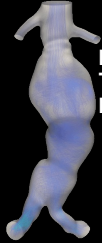




Personalized Treatment of AAAs with AI: The Development of The First Prediction Models of the VASCUL-AID Project

Associate prof. Dr. Kak Khee Yeung
Vascular Surgeon and PI, Amsterdam UMC, the Netherlands

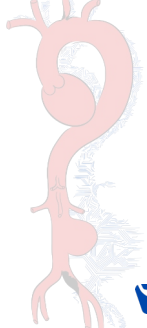

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Disclosures



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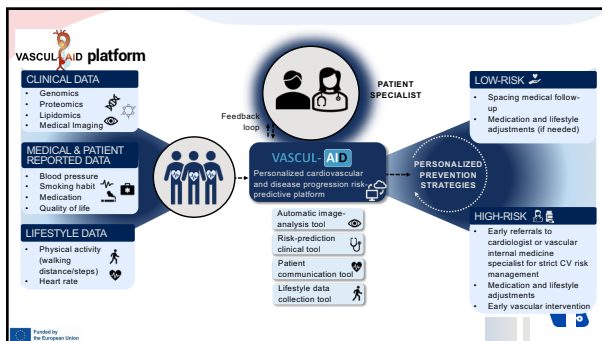
VASCULAID consortium

Nr	Short	Full name	Country
1	VUMC	Amsterdam UMC, location VUmc	NL
2	AMC	Amsterdam UMC, location AMC	NL
3	BFS	Brightfish B.V.	BE
4	UOT	University of Twente	NL
5	FMUP	University of Porto	PT
5.1	UAVE	University of Aveiro (AE)	PT
5.2	HSLJ	Hospital São João (AE)	PT
6	CHUN	Nice University Hospital	FR
7	ALLAI	Alliance for Responsible AI	NL
8	UOB	University of Belgrade	RS
9	HUS	Helsinki University Hospital	FI
10	VINS	Vinča Institute of Nuclear Sciences	RS
11	UIB	University of Bergen	NO
12	MHB	Brandenburg Medical School	DE
13	OX	University of Oxford (AP)	UK
14	AKH	Asklepios Kliniken Hamburg (AP)	DE

16 partners: 12 beneficiaries, 2 affiliated entities (AE), 2 associated partners (AP), 9 EU countries

Prediction of vascular disease progression and the risk of cardiovascular events in AAA and PAD patients

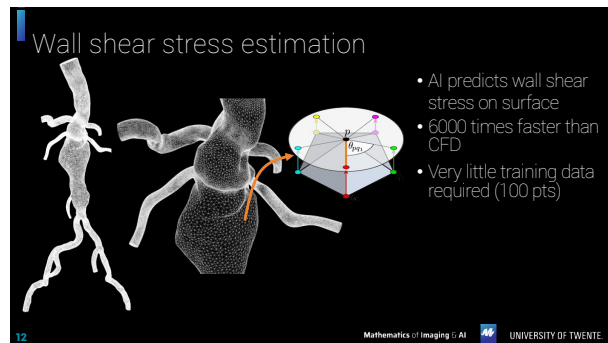
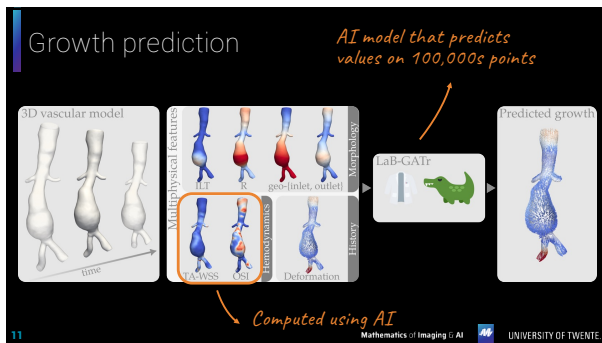
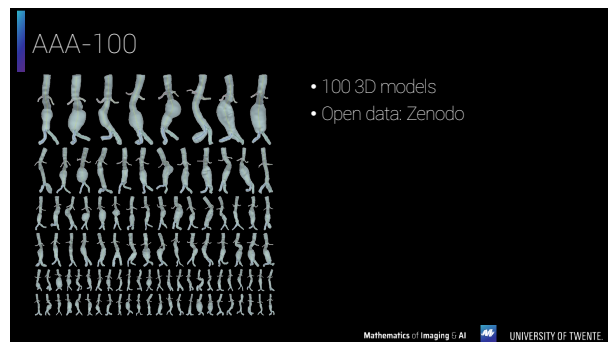
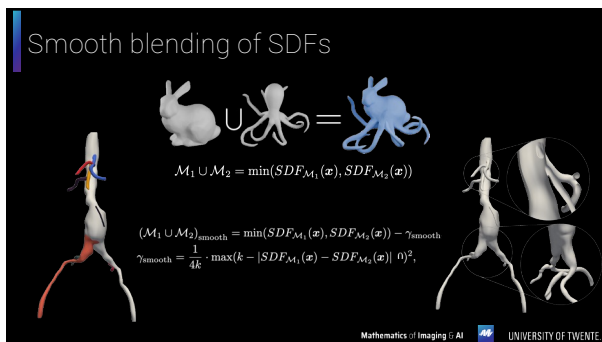
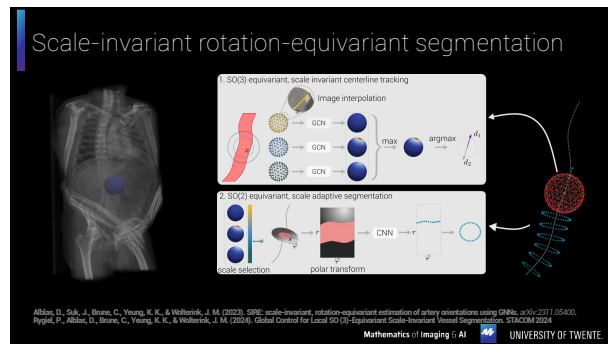
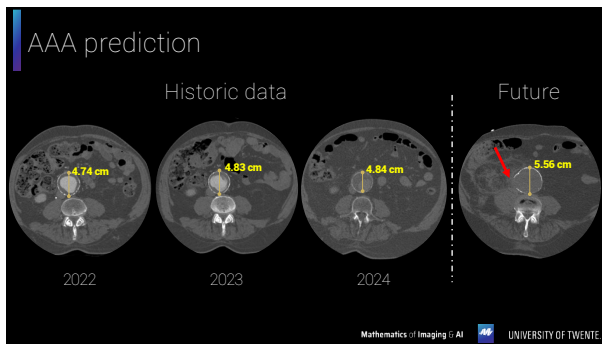



WP3: Predictions based on imaging




Associate Prof. Dr. Jelmer Wolterink
AI & Mathematics, University of Twente





Integration to AI workflow



Graph Neural Networks (GNNs) for Multi-Omics Integration:

- GNNs leverage proteomics data AAA patient classification.
- Nodes in the graph represent proteins (both known and novel predicted), and edges represent relationships between proteins (interactions or co-expression).
- Experimental omics data (protein expression levels in blood and aneurysmal tissue, experiments ongoing) serve as node features.

Patient-level classification:

- Graphs are aggregated at the patient level, and the patient's risk category (e.g. low, medium, high risk for AAA) is predicted based on the protein expression patterns and network structure.

Dynamic Learning:

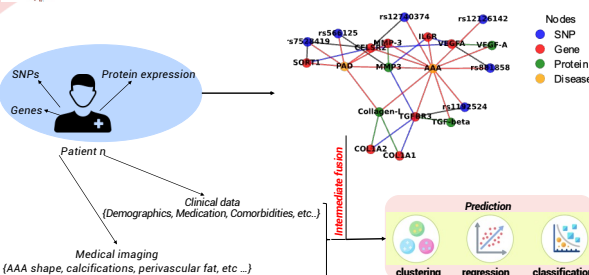
- GNNs can adapt as new data (novel proteins, new pathways, etc.) becomes available.

Clinical Application:

- Personalized treatment strategies for AAA, with precision medicine approaches based on proteomics and pathway data.
- Improved identification of high-risk patients for targeted interventions and monitoring.

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Multi-modal model



Nodes Legend:

- SNP (Blue circle)
- Gene (Red circle)
- Protein (Green circle)
- Disease (Yellow circle)

Input Data for Patient n:

- SNPs
- Protein expression
- Genes
- Clinical data (Demographics, Medication, Comorbidities, etc.)
- Medical imaging (AAA shape, calcifications, perivascular fat, etc...)

Intermediate fusion

Prediction Methods:

- clustering
- regression
- classification

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Thank you!





















<https://vascul-aid.eu>

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