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			sluitingsdag	sluitingsdag		
30	31	1	2	3	4	5




- Theory (50%)
 - morning lectures
 - written exam

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			sluitingsdag	sluitingsdag		
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- Theory (50%)
 - morning lectures
 - written exam
- Project (15%)
 - notebooks:
 - splice site classification
 - data clustering

maandag	dinsdag	woensdag	donderdag	vrijdag	zaterdag	zondag
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- Theory (50%)
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- Micro-teaching (15%)
 - short presentation about specific ML method

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- Theory (50%)
 - morning lectures
 - written exam
- Project (15%)
 - notebooks:
 - splice site classification
 - data clustering
- Micro-teaching (15%)
 - short presentation about specific ML method
- Kaggle contest (20%)
 - short report on best result (written/oral)?

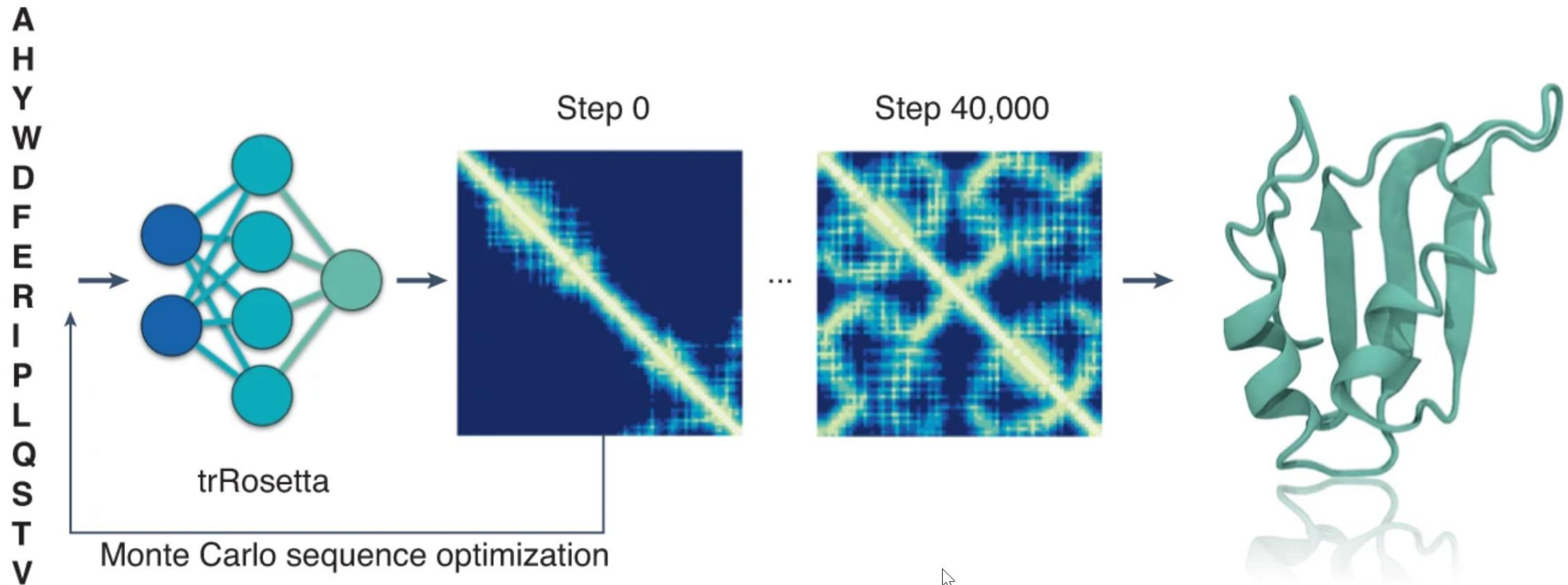
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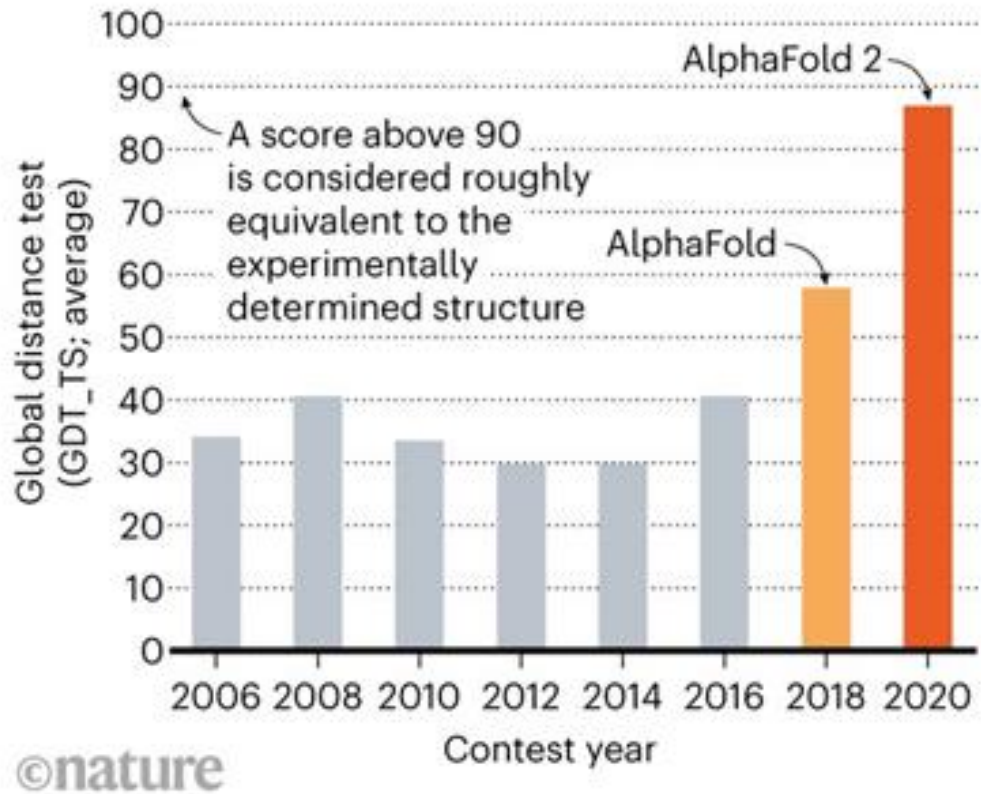
- Major internship
 - TRIM32 interactions
 - AlphaFold2
 - write a paragraph

Random
sequence

De novo
structure



Random amino acid sequences are generated; here a single sequence is shown. These sequences are fed into the trRosetta structure-prediction convolutional neural network. The first predictions (step 0) lead to distance maps with no strong patterns. After a Monte Carlo sampling where the contrast between the trRosetta-predicted distribution of distances and a background distribution is optimized, new sequences are produced in a step-wise manner. The final distance maps (step 40,000) are feature-rich and lead to well-structured de novo proteins.

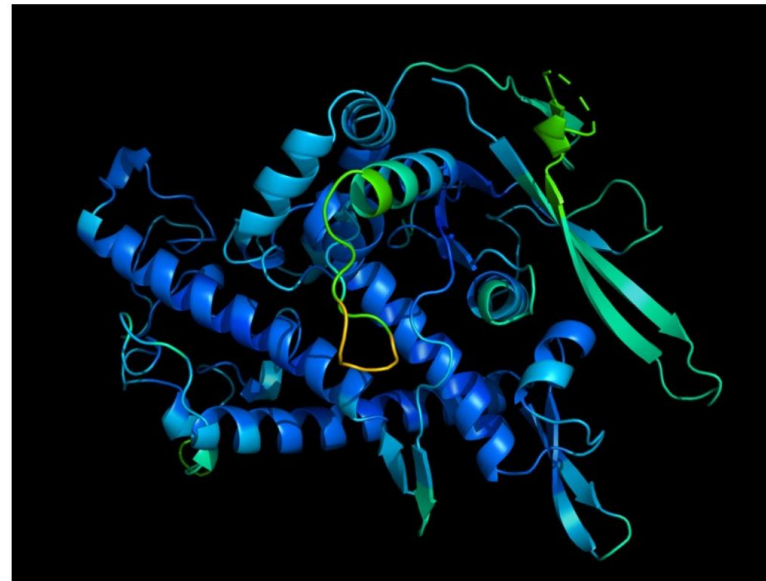


NEWS | 30 November 2020

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Google's deep-learning program for determining the 3D shapes of proteins stands to transform biology, say scientists.

Ewen Callaway



A protein's function is determined by its 3D shape. Credit: DeepMind

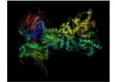
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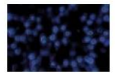
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The computational protein designers



Revolutionary microscopy technique sees individual atoms for first time



Subjects

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Drug discovery

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3D viewer

Model Confidence:

- Very high (pLDDT > 90)
- Confident (90 > pLDDT > 70)
- Low (70 > pLDDT > 50)
- Very low (pLDDT < 50)

AlphaFold produces a per-residue confidence score (pLDDT) between 0 and 100. Some regions below 50 pLDDT may be unstructured in isolation.

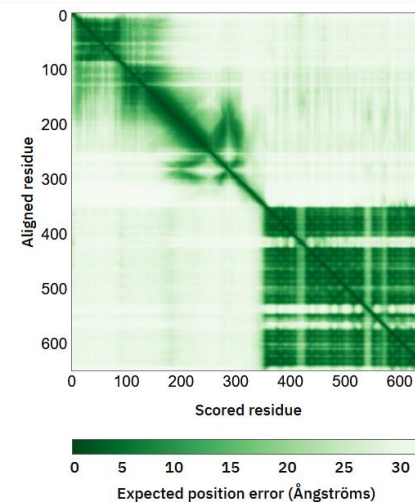
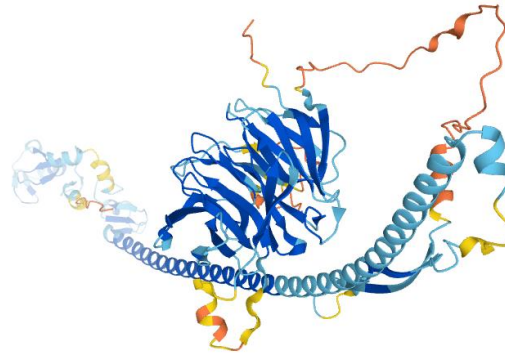
Views

Predicted aligned error

Sequence Features (coming soon)

Sequence of AF-Q13049-F1 1: E3 ubiquitin... A

```
1 11 21 31 41 51 61 71 81 91 101 111 121
MAAAAASHNLDALEVLKLEPICMESFTTEQLRPLKLLHCGHTICRQCLEKLLASSINGVRCFPCSKITRITSLTQLTDNLTVLKIIDTAGLSEAVGLLMCRSCGRRLPQFCRSCGLVLCPEP
131 141 151 161 171 181 191 201 211 221 231 241
CREADHQPFGHCTLPVKEAAEERRRDFGEKLTRELIMGELQRRKAALEGVSKDLQARYKAVLQYGHERRVQDELARSRKFFTGSLAEVEKSNQVVEEQSYLLNIAEVQAVSRCDYFLA
251 261 271 281 291 301 311 321 331 341 351 361
KIQQADVALLEETADEEFELTASLPRELTLQDVELLKVGHVGLQIGQAVKKPRTVNVEDSWAMEATASAASTSVTFREMDMSPEEVVASPRASPAKQGPAAASNIQQCLFLKRMGAKGS
```



<https://alphafold.ebi.ac.uk/>

https://scikit-learn.org/stable/ 110%

scikit-learn
Machine Learning in Python

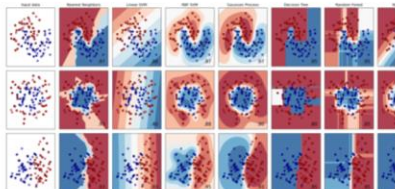
Getting Started Release Highlights for 1.0 GitHub

- Simple and efficient tools for predictive data analysis
- Accessible to everybody, and reusable in various contexts
- Built on NumPy, SciPy, and matplotlib
- Open source, commercially usable - BSD license

Classification

Identifying which category an object belongs to.

Applications: Spam detection, image recognition.
Algorithms: SVM, nearest neighbors, random forest, and more...

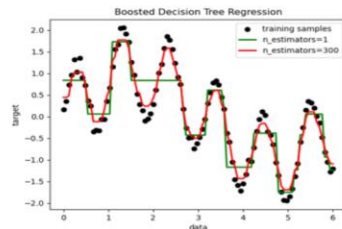


Examples

Regression

Predicting a continuous-valued attribute associated with an object.

Applications: Drug response, Stock prices.
Algorithms: SVR, nearest neighbors, random forest, and more...

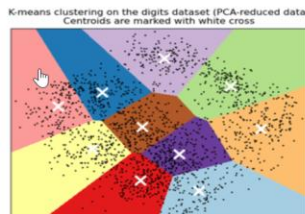


Examples

Clustering

Automatic grouping of similar objects into sets.

Applications: Customer segmentation, Grouping experiment outcomes
Algorithms: k-Means, spectral clustering, mean-shift, and more...

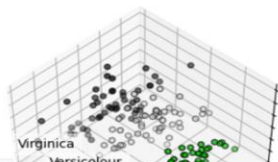


Examples

Dimensionality reduction

Reducing the number of random variables to consider.

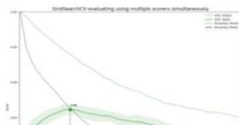
Applications: Visualization, Increased efficiency
Algorithms: k-Means, feature selection, non-negative matrix factorization, and more...



Model selection

Comparing, validating and choosing parameters and models.

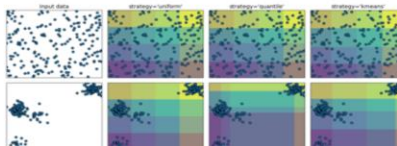
Applications: Improved accuracy via parameter tuning
Algorithms: grid search, cross validation, metrics, and more...



Preprocessing

Feature extraction and normalization.

Applications: Transforming input data such as text for use with machine learning algorithms.
Algorithms: preprocessing, feature extraction, and more...



1.1 Linear regression

In the introduction we constructed an instrument to **classify** a raw dermoscopic image of a lesion as either benign or malignant. This required some kind of decision boundary that **separates** these classes as good as possible.

Suppose we were asked to implement a similar approach to predict the survival time of stage III melanoma patients. In this case the data points will be labeled with a **continuous value** that represents this survival time, i.e. there are no classes.

In statistics and machine learning modeling a continuous value is known as **regression**. Typical regression tasks include modeling drug effectiveness, toxicity, disease progression, and survival times. In genomics, transcriptomics and proteomics regression is successfully applied to for instance calibrate and align experiments, assess data quality, and predict expression levels. Regression is a general term for **modeling the relationship** between a **target** (or **dependent variable**) and one or more **features** (or the **independent** or **explanatory variable(s)**).

To explain regression data analysis we first open a data set that contains relevant information for about 442 patients that are diagnosed with diabetes disease. Each patient is a data point in this data set and is described by 11 features that measure age (AGE), sex (SEX), body mass index (BMI), average blood pressure (BP), together with six blood serum measurements (Sx) as well as the target (Y) that represents a quantitative measure of disease progression one year after baseline.

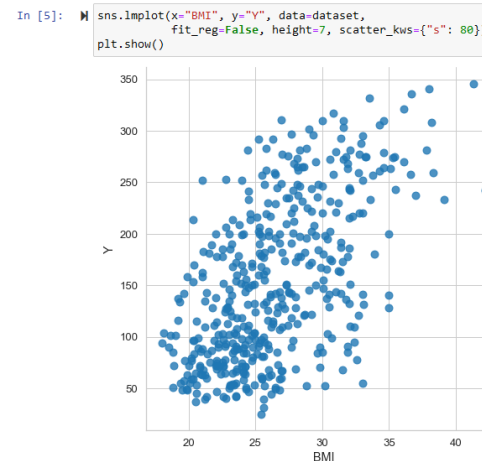
```
In [4]: dataset = pd.read_csv('https://raw.githubusercontent.com/sdgroeve/Machine_Learning_course_UGent_D012554_data/master/notebook_data.csv')
print(dataset.head())
print()
print("Shape of data set: " + str(dataset.shape))
```

	AGE	SEX	BMI	BP	S1	S2	S3	S4	S5	S6	Y
0	59	2	32.1	101.0	157	93.2	38.0	4.0	4.8598	87	151
1	48	1	21.6	87.0	183	103.2	70.0	3.0	3.8918	69	75
2	72	2	30.5	93.0	156	93.6	41.0	4.0	4.6728	85	141
3	24	1	25.3	84.0	198	131.4	40.0	5.0	4.8903	89	206
4	50	1	23.0	101.0	192	125.4	52.0	4.0	4.2905	80	135

Shape of data set: (442, 11)

The data set was created because diabetes disease progression Y observed for a patient is assumed to be dependent on one or more of the features and we want to know what this potential relationship looks like. Can the exploratory variables **explain** the values observed for Y? If they do then we can use this explanation to **predict** diabetes disease progression for future unseen external patients.

We could for instance ask ourselves how Y varies with the Body Mass Index (BMI) of a patient? So can we explain disease progression in terms of the BMI? To investigate this we plot the relationship between BMI and Y for the patients in the data set in a scatter plot.




Just by looking at this patient data we can already see a trend: values for Y seem to be larger for larger values of the BMI. From this data we can estimate or **model** the relationship between the BMI and diabetes disease progression Y, assuming that there is one. Such a **regression model** explains Y in terms of BMI.

To compute such a model, we need to make **assumptions about the true underlying model that generated the data**. A common and straightforward assumption is that the relationship between the two variables is **linear**, i.e. disease progression varies linearly with the BMI.

In this case we use the term **linear regression model** that assumes that the target varies linearly with the features. **Fitting** a linear regression model is known **linear regression**.

To correctly apply linear regression we need to normalize the features.

From scikit learn we use the `StandardScaler` module to standardize the features and the target. We first create `StandardScaler` objects



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Code

 **svendegroeve** updated to 2022


164b3a1 3 minutes ago 109 commits

	notebooks	updated to 2022	3 minutes ago
	practicum/Classification	updated to 2022	3 minutes ago
	slides	initial commit	2 years ago
	README.md	initial commit	2 years ago
	environment.yml	initial commit	2 years ago

README.md

D012554

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GettingStarted Prediction Competition

Spaceship Titanic

Predict which passengers are transported to an alternate dimension

 Kaggle · 1,776 teams · Ongoing

OverviewDataCodeDiscussionLeaderboardRulesTeam

My Submissions









Submit Predictions

...

Leaderboard

[Raw Data](#)[Refresh](#)

This leaderboard is calculated with all of the test data.

#	Team	Members	Score	Entries	Last	Code
1	Rizky R&F YS		0.81669	166	7d	
2	Karl Cini		0.81669	102	4m	
3	CADang		0.81646	201	11h	
4	enescnkr		0.81505	67	3d	
5	Mukharbek Organokov		0.81482	10	21d	
6	Marcello Gomitoni		0.81458	90	1mo	
7	John Mitchell		0.81458	8	6d	< >
8	Deepak Kaura		0.81458	4	5d	

<https://www.kaggle.com/competitions/spaceship-titanic/>

- Sections

- EDA -> description of the features and the target
- Pre-processing (missing values, feature scaling)
- Feature engineering
- Hyperparameter optimization
- Model performance comparison (does your performance estimation match the observed leaderboard score)

- Grades

- Protocol (10)
- Clarity of the report (5)
- Effort (5)