BS12 A NOVEL PHYSICS-BASED ARTIFICIAL INTELLIGENCE TECHNIQUE RAPIDLY RECONSTRUCTS THE 3D VELOCITY, SHEAR STRESS AND PRESSURE FIELDS IN CORONARY ARTERIES.

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Background With the global rise of cardiovascular disease including atherosclerosis, there is a high demand for accurate diagnostic tools that can be used during a short consultation. Abnormal blood flow patterns are strong predictors of atherosclerotic lesion location, progression, and plaque rupture. Patient-specific blood flow patterns are often obtained from 3D-imaging-based computational fluid dynamics. However, the high computational cost makes these methods impractical. Here, we present a new method to expedite the reconstruction of 3D velocity fields using a combination of data-reduction (POD and t-SNE) and deep learning.

Methods and Results We developed a semi-automatic pipeline producing a large dataset of randomly perturbed meshes (n=3,300) obtained from atherosclerotic pig coronary arteries (n=7) to numerically simulate blood flow in the classical way for reference (with Abaqus). This dataset was then used to generate a large covariance matrix, which was decomposed with singular value decomposition to obtain “eigen” modes, of which five modes were selected to represent >90% of signal energy. Next, the meshes of ~110,000 nodes were reduced in size using t-SNE. The reduced dataset was then used to train a group of Neural Network which predicted the pattern of blood flow in an unseen arterial geometry accurately (>95%). The new method was able to reproduce the 3D velocity field and its derivatives (Pressure, WSS) in coronary arteries 200 times faster than before.

Conclusion CFD is inherently too slow to be of significance for clinical decisions. Here, we present a new physics-based technique capable of producing 3D biomechanics maps in human coronary arteries within a minute.

Conflict of Interest No

BS13 ULTRA-HIGHLY FLEXIBLE, ACCURATE, HIGH THROUGHPUT PLATFORM FOR PERSONALISED DRUG SCREENING STUDIES.

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Background Each patient is unique and personalized medicine aims to provide tuned drug treatments. In silico screening of known and unknown synthetic compounds might offer a way to repurpose drugs or discover new drugs. However, success rates of these approaches are low, necessitating to screen large repositories (1060). We aim to solve this problem by a) designing and employing smart artificial intelligence architectures to better select and personalize drug compounds of interest, and b) to integrate this software in a novel CRISPR high throughput platform.

Whole genome screening with CRISPR targeted gene deletion has revolutionized research. We designed a novel, ultra-scalable, highly efficient, programmable, high throughput (HT) scalable knock-out/knock-in system. The HT CRISPR platform consists of a highly efficiently electroporator for (reversed) gene transfection, an ultra-high precision robot dispenser, and a modular parallel plate chamber. Analysis is performed by integrating the platform with an in-house developed single cell analysis software package operating on a high throughput microscope.

Here, we propose a new platform for more efficient drug screening purposes and integrate it in our A.I. algorithms. The idea is to take advantage of the fact that diffusion is far slower than convection, and hence that we can perfuse two drugs in parallel into the same platform next to each other with minimal interference (perpendicular diffusion). When we extent this idea, we can modify the platform with ~100 small pumps, each perfusing a small lane at the HT-platform. This implies that as each pump is capable of testing one drug, and the modification of the slide enables to supply 100 spots, where in each spot we can tag 10 proteins, each drug will be evaluated in 1000 proteins/pathways.

The unique A.I. software consists of a generic part which generates in-silico drug screening, and a personalized part which enables to identify drugs only of interest to the patient. The top 100 predicted drugs will be tested on patient-specific cells for their effects modifying selected pathways of interest.

Conflict of Interest no

BS14 A FULLY AUTOMATED VULNERABLE PLAQUE CLASSIFIER FOR OCT USING CO-REGISTERED HISTOLOGICAL IMAGES AND TRANSFER LEARNING LEARNING.

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Background The high mortality rates of coronary artery disease (CAD) is predominantly associated with a rupture of the thin cap overlying a vulnerable plaque. Intracoronary optical coherence tomography (OCT) is a high resolution, catheter-based invasive imaging system that allows the evaluation of atherosclerotic plaques at the requested high spatial resolution. Currently, plaque characterization and classification are done by visual evaluation, making diagnosis of OCT images subjective and time-consuming. Initial AI classifiers suffer from the fact they cannot detect the plaque embedded in healthy tissue. In this study, we overcome this problem, and propose to fully automate OCT-based atherosclerotic plaque diagnosis using a unique and accurate co-registration of histology and OCT in a validated experimental pig model.

Methods A PCSK transgenic pig model was instrumented with a stenotic stent to expedite advanced plaque formation. OCT images of the plaques were acquired and carefully co-registered with its histology using a previously developed and validated 3D histological method. Labelling was performed by