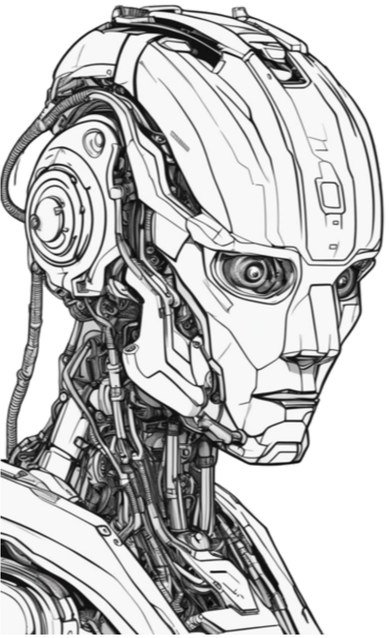
ICG INSTITUTE FOR COMPARATIVE GENOMICS

DALHOUSIE UNIVERSITY
FACULTY OF MEDICINE

ACENET
accelerate discovery



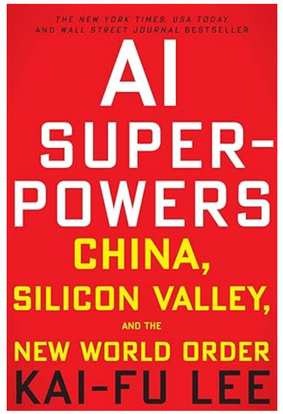
Artificial Intelligence Meets Biology

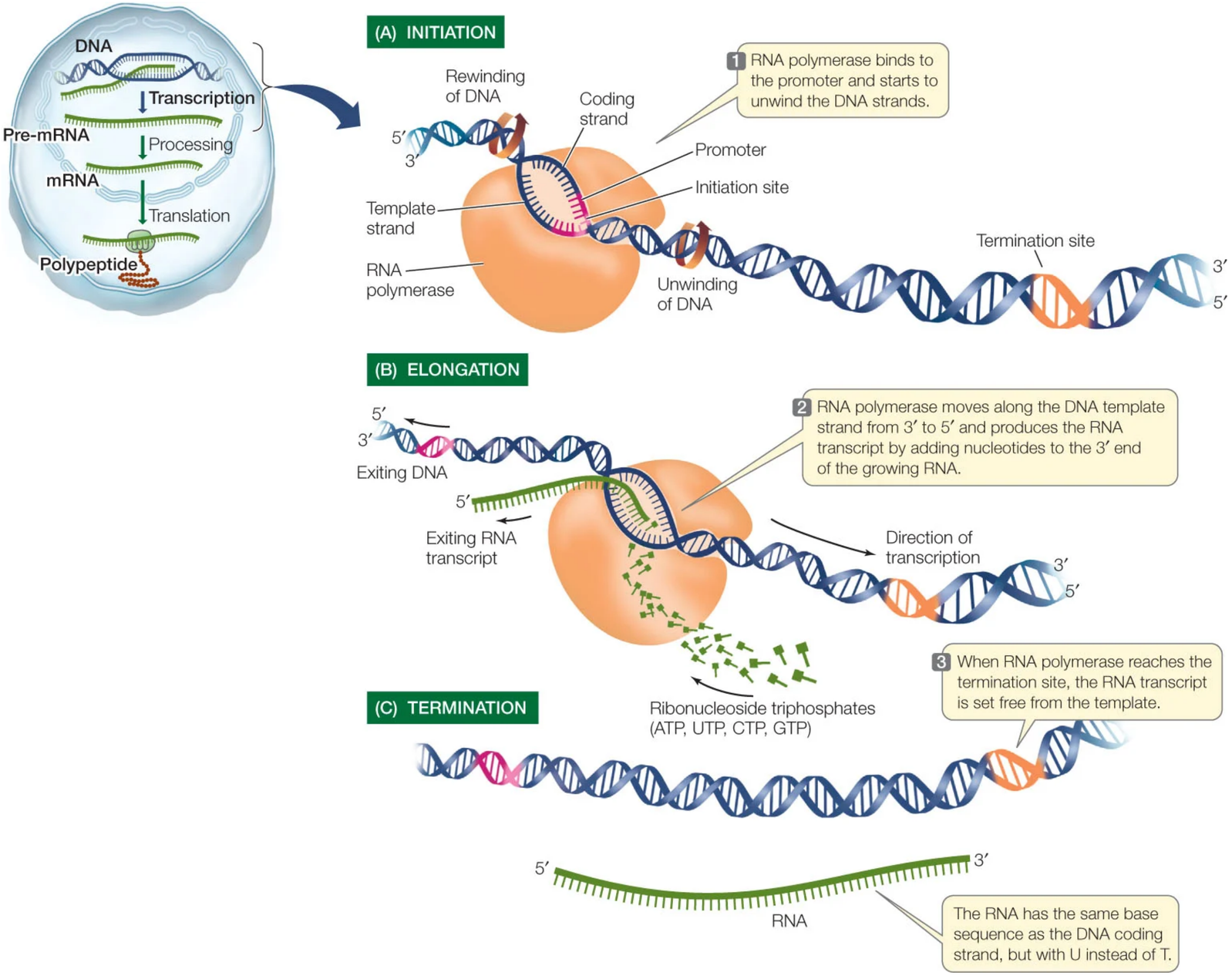
AI-based prediction of genomic elements.

Dr. Gustavo Sganzerla Martinez

“[...] with more data, an algorithm projected mid a mid-level team of engineers generally is better than one projected by an elite team of engineers.

Having the monopoly of the most brilliant minds does not mean having the best results.”





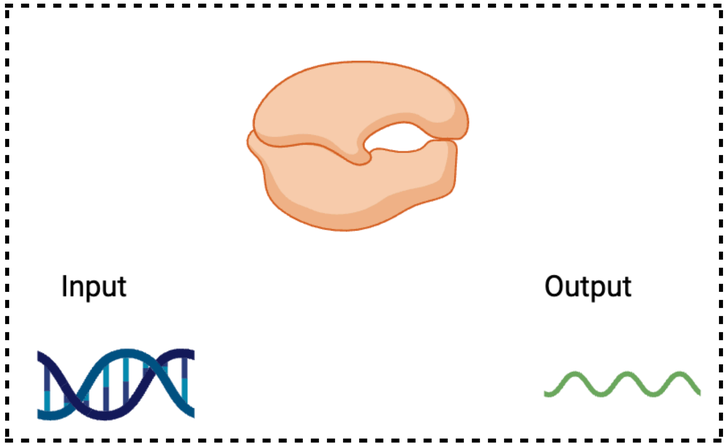
Aryal, 2022. *Microbe Notes*

system ☆

/ ˈsɪstəm /

noun

1 a group or combination of interrelated, interdependent, or interacting elements forming a collective entity; a methodical or coordinated assemblage of parts, facts, concepts, etc



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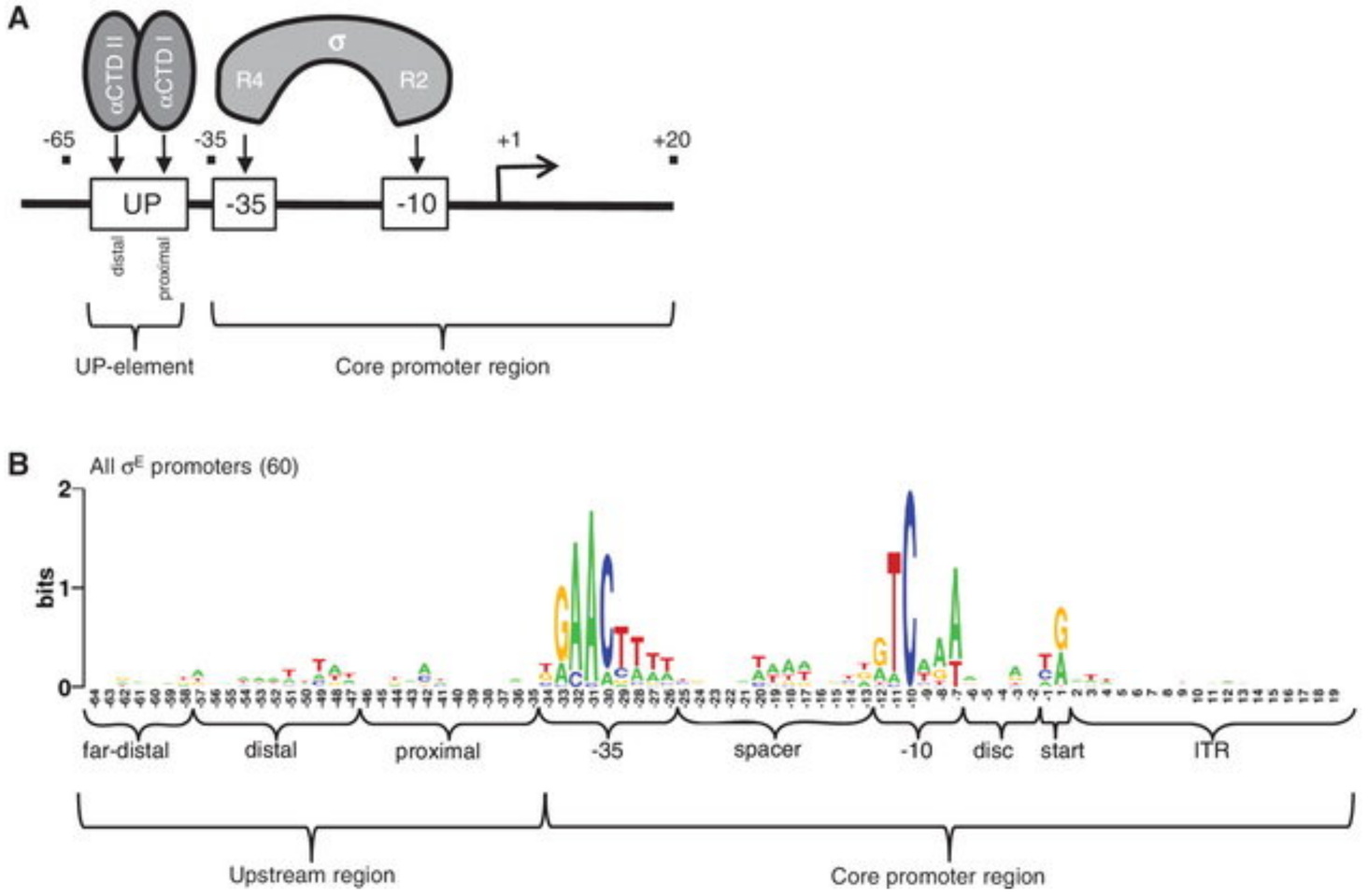
“Regulation of the gene expression ensures the right gene is expressed at the right moment.”

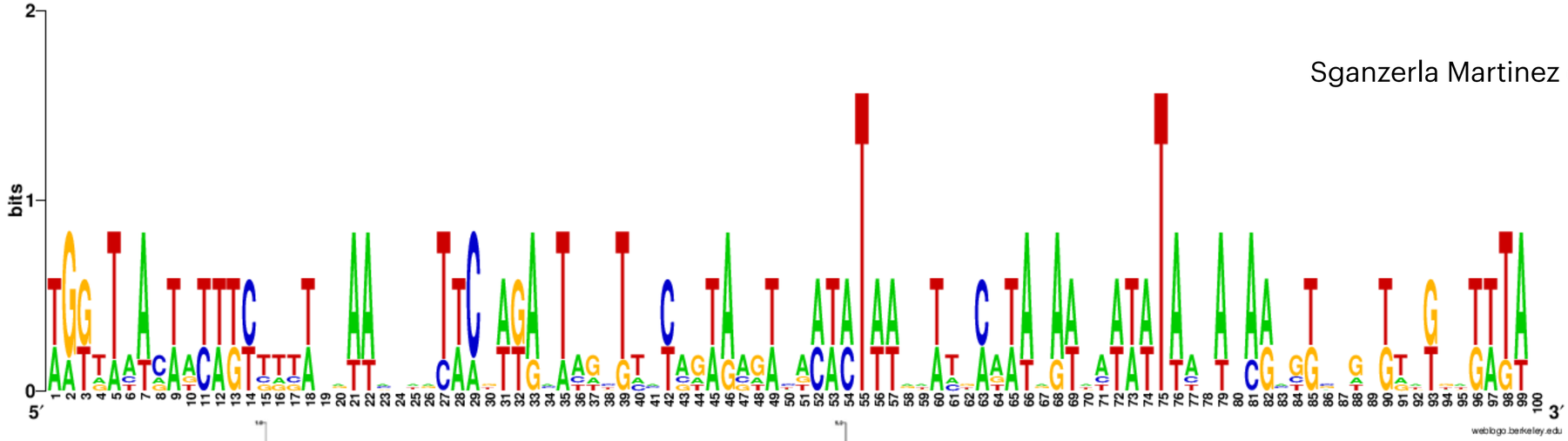


Rhodius *et* al, 2011. *Nucleic Acids Research*

Promoters are conserved DNA segments

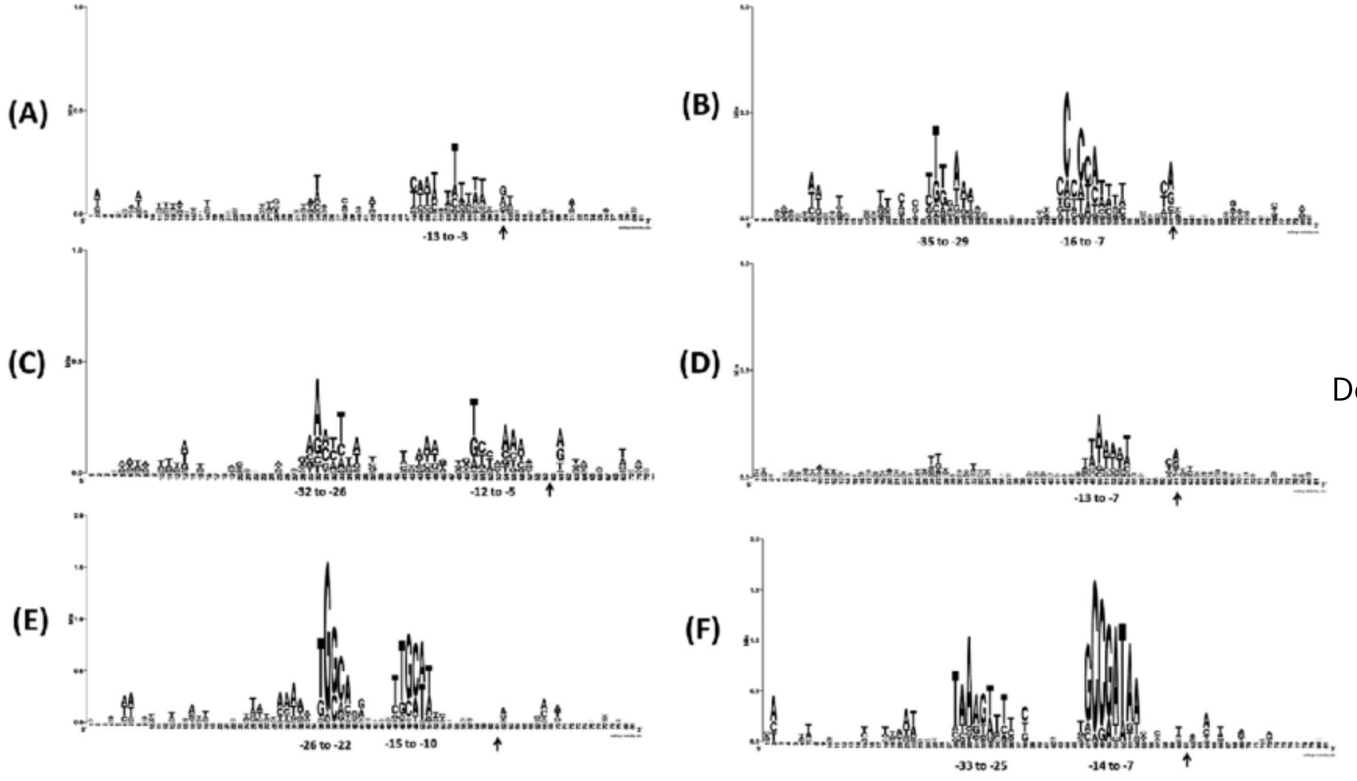
Archaea

Sganzerla Martinez et al, 2024. *Unpublished*



Bacteria

De Avila e Silva et al, 2013. *Biologicals*



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Where does AI fit in?

What is AI? IBM, 2024.

Artificial intelligence, or AI, is technology that enables computers and machines to simulate human intelligence and problem-solving capabilities.

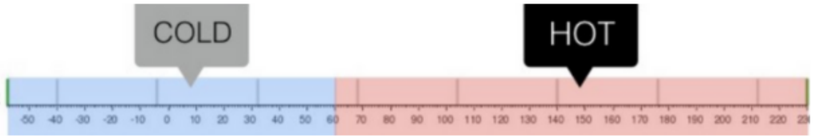
Regression

What will be the temperature tomorrow?

Fahrenheit

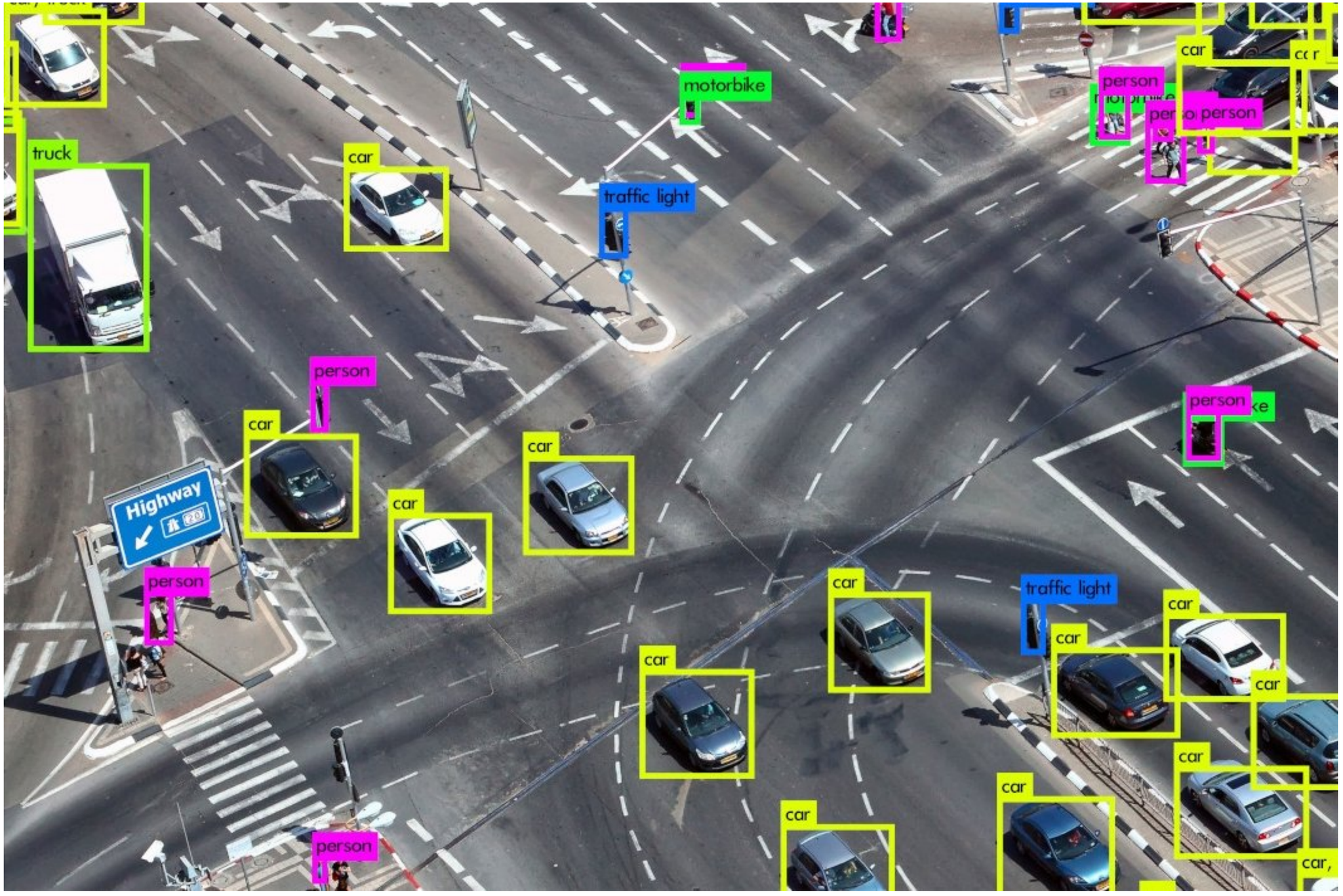
Classification

Will it be hot or cold tomorrow?



Fahrenheit

- Disease severity;
- Gene expression prediction;
- Population growth;
- Is a sequence a promoter?


motorbike
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Highway
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traffic light
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person
car,

martinez.ace-net.training

usernames: user[001-099]

password: scarcely.daily.caring.redfish

X and y

f(x) = y

	0	1	2	3	4	5	6	7	8	9	...	50	51	52	53	54	55	56	57	58	label
0	-1.45	-1.30	-2.27	-1.28	-1.44	-2.27	-1.84	-2.24	-1.84	-1.44	...	-1.84	-1.30	-1.30	-1.44	-1.28	-1.28	-1.44	-1.30	-1.45	1
1	-1.28	-2.24	-1.30	-0.88	-1.28	-1.45	-1.00	-1.45	-1.28	-1.28	...	-1.30	-1.84	-1.30	-1.45	-1.28	-1.44	-1.84	-1.30	-0.88	1
2	-1.45	-1.45	-1.28	-0.58	-1.45	-1.45	-1.30	-1.44	-1.00	-0.58	...	-1.00	-1.44	-1.30	-1.30	-1.84	-1.30	-1.00	-0.88	-1.00	1
3	-0.88	-0.58	-0.88	-1.44	-1.84	-2.27	-1.84	-1.45	-1.45	-2.24	...	-2.27	-1.84	-1.45	-1.45	-1.45	-1.00	-1.00	-1.00	-1.00	1
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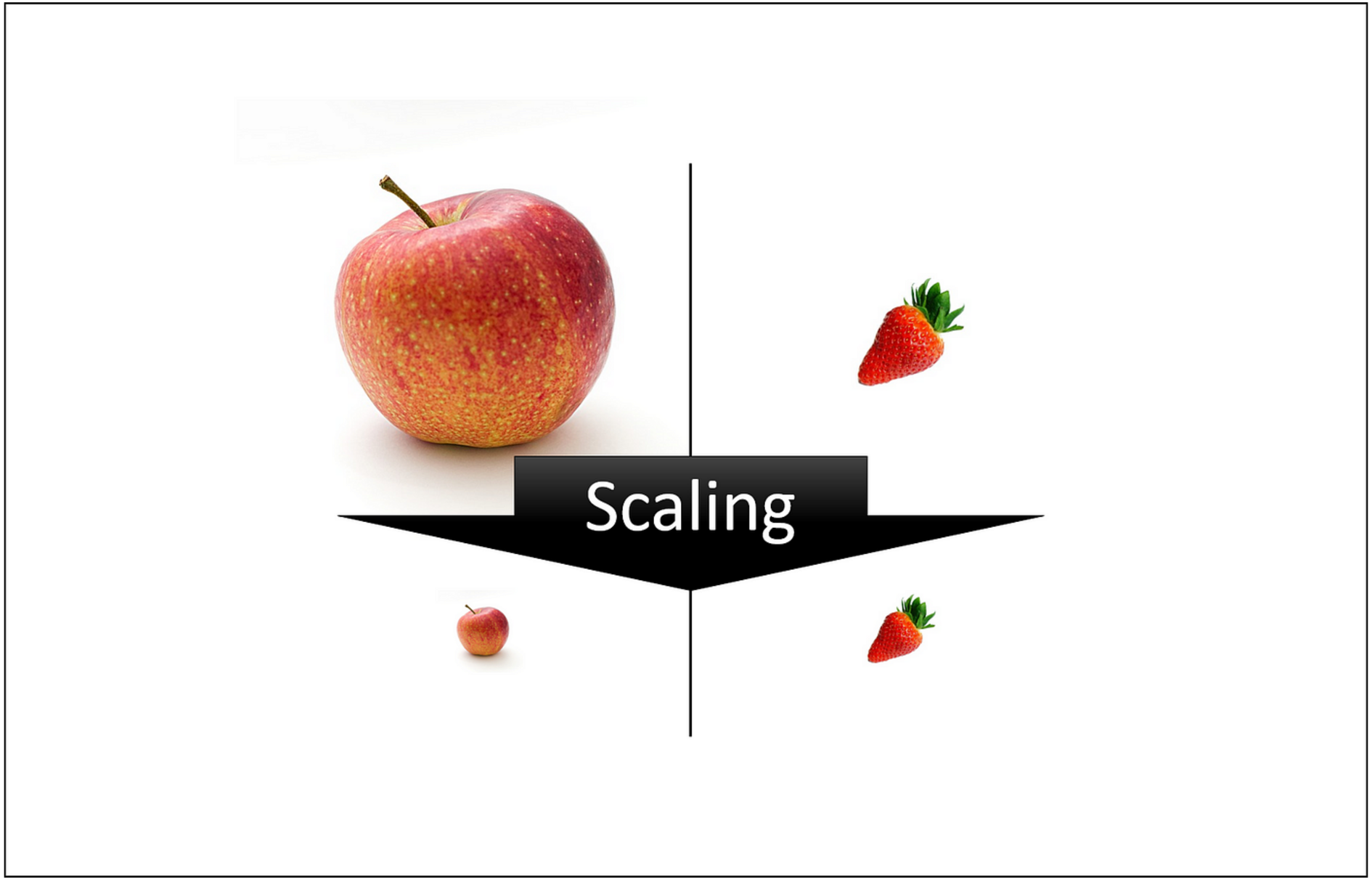
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...
3645	-0.88	-0.58	-1.30	-1.44	-0.58	-0.88	-1.28	-2.24	-2.27	-1.28	...	-1.00	-0.58	-0.88	-0.58	-0.88	-0.58	-1.00	-1.00	-1.00	0
3646	-1.00	-0.88	-1.00	-1.00	-0.58	-1.45	-1.84	-1.28	-0.58	-1.45	...	-1.84	-1.45	-1.30	-1.30	-0.88	-1.00	-1.28	-1.84	-1.45	0
3647	-1.30	-1.30	-1.30	-1.45	-1.28	-0.58	-1.30	-1.30	-0.88	-1.00	...	-0.88	-1.00	-1.44	-1.44	-1.00	-1.00	-0.58	-1.45	-2.24	0
3648	-1.28	-1.28	-1.45	-0.88	-1.00	-1.00	-1.44	-1.84	-1.30	-0.88	...	-0.88	-1.28	-2.24	-1.44	-1.28	-1.84	-2.24	-1.44	-1.00	0
3649	-1.00	-1.30	-1.30	-1.00	-0.88	-1.28	-1.28	-1.00	-0.58	-0.88	...	-1.44	-1.00	-1.44	-1.44	-1.00	-0.58	-0.88	-0.58	-1.45	0

3650 rows × 60 columns

Data scaling



Measuring binary classification performance

actual vs predicted

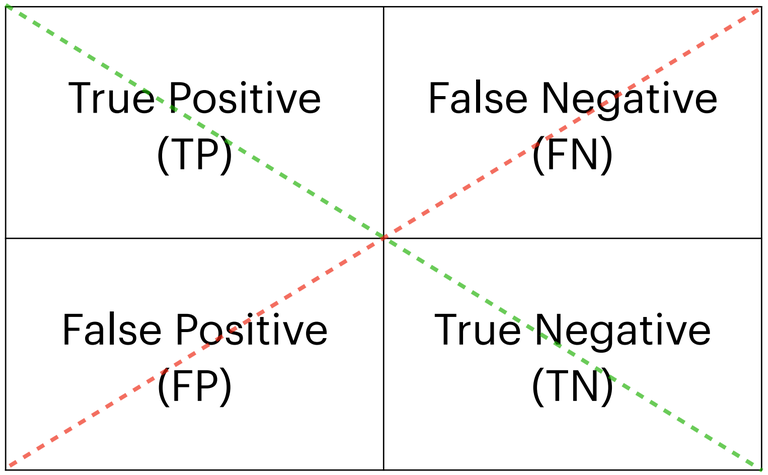
TP = promoter classified as *promoter*

TN = non-promoter classified as *non-promoter*

FP = non-promoter classified as *promoter*

FN = promoter classified as *non-promoter*

confusion matrix



accuracy = (TP+TN)/(TP+TN+FP+FN)

precision = TP/(TP+FP)

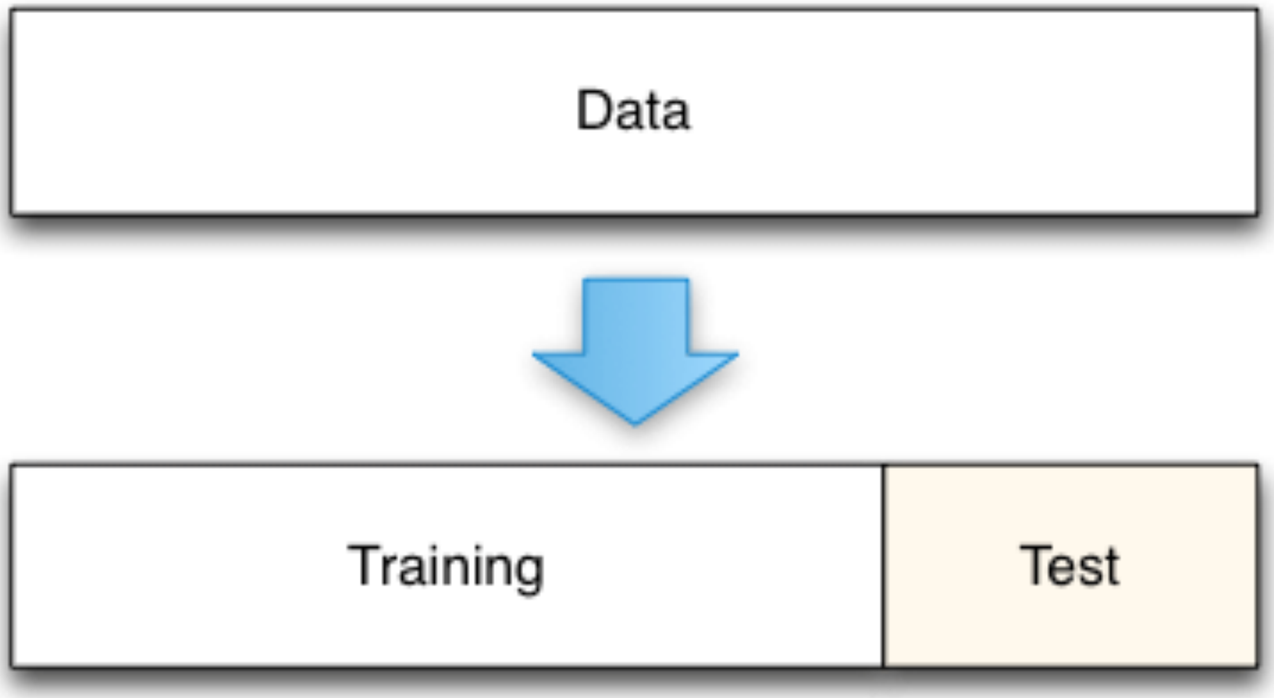
recall = TP/(TP+FN)

specificity = TN/(TN+FP)

main diagonal (correct)

opposing diagonal (incorrect)

Data split



Model interpretation