### AI in medicinal products

**Liam Childs** Artificial Intelligence and Big Data Working Group

Bundesinstitut für Impfstoffe und biomedizinische Arzneimittel Federal Institute for Vaccines and Biomedicines



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#### Outside



#### Inside



Not medical devices (please see BfArM)

**Authorisation** 



# **INTRODUCTION TO AI**

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### What is artificial intelligence?

*"AI is the simulation of human-like intelligence using computer systems"* 

"Al is the use of computers to perform tasks that require human-like intelligence"



"AI combines computer science and robust datasets to enable problem solving"

"Artificial intelligence (AI) is the intelligence of machines or software, as opposed to the intelligence of humans or animals."



#### A step: the atomic unit of data science





#### Bioinformatics: Data science using biological data





### AI: Data science using machine learning





### AI: Data science using machine learning



AI in medicinal products | Liam Childs | FoG3 - AI



## The hype around AI





### What is machine learning?





# Training and Testing





#### Performance measures

	F	Predicte	ed
ved		0	1
ser	0	ΤN	FP
<b>O</b> p	1	FN	TP

Precision (P)	TP/(TP+FP)	How many of the positive predictions are true?
Recall (R)	TP/(TP + FN)	How many of the observed positives did we predict?
F1-Value	$\frac{2PR}{P+R}$	How well are precision and recall balanced?

All measures range between 0 and 1, where 1 is the best performance.

Performance measures come in pairs (e.g. sensitivity/specificity).

Optimising one measure usually requires compromises on the other.

Algorithms are never perfect (you should rarely see a "1").



#### Assessments at the Paul Ehrlich Institute

#### Regulatory Assessments of Bioinformatics and Artificial Intelligence





# AI IN MEDICINAL PRODUCT LIFECYCLE



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#### Medicinal Product Lifecycle





# AI in drug discovery



Mesrabadi et. al. (2023) J. Drug-target interaction prediction based on protein features, using wrapper feature selection. Sci Rep



## AI in manufacturing



#### **Quality assurance of tablet coating quality**



Hirschberg et. al. (2020) Image-Based Artificial Intelligence Methods for Product Control of Tablet Coating Quality. pharmaceutics



#### AI in biomedicines

Machine learning can learn subtle and complex patterns in high dimensional spaces connecting measurements with outcomes

There are many tools and models available

Machine learning has made certain products possible Neoantigen-based therapies: peptide-MHC/pMHC-T-Cell binding prediction CRISPR-Cas off target site editing prediction



# AI IN NEO-ANTIGEN-BASED PRODUCTS



#### Cancer progression and mutation accumulation





### Adaptive immune response to cancer neoantigens





**Neoantigens** are newly formed peptides which arise from somatic mutations in cancer cells

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### Training the adaptive immune system using neoantigens



Clinical trials ongoing Nothing on market

Credit: ScienceDirect

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#### Computational neoantigens identification



Fan, T. et al. (2023) Therapeutic cancer vaccines: advancements, challenges and prospects. Sig Transduct Target Ther.



#### How to predict peptide binding affinity?

?	
Pseudo sequence	Log-affinity

Peptide	Pseudo sequence	Log-affinity
AEFWDVFLS	YFAMYGEKVAHTHVDTLYVRYHYYTWAVLAYTWY	0.0847
ADPVDAVIN	YYAMYGEKVAHTHVDTLYVRYHYYTWAVLAYTWY	0.2890
IRHHVRWAL	YHTEYRNICAKTDVGNLYWTYNFYTWAVLAYEWH	0.4350
YIRRNMINK	YYAMYRNNVAQTDVDTLYIMYRDYTWAVWAYTWY	0.5266
KAGQYVTIW	YDSGYREKYRQADVNKLYLWYDSYTWAEWAYTWY	0.3436
YTAVVPLVS	YTAMYLQNVAQTDANTLYIMYRDYTWAVLAYTWY	0.0014



#### History of neural networks





### Availability of binding affinity data

Number of epitopes curated by year in the Immune Epitope Database



Vita R. et. al. (2019) The Immune Epitope Database (IEDB): 2018 update, Nucleic Acids Research

# How neural networks are applied to peptide-MHC binding prediction

Peptide	Pseudo sequence	Log-affinity
AEFWDVFLS	YFAMYGEKVAHTHVDTLYVRYHYYTWAVLAYTWY	0.0847
ADPVDAVIN	YYAMYGEKVAHTHVDTLYVRYHYYTWAVLAYTWY	0.2890
IRHHVRWAL	YHTEYRNICAKTDVGNLYWTYNFYTWAVLAYEWH	0.4350
YIRRNMINK	YYAMYRNNVAQTDVDTLYIMYRDYTWAVWAYTWY	0.5266
KAGQYVTIW	YDSGYREKYRQADVNKLYLWYDSYTWAEWAYTWY	0.3436
YTAVVPLVS	YTAMYLQNVAQTDANTLYIMYRDYTWAVLAYTWY	0.0014



43 input neurons (one per sequence position)

 $5 \times 10^{50}$  possible amino acid combinations

Nielsen et. al. (2007). NetMHCpan, a Method for Quantitative Predictions of Peptide Binding to Any HLA-A and -B Locus Protein of Known Sequence. PLoS ONE



#### Performance

- Binding affinity data:
  - 134281 IC<sub>50</sub> measurements from IEDB
  - 4 distinct MHC II alleles
- Eluted ligand data:
  - 372639 MHC measurements
  - 74 distinct MHC II alleles
  - Negative peptides sampled from UniProt



*F-rank: the ratio between the number of peptides with a prediction score higher than the positive peptide and the number of peptides contained within the source protein.* 



**CD4+** 



Reynisson et. al. (2020), NetMHCpan-4.1 and NetMHCIIpan-4.0: improved predictions of MHC antigen presentation by concurrent motif deconvolution and integration of MS MHC eluted ligand data, NAR



# AI IN CRISPR-CAS-BASED PRODUCTS



#### **CRISPR-Cas9**



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### Example indication

#### Sickle cell anaemia



#### BCL11A KO restores Foetal Hb expression

BCL11A blocks gamma globin to repress HbF expression causing sickle hemoglobin

CRISPR-Cas9 gene editing targets BCL11A in erythroid lineage increasing HbF expression and rescuing adult hemoglobin

Normal red blood cells





Credit: Morayo G. Adebiyi, (2024) Tackling sickle cell disease with precise and efficient gene editing. DT

Casgevy FDA approved December 2023 EMA authorised February 2024



### **Off-target editing**



Lin Y. et. al. (2014) CRISPR/Cas9 systems have off-target activity with insertions or deletions between target DNA and guide RNA sequences, Nucleic Acids Research



### Off-target editing site prediction





### Mismatch position and identity affect editing activity



Doench, J. et al. (2016) Optimized sgRNA design to maximize activity and minimize off-target effects of CRISPR-Cas9. Nat Biotechnol



### Prediction of off-target site editing

#### Example input data

Site	Sequence	Mutation (%)
On-target	CTTGCCCCACAGGGCAGTAACGG	78.8
Off-target-1	TCAGCCCCACAGGGCAGTAACGG	85.8
Off-target-3	GCTGCCCCACAGGGCAGCAACGG	4.4

#### Data encoding

					Ins	er	tior	ı					Mismatch Deleti									ior	on										
On-target s (5'→3')	site	A	G	С	_	•	·	С	Α	G	G		A G C T · · C A G G A G C T ·									•	С	Α	G	G							
Off-target s (5'→3')	site	A	G	С	Т	•	•	С	A	G	G		A C G T · · C A G G A G _ T ·								•	•	С	A	G	G							
	Α	1	0	0	0	•	•	0	1	0	0		1 0 0 0 0 1 0 0 1 0 0 0								0	•	•	0	1	0	0						
	т	0	0	0	1	·	•	0	0	0	0	Γ	0 0 0 1 0 0 0 0 0 0 0						1	•	•	0	0	0	0								
On- and	G	0		0	0	·	·	0	0				0 1 1 0 • • 0 0 1 1 0 1 0						0	•	•	0	0	1	1								
off-target	С	0	0	1	0	•	•	1	0	0	0		0			0	•	·	1	0	0	0		0	0	1	0	•	•	1	0	0	0
pair code	-	0	0	0		•	•	0	0	0	0		0	0	0	0	•	·	0	0	0	0		0	0		0	•	•	0	0	0	0
		0	0	0	0	•	÷	0	0	0	0		0 1 0 0 0 0 0 0 0 0 1 0						•	•	0	0	0	0									
		0	0	0	1	•	•	0	0	0	0		0	0	1	0	•	÷	0	0	0	0		0	0	0	0	•		0	0	0	0
							_	_						_			_	_					_		_						_		

#### Neural network architecture



Lin et. al. (2020). CRISPR-Net: A Recurrent Convolutional Network Quantifies CRISPR Off-Target Activities with Mismatches and Indels. Advanced Science.



#### Performance

Type / No.	Technique	Total	Validated Off-targets	Guide RNAs	With Indel	Literature
I / 1	CIRCLE-Seq	584 949	7371	10	Yes	Tasi et al. <sup>[19]</sup>
/2	GUIDE-Seq	213 943	60	6	Yes	Listgarten et al.
II / 1	Protein knockout detection	4853	2273	65	No	Doench et al. <sup>[</sup>
II / 2	PCR, Digenome- Seq and HTGTS	10 129	354	19	No	Haeussler et al. <sup>[40]</sup>
II / 3	SITE-Seq	217 733	3767	9	No	Cameron et a I. <sup>[18]</sup>
II / 4	GUIDE-Seq	294 534	52	9	No	Tasi et al. <sup>[16]</sup>
II / 5	GUIDE-Seq	95 829	54	5	No	Kleinstiver et al. <sup>[44]</sup>
II / 6	GUIDE-Seq	383 463	56	22	No	Listgarten et al. <sup>[13]</sup>

Kim et. al. (2015). Digenome-seq: genome-wide profiling of CRISPR-Cas9 off-target effects in human cells. *Nature Methods* Lin et. al. (2020). CRISPR-Net: A Recurrent Convolutional Network Quantifies CRISPR Off-Target Activities with Mismatches and Indels. *Advanced Science*.



# **USING AI**



### Practically integrating AI into your product



- Data cleaners
- Data scientists
- Bioinformaticians
- Developers
- Domain experts
- System admins
- Scrum masters
- UI/UX experts
- Product owners





Skilled

integration



# What to consider when using AI in the development of medicinal products



- Risk of false predictions
- Risk of tools used



Should we develop our own machine learning models?



RISK

#### How well does the step perform?

 Analytical validation as part of risk assessment

#### How are risks mitigated?

- Accept, avoid, transfer, reduce
- Verification, filtering



What dataset should be used?

• Published, purchased, in-house, synthetic



- How is change managed?
- Major/minor changes
- Reporting



### **Regulatory guidelines**



EMA: https://www.ema.europa.eu/en/news/reflection-paper-use-artificial-intelligence-lifecycle-medicines

EU: https://artificialintelligenceact.eu/

WHO: https://www.who.int/publications/i/item/9789240078871

FDA: https://www.fda.gov/science-research/science-and-research-special-topics/artificial-intelligence-and-machine-learning-aiml-drug-development



# OUTLOOK



Outlook

### Al is becoming an integral part of the medicinal product life cycle. The discussion of how Al will be regulated is ongoing (see slide 36)

#### Two examples where AI could be used directly in design of biomedicine Would love to hear about more



### Acknowledgements





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# THANK YOU VERY MUCH

FOR YOUR ATTENTION