Last Name	Nietert
First Name	Manuel M.
Institution	University Medical Center Göttingen & Campus Institut Data Science CIDAS
Short CV	**Group Leader** of **Applied Bio(chem)informatics and Image Analysis** in the Department of Medical Bioinformatics **Position and employment** 2019- Project Leader, AutoBuSTeD, UMG, Germany https://s.gwdg.de/xv5Uzr 2017- Project Leader, CandActCFTR, UMG, Germany https://s.gwdg.de/xvtIlC 2013-2016 Researcher & Project manager, MetastaSys, UMG, Germany 2010-2013 Researcher & Project manager, BreastSys, UMG, Germany 2007-2009 Research Assist., Inst. of Microbiology and Genetics, TU Darmstadt, Germany 2004-2007 Research Assist., Dep. of Chemical and Pharmaceutical Sciences, Goethe University, Frankfurt a. M. Germany **Education and training** 08/2008 PhD in Chemistry, Goethe University, Frankfurt a. M. - Germany 08/2004 Master Level Degree in Biochemistry, Goethe University, Frankfurt a. M. - Germany **Awards** Christiane Herzog-Foundations "Forschungsförderpreis für wissenschaftliche Nachwuchsförderung 2018", initial funding for the Automatic bubble sweat test diagnostic project – AutoBuSTeD **Other Academic Roles** • Vice spokesperson of the working group *Data quality and transparency in medical research* of the TMF e.V. - the umbrella organization for networked medical research in Germany. https://s.gwdg.de/70QJZO • Member of the FAIRDOM Systems Biology Developers Foundry since 2012 https://s.gwdg.de/K3Ywvu
List of five relevant publications within the last five years	**1.** Vinhoven, L.; Stanke, F.; Hafkemeyer, S.; Nietert, M.M. *CFTR Lifecycle Map—A Systems Medicine Model of CFTR Maturation to Predict Possible Active Compound Combinations.*Int. J. Mol. Sci. 2021, 22(14), 7590; https://doi.org/10.3390/ijms22147590; **2.** Jo P, Bernhardt M, Nietert M, ..., Ströbel P, Schildhaus HU, Gaedcke J. *KRAS mutation status concordance between the primary tumor and the corresponding metastasis in patients with rectal cancer.* PLoS One. 2020 Oct 1;15(10):e0239806. doi: 10.1371/journal.pone.0239806. PMID: 33002027 **3.** Uhlig J, Biggemann L, Nietert MM, ..., Uhlig A. *Discriminating malignant and benign clinical T1 renal masses on computed tomography: A pragmatic radiomics and machine learning approach.* Medicine (Baltimore). 2020 Apr;99(16):e19725. doi: 10.1097/MD.0000000000019725. PMID: 32311963 **4.** Lowes M, Kleiss M, Lueck R, Detken S, Koenig A, Nietert M, ..., Ghadimi M, Conradi LC, Homayounfar K. *The utilization of multidisciplinary tumor boards (MDT) in clinical routine: results of a health care research study focusing on patients with metastasized colorectal cancer.* Int. journal of colorectal disease. 2017; PMID: 28779354, PMCID: PMC5596058 **5.** Linke F, Zaunig S, Nietert M, ..., Wilting J, Kube D. *WNT5A: a motility-promoting factor in Hodgkin lymphoma.* Oncogene. 2017; 36(1):13-23. PMID: 27270428

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Research focus

Major Research Interests

For the past years we focus our research in the field of cystic fibrosis (CF), where we still see an unmet demand for IT solutions to help this field. In general our work group aims at providing IT based solutions for biochemical aspects of the systems biology and systems medicine projects, but if necessary can even venture out to help improve the acquisition setup. We thus develop and adapt software solutions to provide the required tools for medical research.

At a first glance, CF is a monocausal disease in which over 2000 putative mutations leading to various forms of phenotypes have been identified. Among these, about 300 variants define the more common types. The CFTR protein is only effective as an integral membrane protein, and as such, it is affected by transcription, translation, folding and degradation, as well as protein trafficking processes. Thus, this monogenic disease has multiple sites for potential drug intervention during its life cycle and covers also protein structure variants. This makes it an interesting target for a system medicine approach. The life cycle of the protein offers also multiple modes to obtain information to annotate the system and the existing literature offers various annotations for specific combinations of mutations and read-outs (e.g. protein expression, functional patch clamp measurements, up to structure models and molecular dynamic simulations).

Current projects

Automated Bubble Sweat Test Diagnostics – AutoBuSTeD - https://s.gwdg.de/xv5Uzr
AutoBuSteD is an example of the work we do on the automation of image analysis workflows, e.g. the AutoBuSTeD project, and we also cover various other image input sources for other projects as well. E.g. microscopy data in the project Pulmonary transplantation of macrophages as a cell-based therapy to treat chronic infections in the cystic fibrosis lung, where we are the collaboration partner to automate the LysoSensor image analysis.

Curated database of candidate therapeutics for the activation of CFTR-mediated ion conductance – CandActCFTR – https://s.gwdg.de/xvtIlC
CandActCFTR is a curated compound database which annotates the chemical structure library with information on where and how in the protein life cycle a compound likely interacts, thus comprising a good starting point for modelling the disease and enhancing ligand based approaches. In the upcoming extension of CandActCFTR, this ligand-based approach will be complemented by structure-based annotations, including the means to predict the interactions between CandActCFTR substances and CFTR by using existing molecular dynamics trajectories, and by adding more organisation and annotation modules