Inteligencia Artificial y Biomedicina: Evolución, actualidad y perspectivas futuras.

Nahuel Costa Cortez

Presentación

Nahuel Costa
Inteligencia Artificial y Biomedicina

2020 - 2023

Universidad de Oviedo

Doctorado en Inteligencia Artificial

2019 - 2020

Universidad de Oviedo

Máster en Ingeniería Informática

2015 - 2019

Universidad de Oviedo

Grado en Ingeniería Informática

Profesor en Universidad de Oviedo

Investigador en IA

nahuelcosta.com

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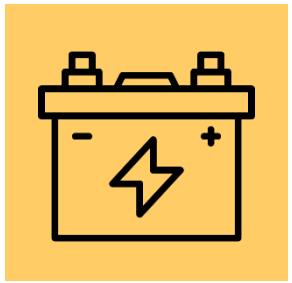
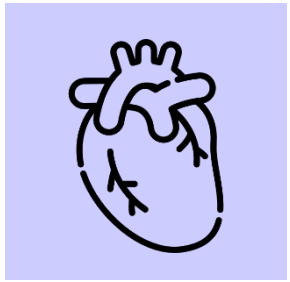
IA aplicada a monitorización de sistemas



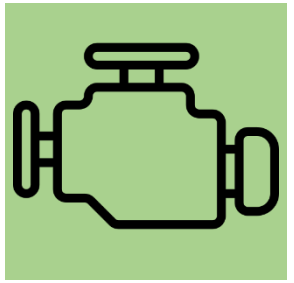
Baterías de Litio

Monitorización de datos de celdas



Marcapasos

Monitorización de datos intracardiacos



Motores de aviación

Monitorización de sensores de aviones

Presentación

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Medtronic

Inteligencia Artificial

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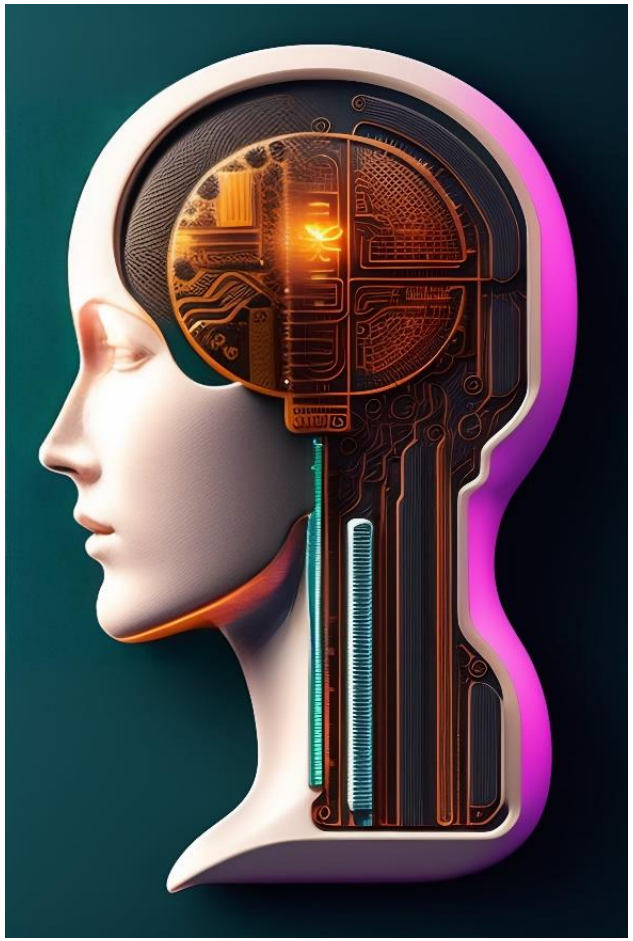
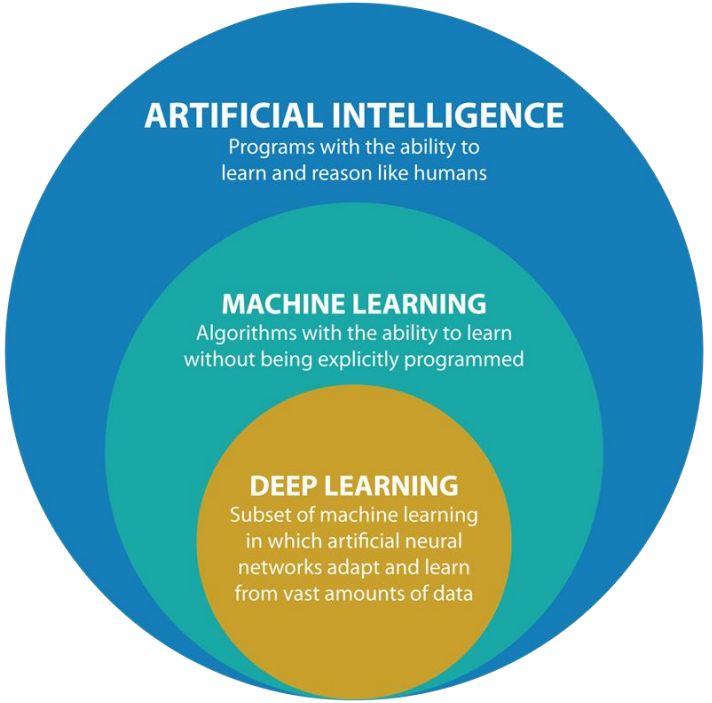


"Capacidad de las máquinas y los sistemas de software para realizar tareas que, en teoría, requerirían inteligencia humana para ser realizadas"



Inteligencia Artificial

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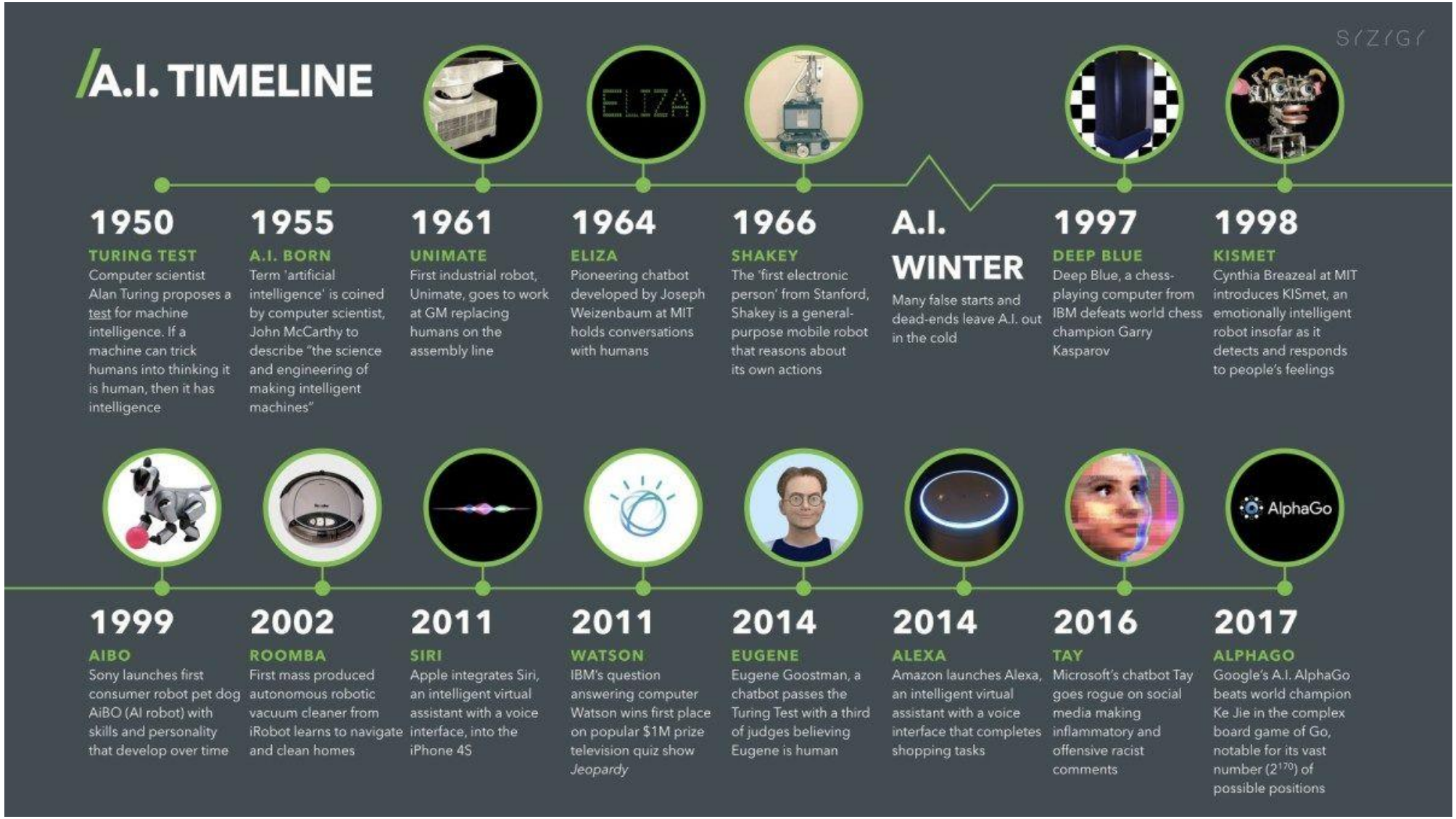


Evolución

2012

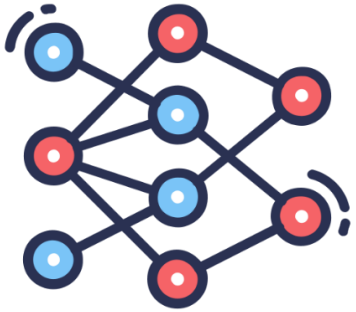
IMAGENET

Reconocimiento de objetos

Desbloqueo móvil

Sistemas de recomendación

2015



EVOLUCION MODELOS

Autocorrector móvil

Asistentes virtuales

Detección de spam

2016

MODELOS GENERATIVOS

Filtros en redes sociales

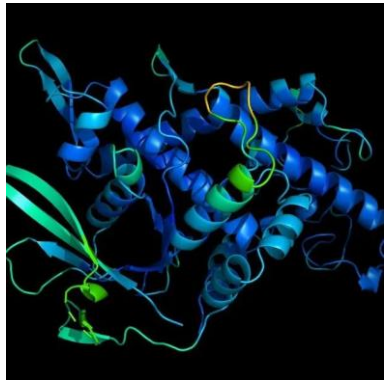
Aplicaciones de diseño

Evolución

2017

Transformers

Alphafold



Plegado de proteínas

Github Copilot

Predicción de código

ChatGPT

Predicción de texto

Dalle2, Midjourney...

Generación de imágenes

Alphafold

DeepMind

Alphafold

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PLEGADO DE PROTEÍNAS

Proteínas - Secuencias de aminoácidos

Alphafold

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PLEGADO DE PROTEÍNAS

Proteínas - Secuencias de aminoácidos

⚠ Mal plegado

↓

Enfermedades: Alzheimer, Parkinson...

Alphafold

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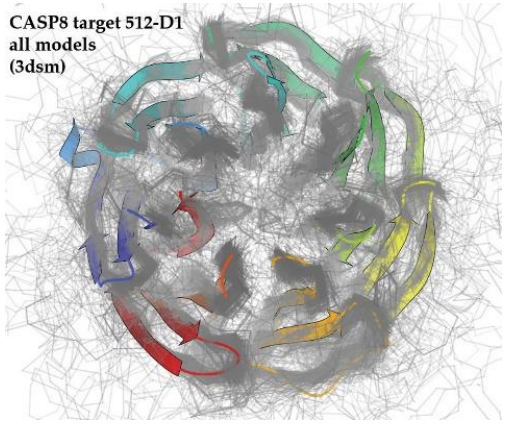
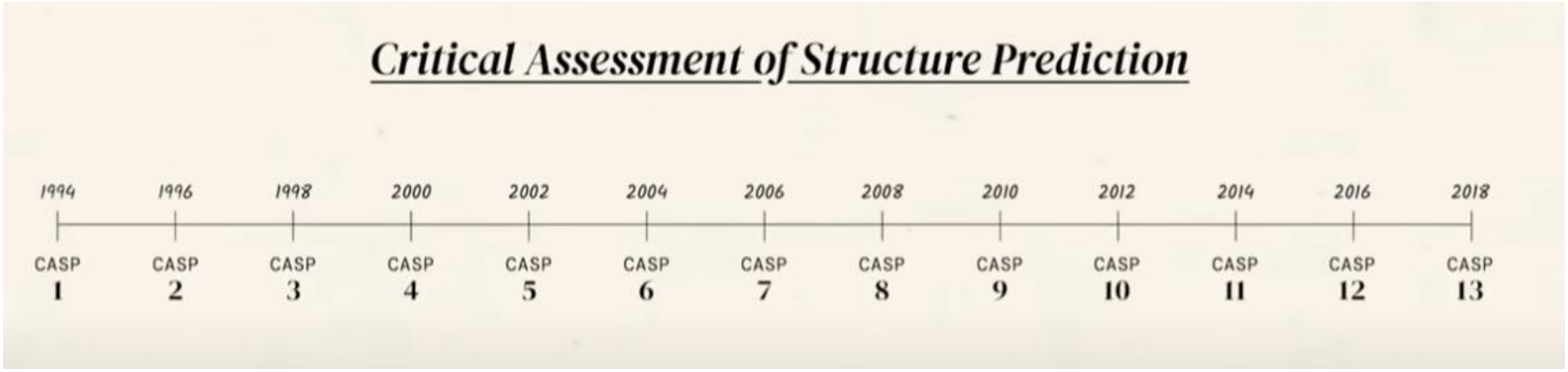


COMPETICIÓN CASP

Métodos tradicionales -
Computacionalmente muy costosos



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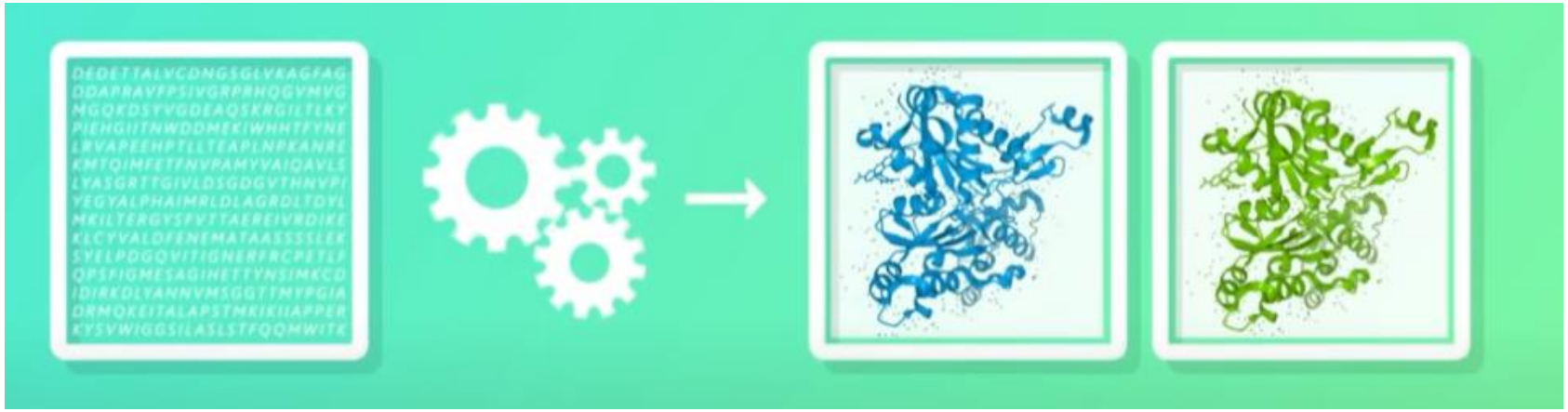
COMPETICIÓN CASP

SECUENCIA DE AMINOÁCIDOS

ESTRUCTURA 3D PROTEINA



Alphafold

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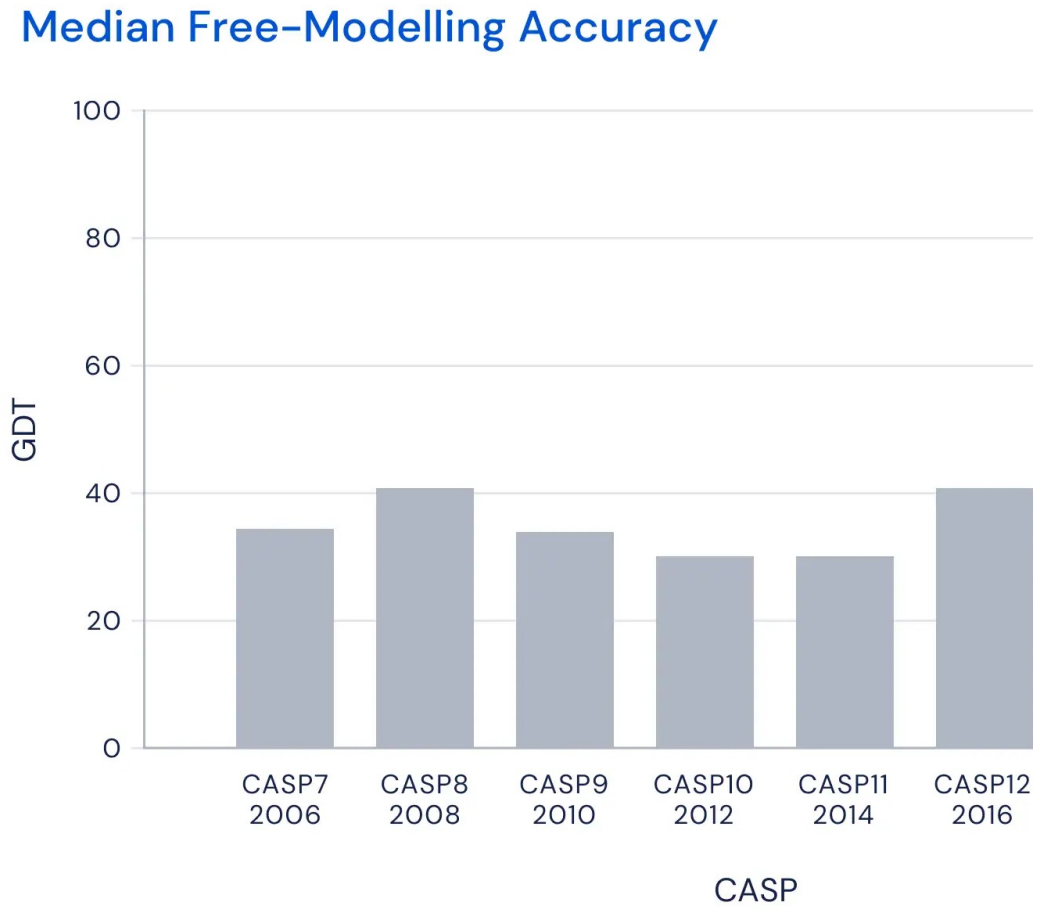
Métrica - Global Distance Test (GDT)

Indica el porcentaje de aminoácidos que se localizan en la posición correcta

DeepMind



Alphafold

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Métrica - Global Distance Test (GDT)

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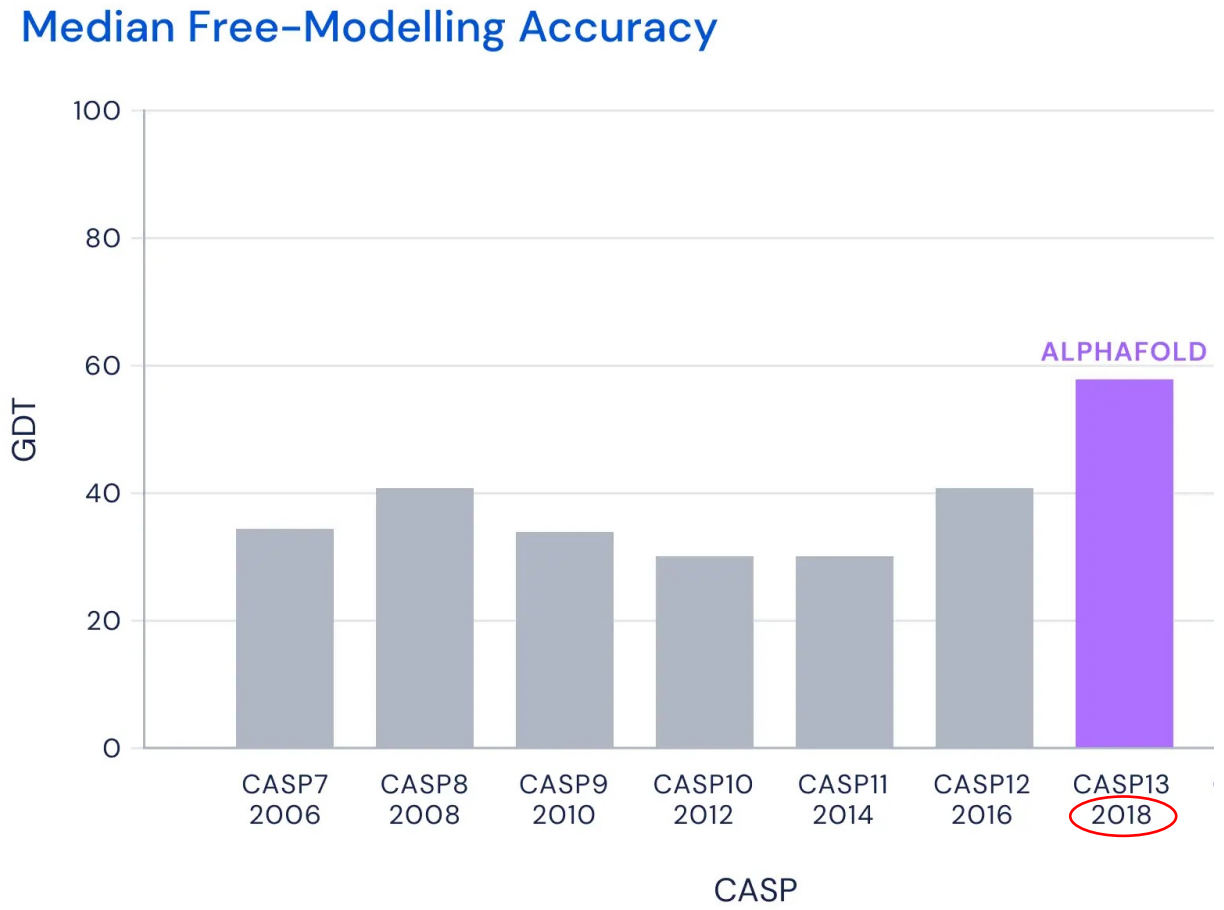

Alphafold

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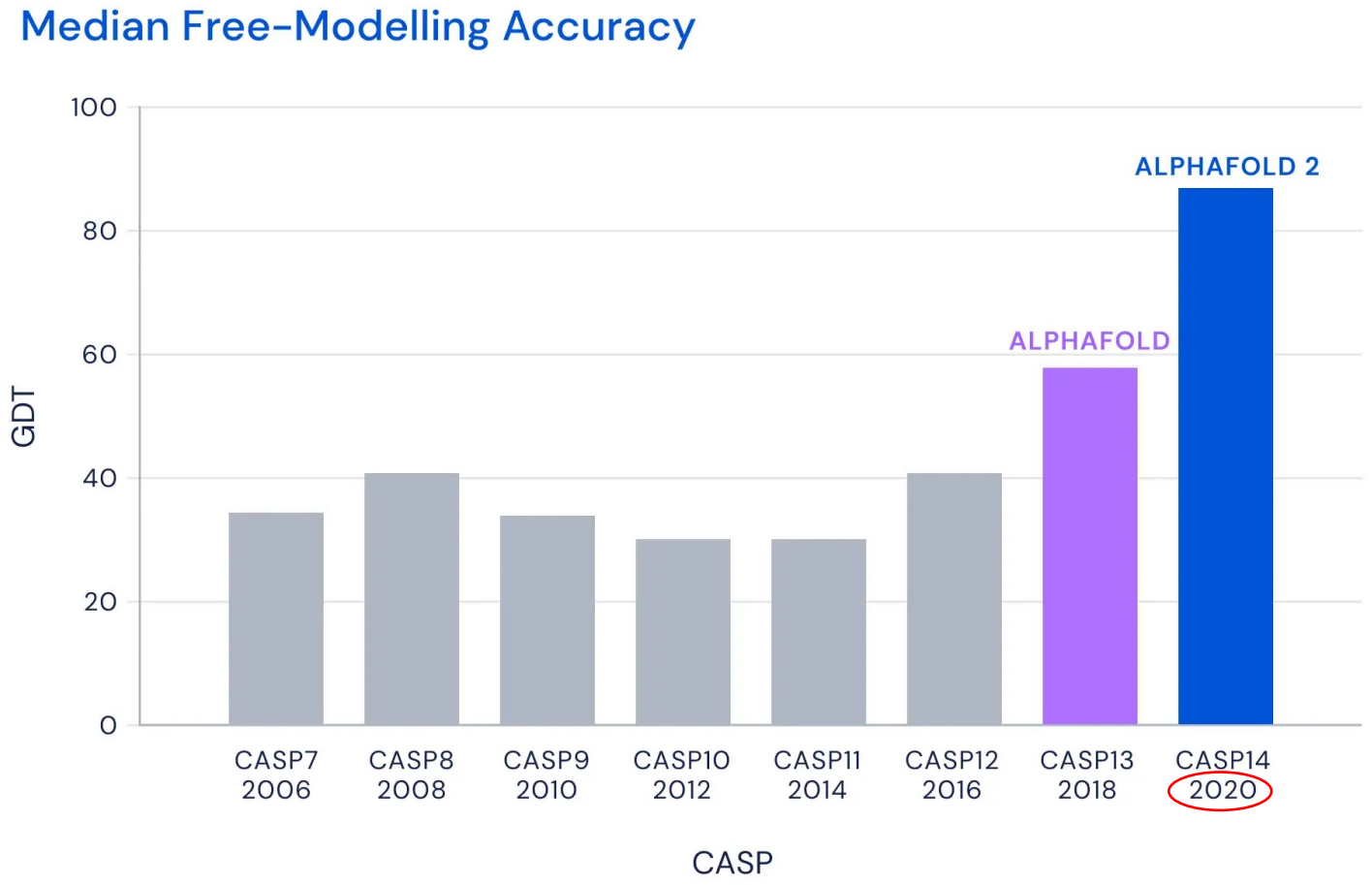
Métrica - Global Distance Test (GDT)

Indica el porcentaje de aminoácidos que se localizan en la posición correcta

¡Problema resuelto!



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ALPHAFOLD 1

Convertir una secuencia unidimensional a una estructura tridimensional

ALPHAFOLD 1

Convertir una secuencia unidimensional a una estructura tridimensional → Convertir una imagen a otra imagen

Alphafold

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Tomar una imagen y modificar su estilo

Alphafold

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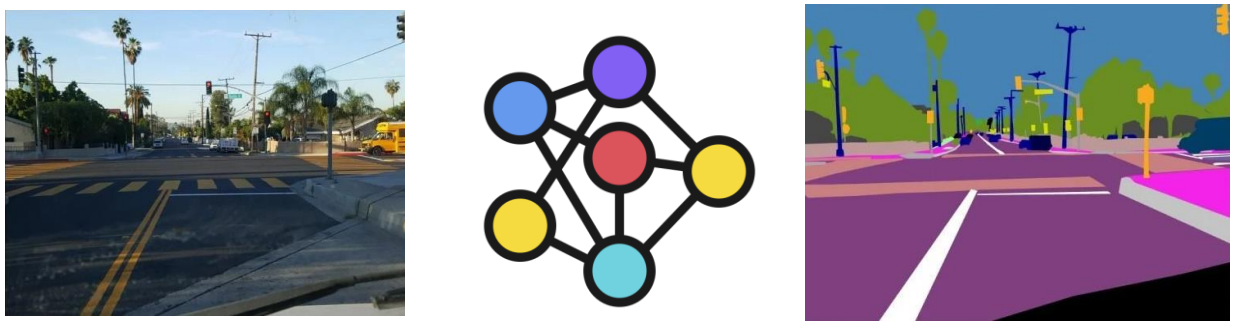
Inteligencia Artificial y Biomedicina

Tomar una imagen y modificar su estilo

Tomar una imagen y generar un mapa de segmentación



Alphafold

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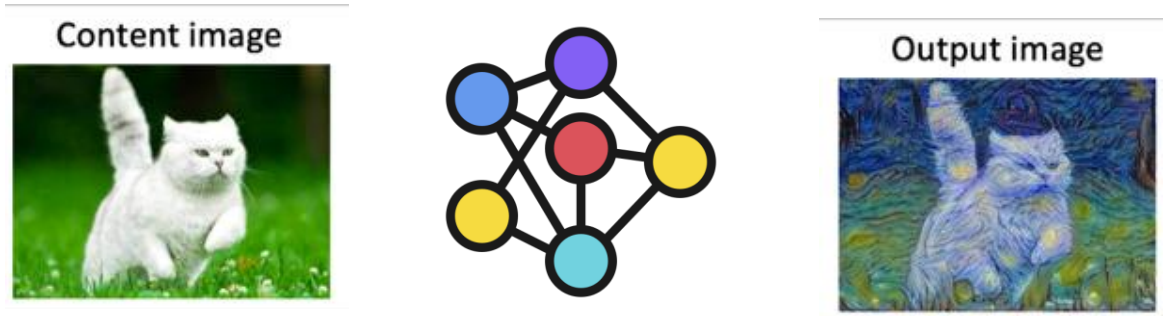
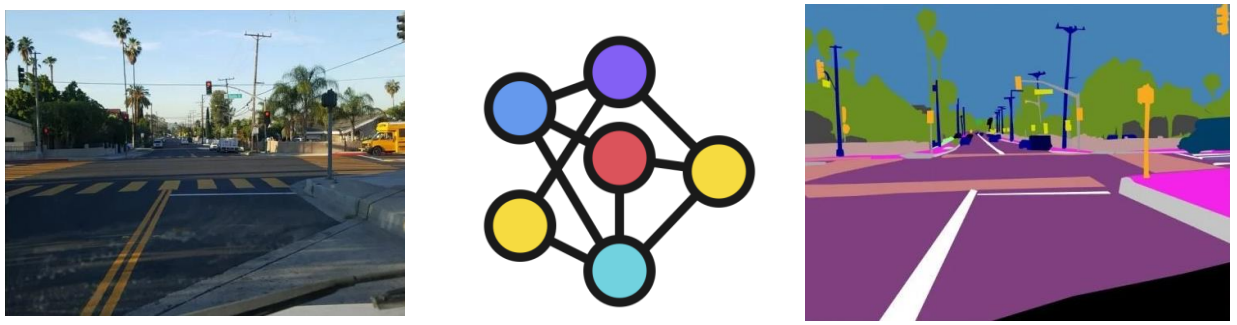
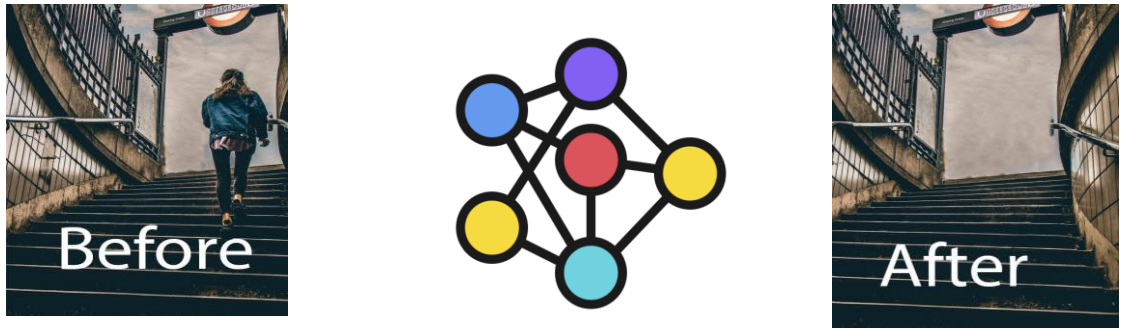
Tomar una imagen y modificar su estilo



Tomar una imagen y generar un mapa de segmentación



Tomar una imagen y borrar partes



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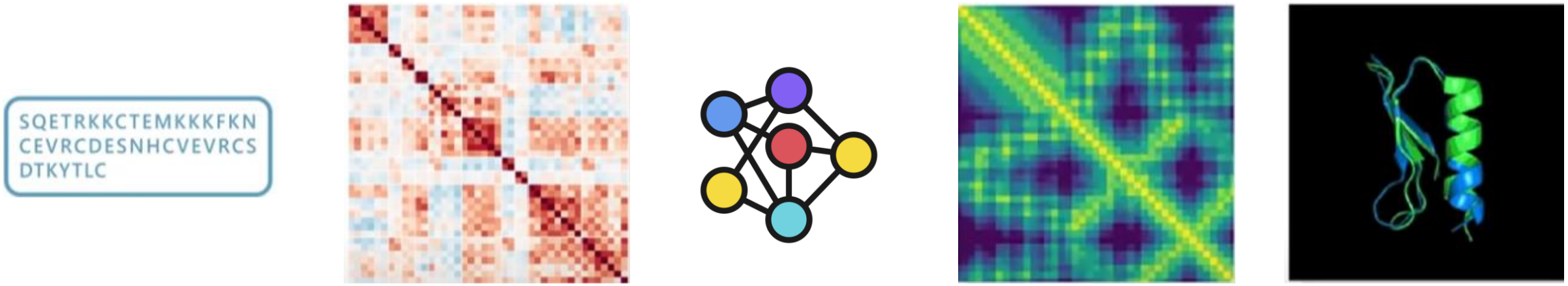
ALPHAFOLD 1



Alphafold

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Multiple sequence alignment

Alphafold

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Multiple Sequence Alignment (MSA)

Aminoácidos que coevolucionan

Qué interacción se produce dentro de la estructura tridimensional

Predecir plegado

Alphafold

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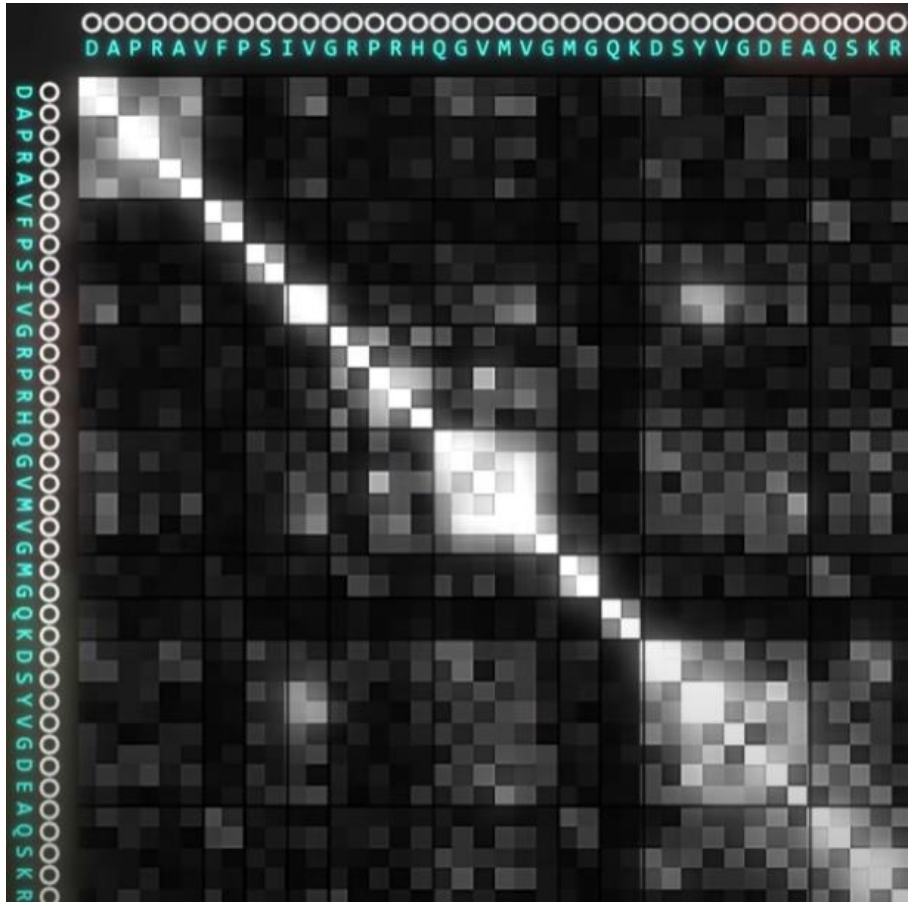
Multiple Sequence Alignment (MSA)

Aminoácidos que coevolucionan

Qué interacción se produce dentro de la estructura tridimensional

Predecir plegado

Interacción de aminoácidos



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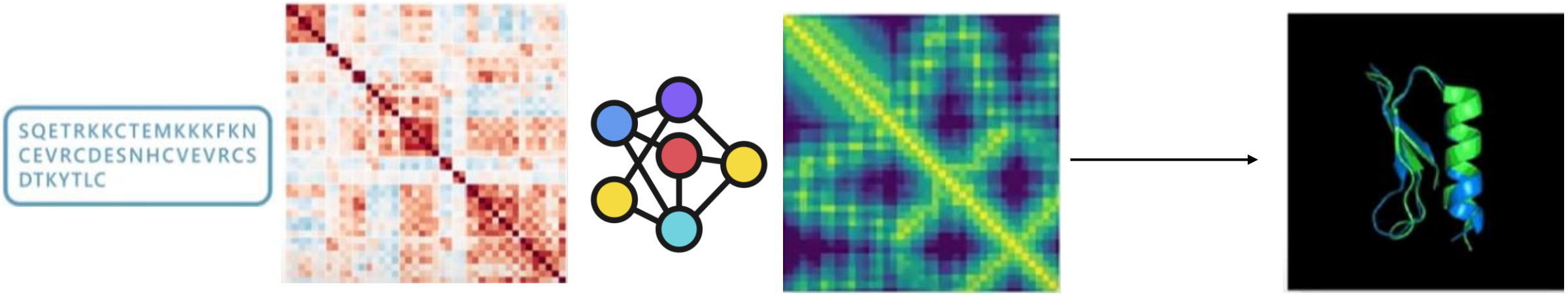

INPUT
Información de la secuencia de aminoácidos

OUTPUT
Matriz de distancia de la proteína

OUTPUT FINAL
Estructura 3D de la proteína

ALPHAFOLD 2

Convertir una secuencia unidimensional a una estructura tridimensional → Modelarlo como un problema de texto

Transformers

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ALPHAFOLD 2

Convertir una secuencia unidimensional a una estructura tridimensional → Modelarlo como un problema de texto

Transformers

Permiten atender a las partes más importantes de una secuencia

ALPHAFOLD 2

Convertir una secuencia unidimensional a una estructura tridimensional → Modelarlo como un problema de texto

Transformers

- Permiten atender a las partes más importantes de una secuencia
- Pueden ser entrenados en paralelo

Alphafold

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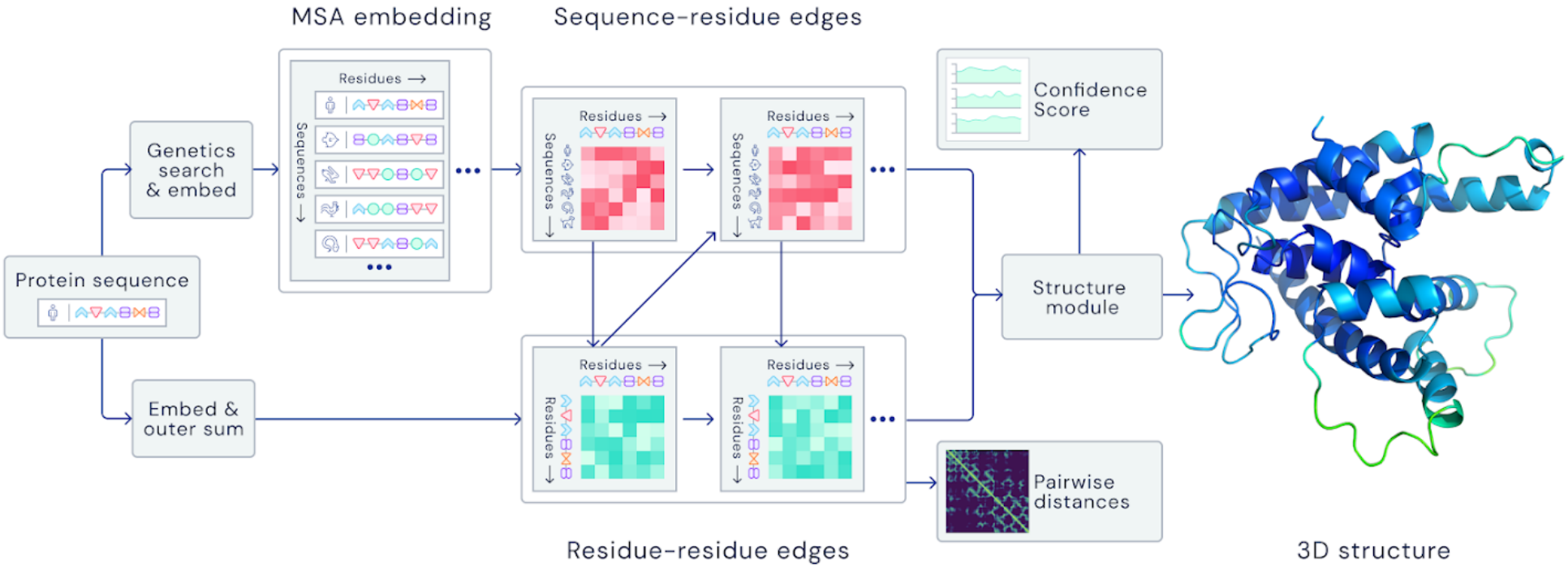

Encuentra secuencias similares a la entrada y pasa esa información a otra red neuronal que produce la estructura 3D final

Fibrilación Auricular

Fibrilación Auricular

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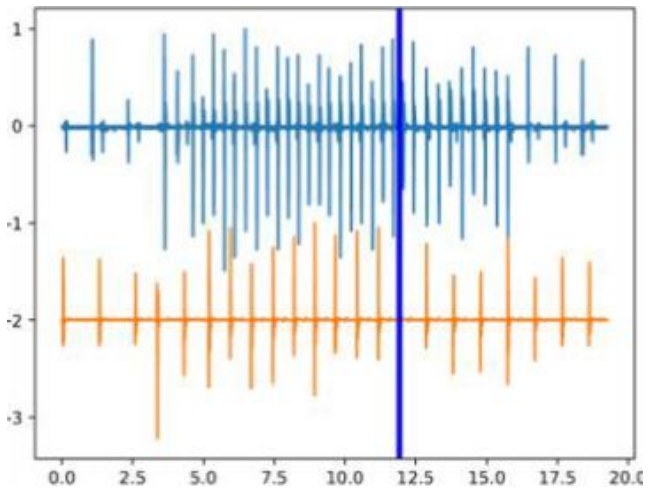

DATOS INCOMPLETOS

REGISTROS LIMITADOS

Fibrilación Auricular

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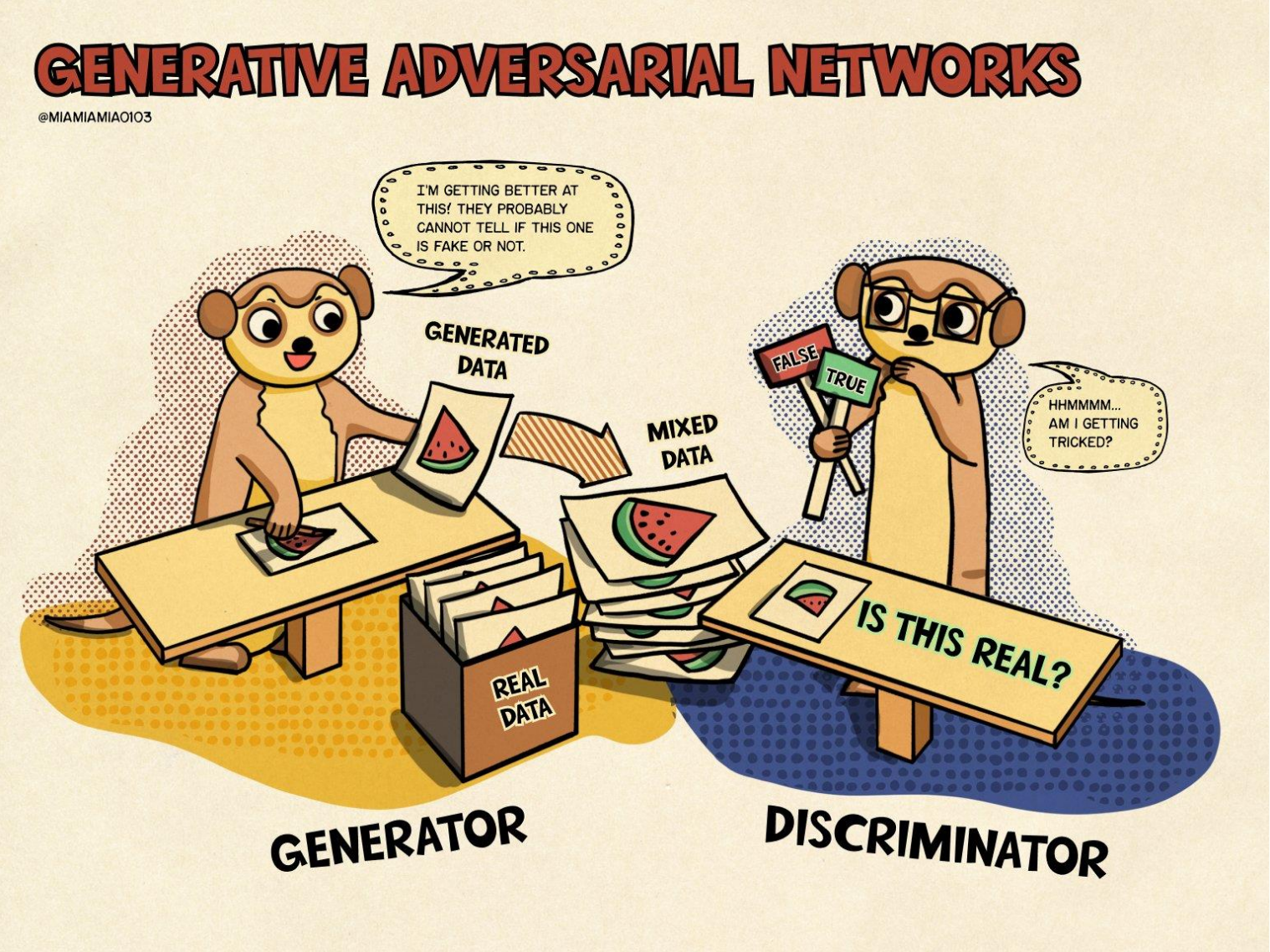
GANs



Fibrilación Auricular

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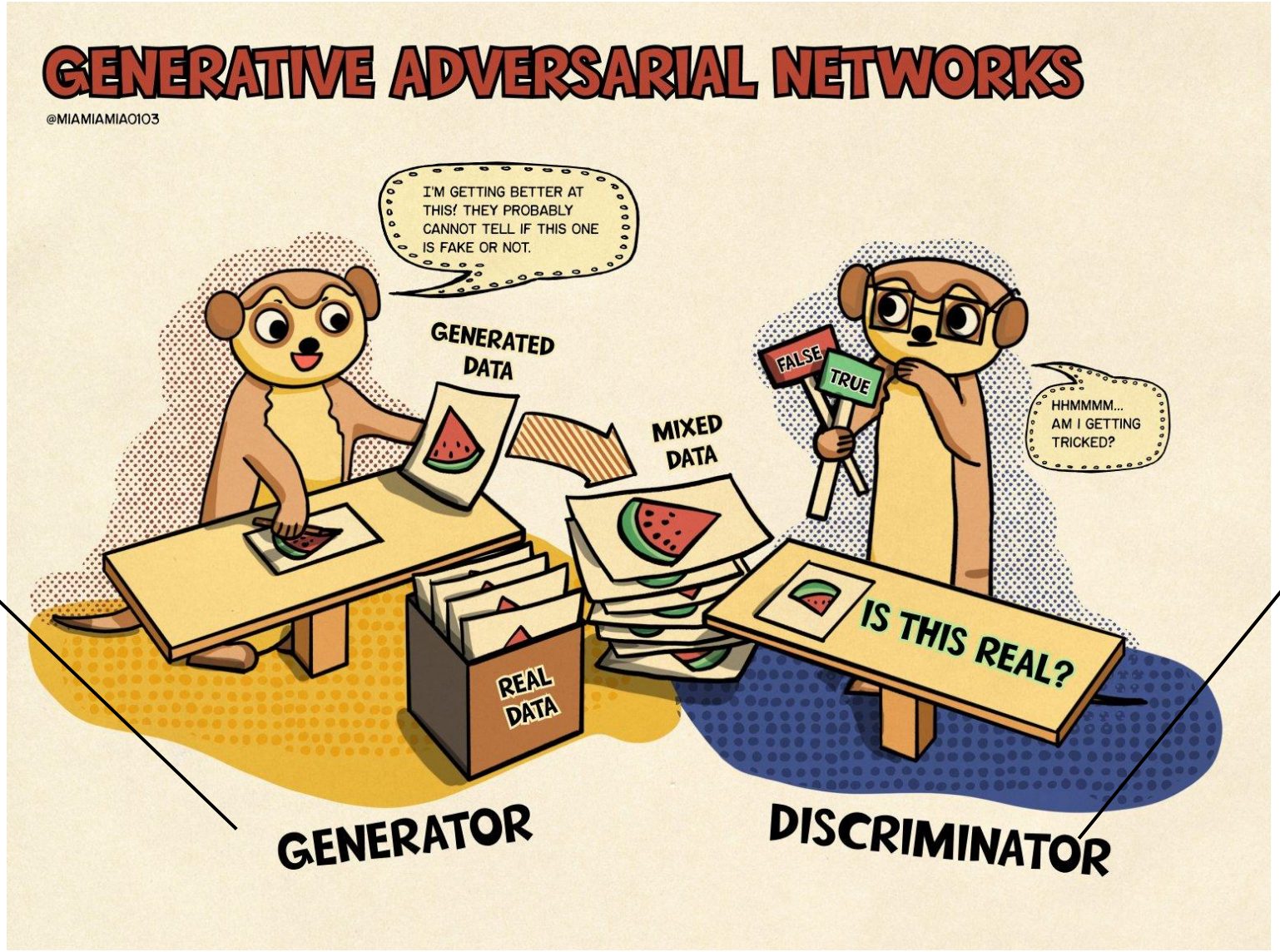
GANs



Generar datos

[thisxdoesnotexist]

Reconocer datos

Fibrilación Auricular

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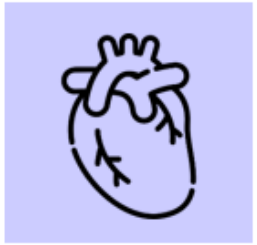

Atrial Fibrillation

Fibrilación Auricular

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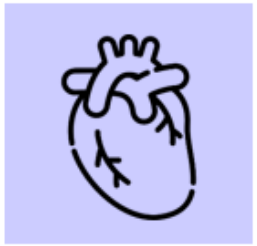

Atrial Fibrillation

Class 1

Class 2

Class 3

Class 4

Class 5

Class 6

Fibrilación Auricular

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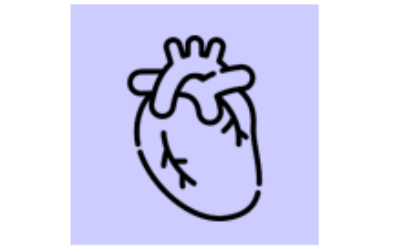
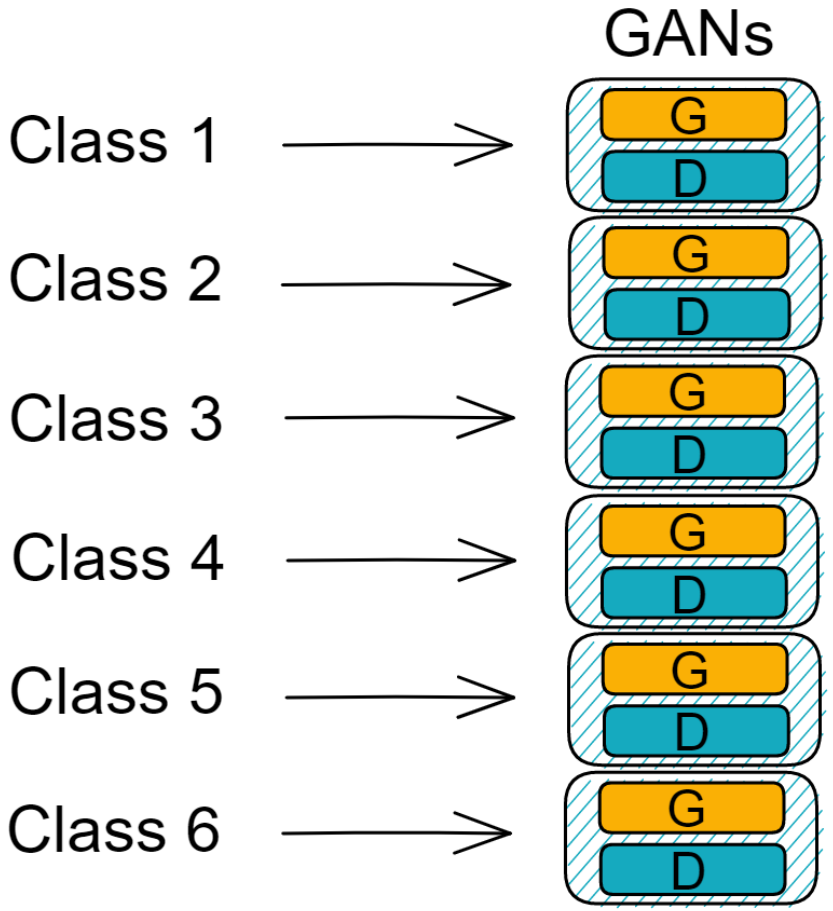


Atrial Fibrillation



Fibrilación Auricular

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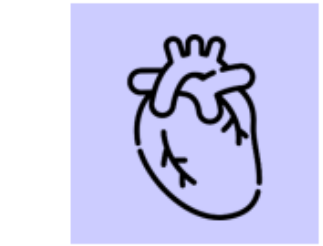
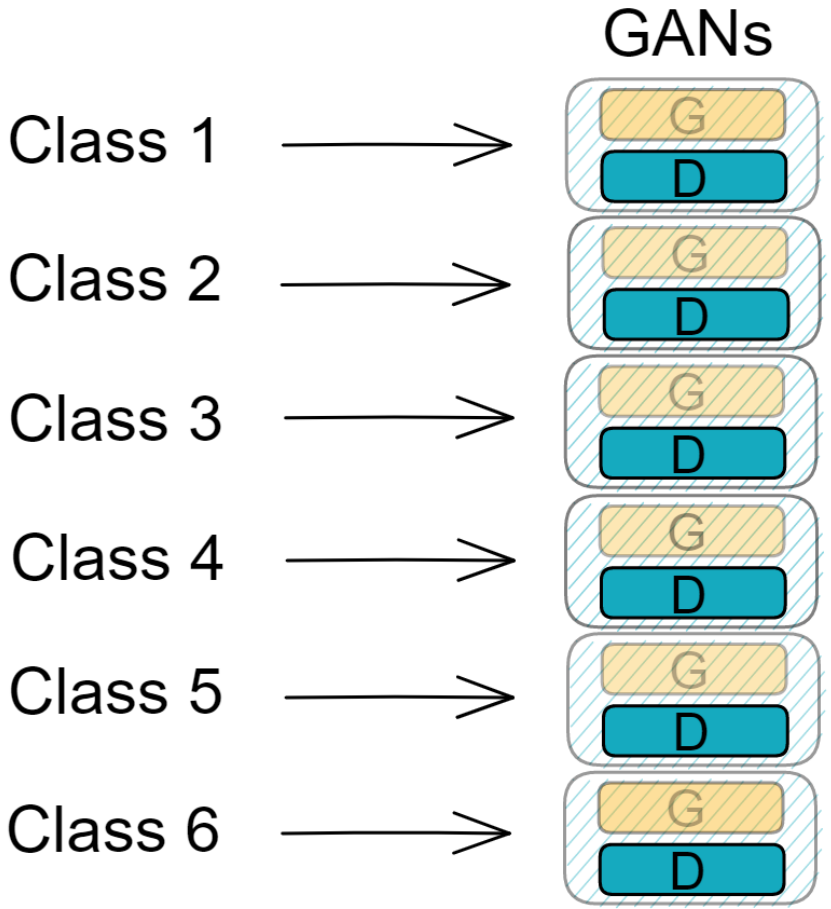


Atrial Fibrillation



Fibrilación Auricular

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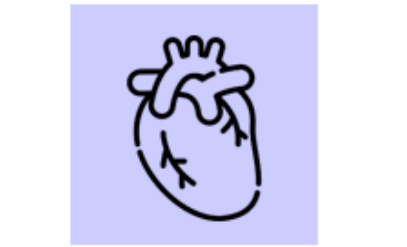
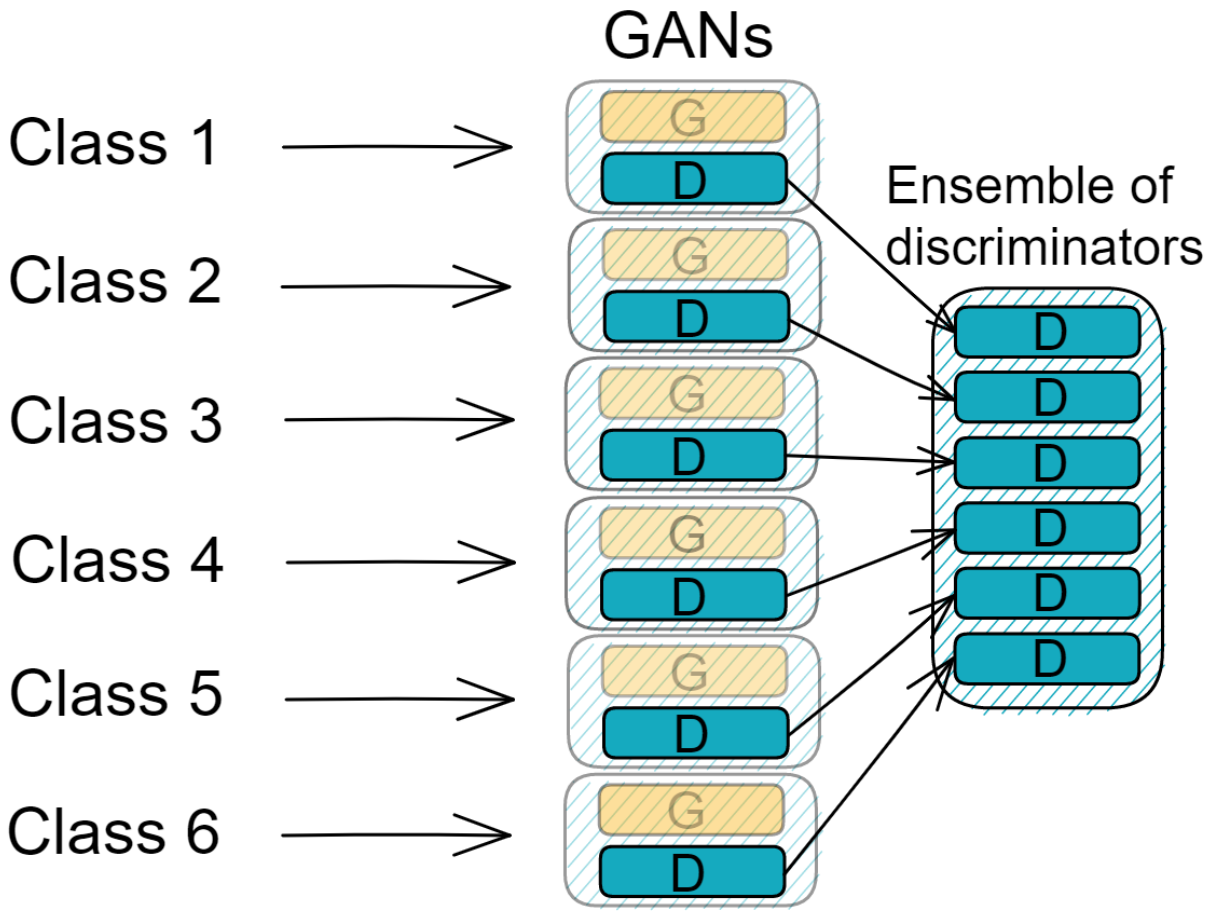


Atrial Fibrillation



Fibrilación Auricular

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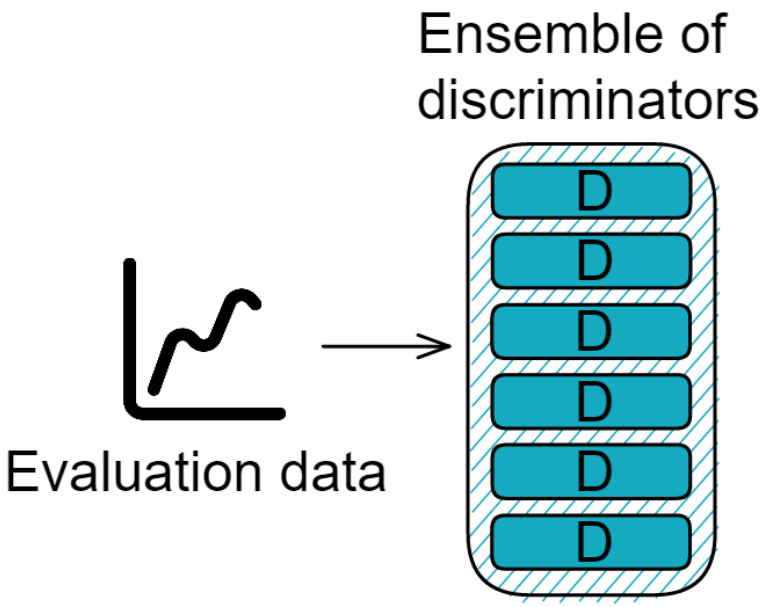
Inteligencia Artificial y Biomedicina



Fibrilación Auricular

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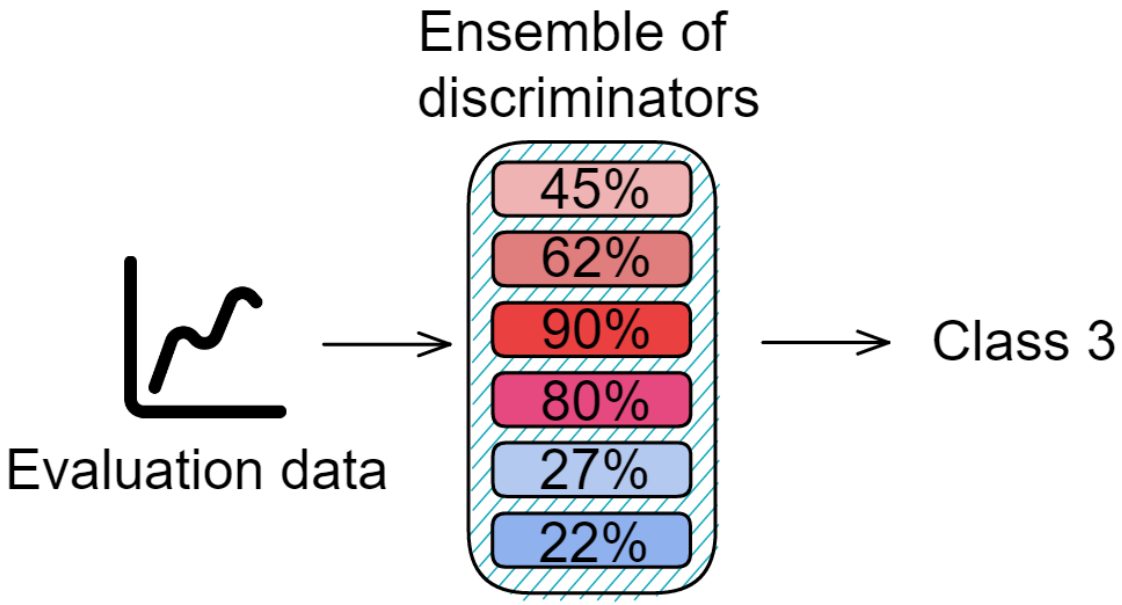
Inteligencia Artificial y Biomedicina



Fibrilación Auricular

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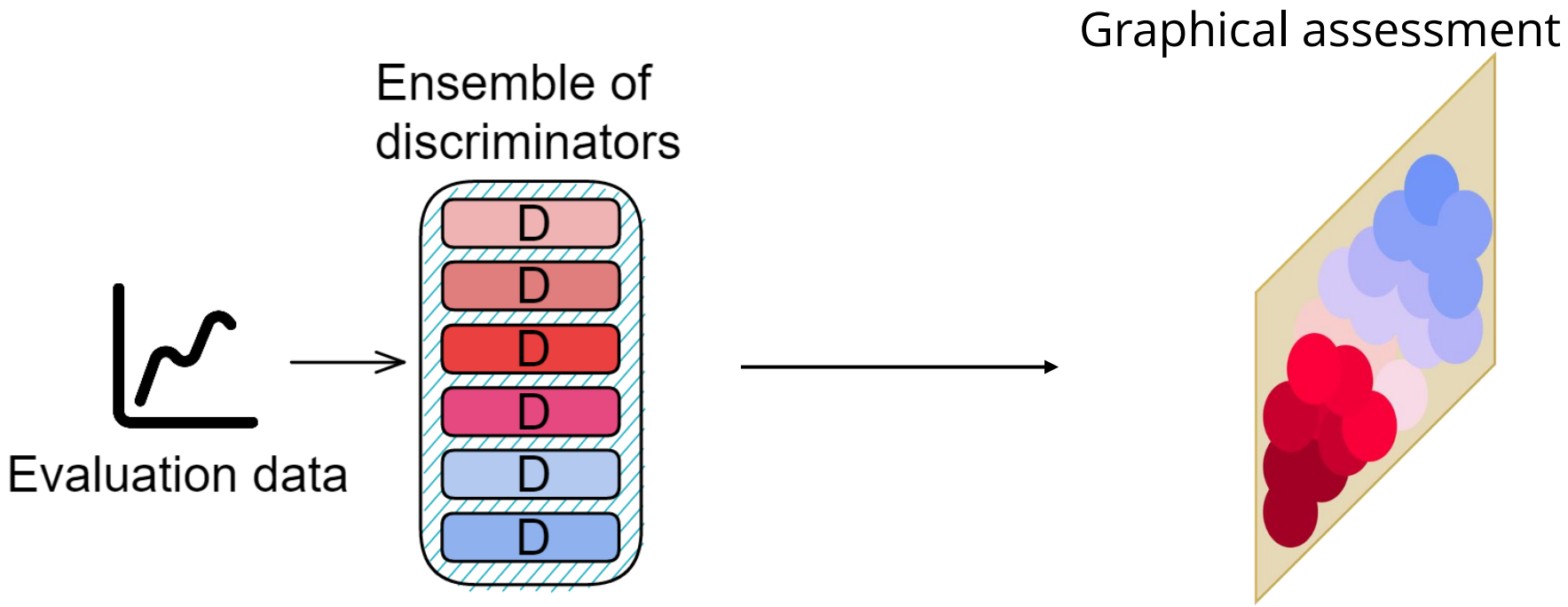
Inteligencia Artificial y Biomedicina



Atrial Fibrillation

Atrial Fibrillation

Class 1

Class 2

Class 3

Class 4

Class 5

Class 6

α = velocidad de progresión hacia arritmia permanente

β = tiempo medio entre episodios de arritmia

Atrial Fibrillation

Atrial Fibrillation

Class 1

Class 2

Class 3

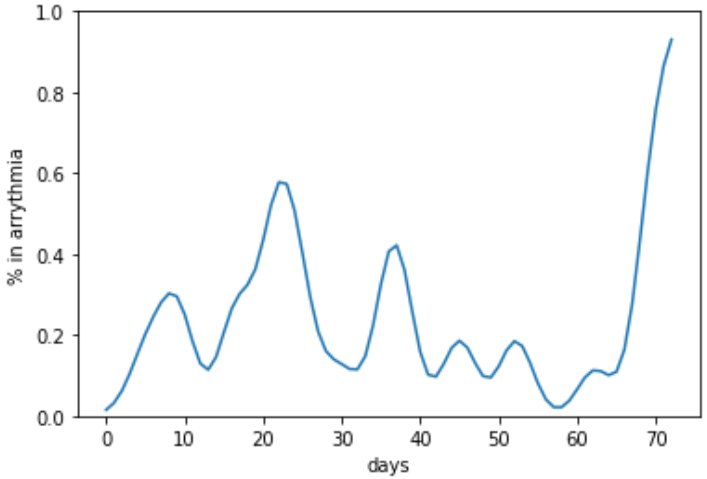
Class 4

Class 5

Class 6

Muchos episodios, progresión rápida hacia permanente

α alta, **β baja**



α = velocidad de progresión hacia arritmia permanente

β = tiempo medio entre episodios de arritmia

Atrial Fibrillation

Atrial Fibrillation

Class 1

Class 2

Class 3

Class 4

Class 5

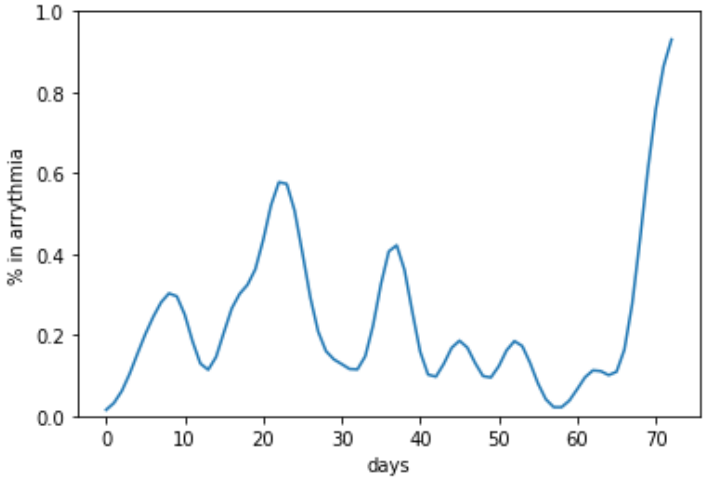
Class 6

α = velocidad de progresión hacia arritmia permanente

β = tiempo medio entre episodios de arritmia

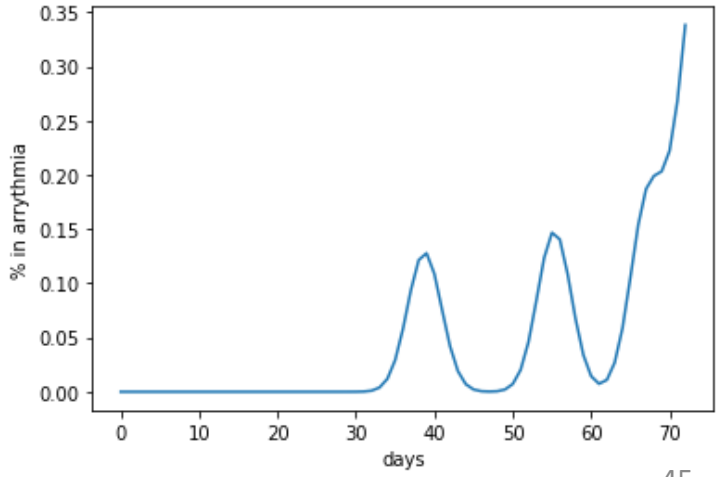
α alta, **β baja**

Muchos episodios, progresión rápida hacia permanente



α baja, β alta

Pocos episodios, pero también progresión rápida hacia permanente



Atrial Fibrillation

Atrial Fibrillation

Class 1

Class 2

Class 3

Class 4

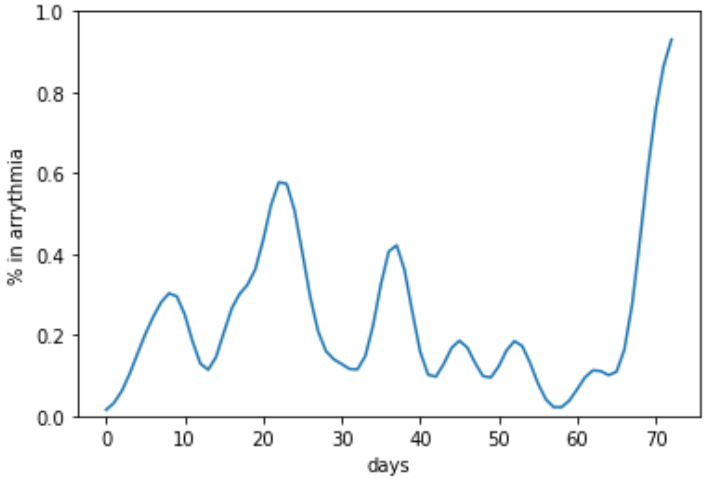
Class 5

Class 6

Criticidad es la misma
Independientemente del
número de episodios

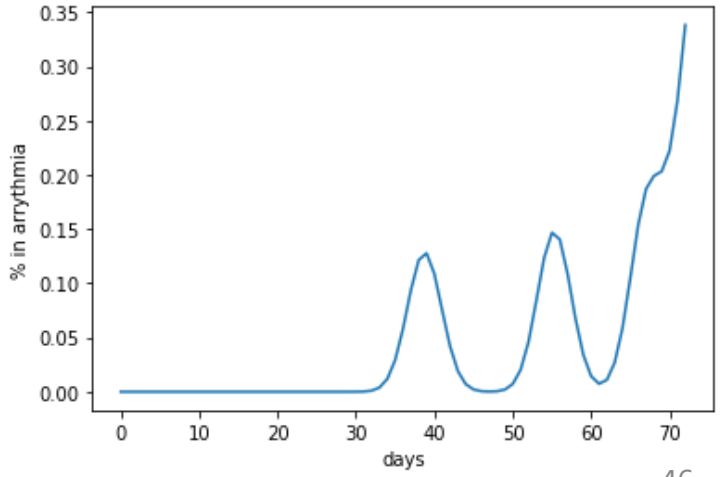
Muchos epidosios,
progresión rápida
hacia permanente

α alta, **β baja**



Pocos episodios,
pero también
progresión rápida hacia
permanente

α baja, β alta



α = velocidad de progresión hacia arritmia permanente

β = tiempo medio entre eposidios de arritmia

Fibrilación Auricular

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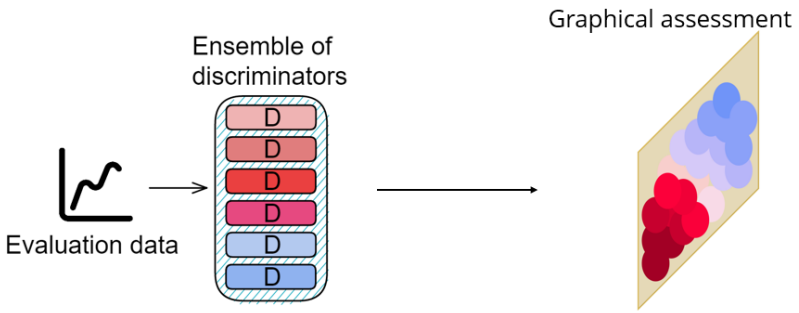
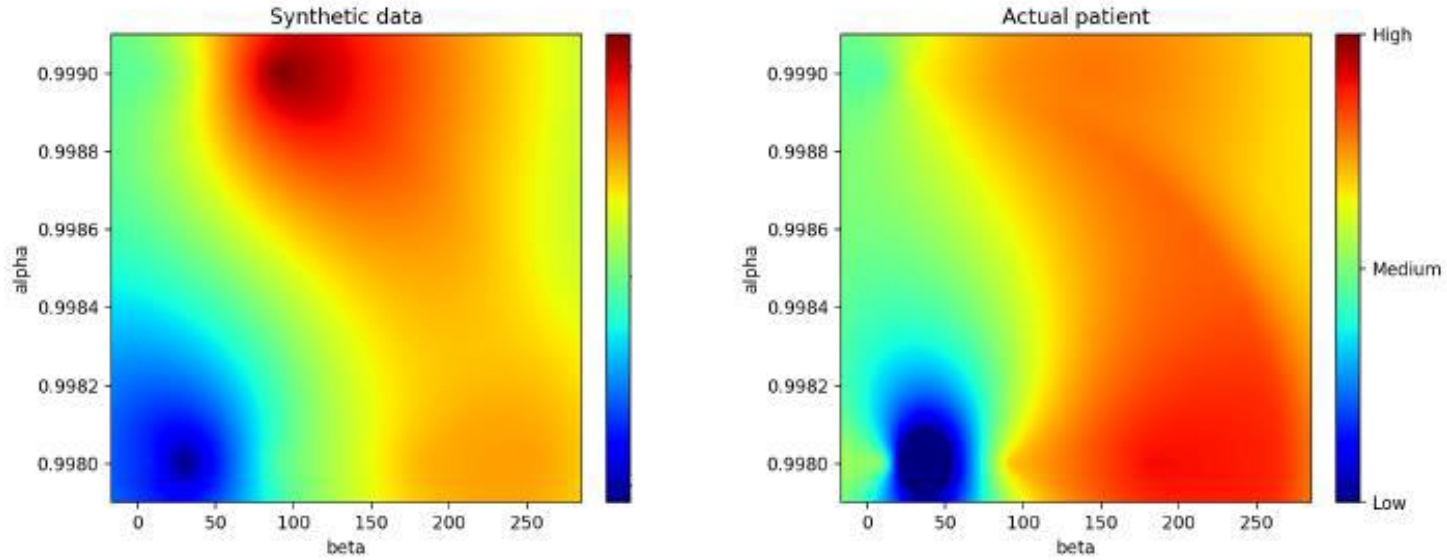
Mapa gráfico de las activaciones de las últimas capas de cada discriminador





Otras aplicaciones

Otras aplicaciones

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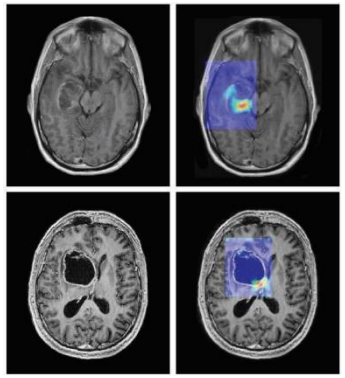
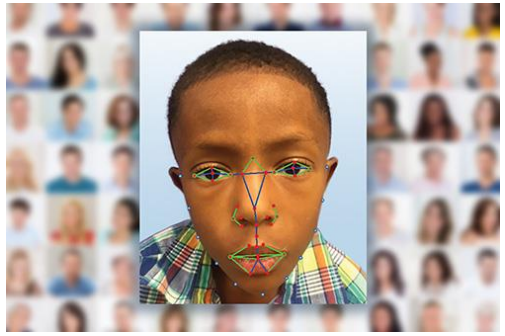


Análisis de imágenes médicas

Tratamientos farmacológicos

Prótesis



Genética

Obstetricia y ginecología

Por dónde empiezo?

Recursos

Andrés Torrubia

Aurelia Bustos

SOFTWARE 2.0

Recursos

Andrés Torrubia

Aurelia Bustos

SOFTWARE 2.0

Jeremy Howard

Rachel Thomas

FASTAI

Recursos

[DotCSV]

Divulgador de Inteligencia Artificial

[La hiperactina]

Divulgadora biomedicina

Recursos

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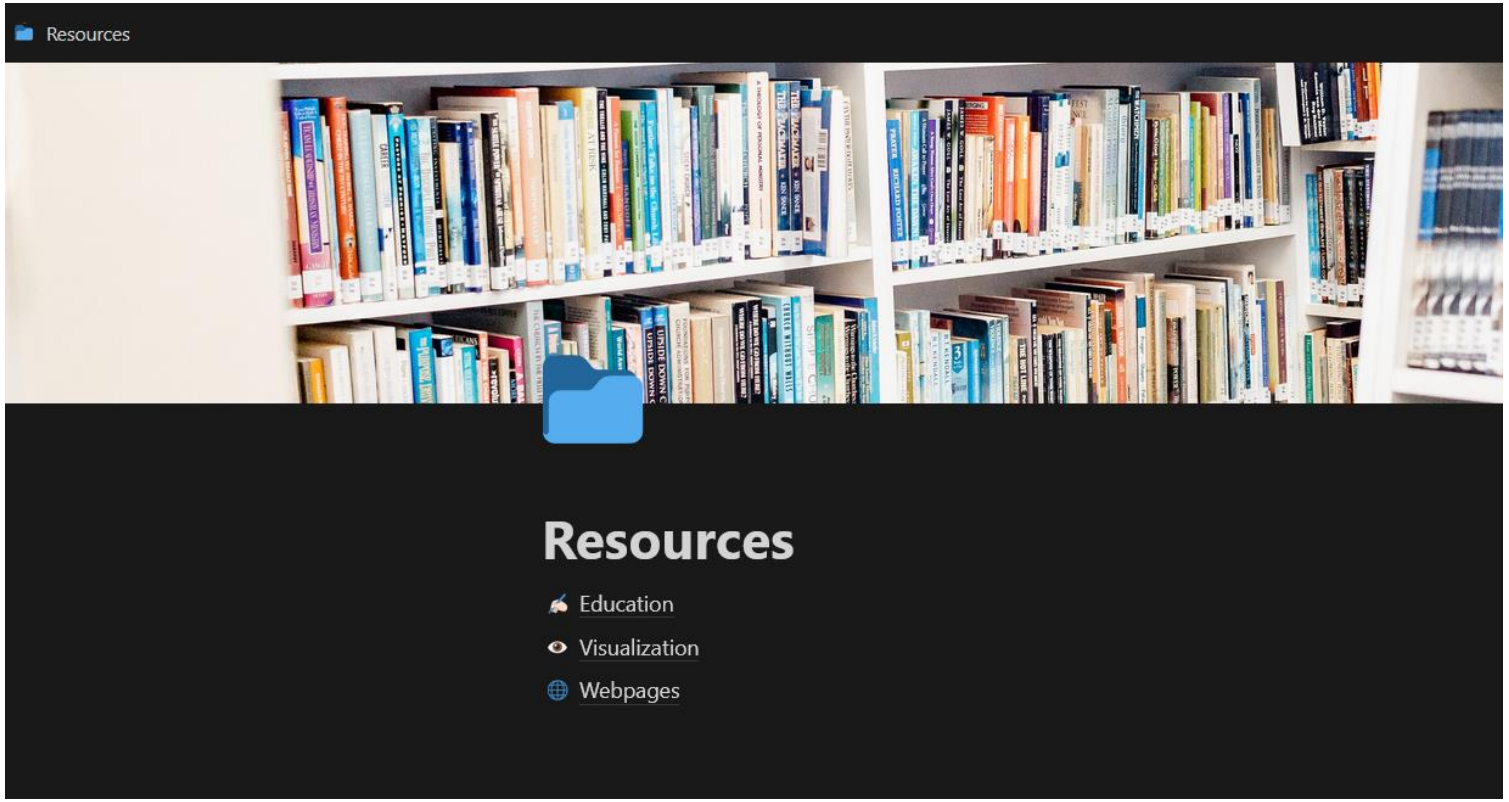
Inteligencia Artificial y Biomedicina

[Lista de recursos]



Perspectivas futuras

Perspectivas futuras

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```
import random
import tensorflow as tf
from tensorflow import keras
from tensorflow.keras.layers import Input, Dense, LSTM, Bidirectional, Masking

# keeping the random seed constant from one experiment to the next makes it
# easier to interpret the effects of hyper-parameters values
seed = 99
random.seed(seed)
tf.random.set_seed(seed)

def create_model(timesteps, input_dim, intermediate_dim, batch_size, latent_dim, epochs,
optimizer): the network parameters:
    timesteps = timesteps
    input_dim = input_dim
    intermediate_dim = intermediate_dim
    batch_size = batch_size
    latent_dim = latent_dim
    epochs = epochs
    if optimizer == 'adam':
        optimizer = keras.optimizers.Adam(learning_rate=0.001)
    else:
        print("unimplemented optimizer")
        exit(-1)
    masking_value = -99.

    class Sampling(keras.layers.Layer):
        """Uses (z_mean, sigma) to sample z, the vector encoding an engine trajetory."""
        def call(self, inputs):
            mu, sigma = inputs
            batch = tf.shape(mu)[0]
            dim = tf.shape(mu)[1]
            epsilon = tf.keras.backend.random_normal(shape=(batch, dim))
            return mu + tf.exp(0.5 * sigma) * epsilon

    # ---------------------- Encoder ----------------------
    inputs = Input(shape=(timesteps, input_dim,), name='encoder_input')

    mask = Masking(mask_value=masking_value)(inputs)

    # LSTM encoding
    h = Bidirectional(LSTM(intermediate_dim))(mask)

    # VAE Z layer
    mu = Dense(latent_dim)(h)
    sigma = Dense(latent_dim)(h)

    z = Sampling()([mu, sigma])

    # Instantiate the encoder model:
    encoder = keras.Model(inputs, [z, mu, sigma], name='encoder')
    print(encoder.summary())
    # -----------------------------------------------------------

    # ---------------------- Regressor --------------------
    reg_latent_inputs = Input(shape=(latent_dim,), name='z_sampling_reg')
    reg_intermediate = Dense(200, activation='tanh')(reg_latent_inputs)
    reg_outputs = Dense(1, name='reg_output')(reg_intermediate)
    # Instantiate the classifier model:
    regressor = keras.Model(reg_latent_inputs, reg_outputs, name='regressor')
    print(regressor.summary())
    # -----------------------------------------------------------
  return go(f, seed, [])
}
```

Perspectivas futuras

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}
```

"Procesa mis datos y aplica una red convolucional para aprender patrones que ayuden a identificar X patología"

Perspectivas futuras

Nahuel Costa
Inteligencia Artificial y Biomedicina

- Creatividad para combinar modelos
- Explicabilidad
- Ética y privacidad