FINAL CONCLUSIONS



SYNTHETIC BIOLOGY

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UNLEASHING CHAOS

We can create "a living being on demand"



HAVE IN MIND

With great power comes great responsibility

Thanks!



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[marinamorolopez](https://github.com/marinamorolopez) / [synvirus-europython24](https://github.com/synvirus-europython24)



We look forward to
seeing you at PyConES!
(October 4-6th) ;)