Poster Abstracts

Mining Metagenomic Data for Predictors of Yersinia enterocolitica Infection Outcome

Sina Beier (Centre for Bioinformatics, University Tübingen)

Yersinia enterocolitica infection in healthy mice leads to two outcome scenarios: Rapid weight loss and strong inflammation or moderate weight loss leading to recovery. 16S sequencing indicates potentially predictive bacterial species which make it possible to predict the outcome of infection.

Systems Biology Supports Multiscale Analysis of Imaging, Omics and Clinical Data to Improve Diagnosis and Therapy of HCCs

Michael Bitzer (Internal Medicine I, University Hospital Tübingen)

The aim of this feasibility study within the e:med project "Multiscale HCC" is to get a comprehensive image and molecular fingerprint of individual tumors, treated with transarterial chemoembolization (TACE) or sorafenib with the intention to govern therapy decisions.

MDR1 Promotor Methylation on Primary Glioblastoma (WHO grade IV) Patients

Sedat Cetin (Yuzuncu Yil University, Department of Biochemistry, Van, Turkey)

The most frequent and malignant brain tumor seen in the adults is Glioblastoma (GB). Tumor tissue were taken from the patients. Patients' clinical information and MDR1 methylation status of tumor tissues are compared for the effect on patients survival, resistance to chemotherapy and recurrence of the tumor.

Amelioration of cardiotoxic impacts of diclofenac sodium by vitamin B complex

Nadi Amin Abdulmajeed (Faculty of Science, King Abdulaziz University)
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Predicting Compound Synergy in the DREAM Challenge

Tjeerd M.H. Dijkstra (Department of Computer Science, Center for Bioinformatics Tübingen)

The DREAM consortium launched an open challenge to foster the development of in silico methods to computationally rank 91 compound pairs, from the most synergistic to the most antagonistic, based on gene-expression profiles of human B cells treated with individual compounds.

Analysis of MRSA and ESBL colonisation patterns using machine learning methods

Anna Górska (Department of Computer Science, Center for Bioinformatics Tübingen)

Since the introduction of antibiotics for human therapy, physicians have witnessed growing number of antibiotic-resistant bacterial strains. Antibiotics exert ecological pressure on the community of human micro flora what allows colonisation by the multi-drug resistant strains such as MRSA or ESBLs.

Ciprofloxacin Impact on Human Gut Microbiome and Resistome

Mohamed El-Hadidi (Department of Computer Science, Center for Bioinformatics Tübingen)

We monitored the impact of Ciprofloxacin on intestinal microbiome and resistome of 2 subjects based on metagenomic sequencing data. Due to interpersonal differences, we observed differences in the abundance profile of antibiotic resistant genes (ARGs) and phylogenetic dynamics during and beyond the course of Ciprofloxacin administration.

Factor-based Experimental Design and Visualization and their Applications for Personalized Medicine

Andreas Friedrich (Department of Computer Science, Center for Bioinformatics Tübingen)

High-throughput biomedical methods make it possible to investigate human variation on an unprecedented scale. While enabling promising approaches in personalized medicine, the wealth of data poses challenges. We present a web-based solution to plan and execute large-scale biomedical experiments.

Translational oncology: Identification of biomarkers from primary ovarian cancer tissue using DigiWest multiple protein profiling technology.

R.S. Haeussler (NMI Reutlingen, Germany)

Profiling of cellular signaling cascades requires more than RNA profiling, namely the detection of protein expression and activation. Our novel DigiWest protein profiling technology enables the parallel analysis of up to 600 total and phospho proteins, from <50µg of protein sample

Epigenomics in Parkinson's Disease – Genome-wide analysis of epigenetic signatures in a PD mouse model under environmental influences

Thomas Hentrich (Inst. f. Medical Genetics and Applied Genomics, Uni. Tübingen, Germany)

While genomic mutations and multiplications have been linked to familial cases of PD, they constitute only for about ten percent of all patients. The preponderance of PD cases cannot be explained by genetics alone and seems to occur sporadically.

Using cell-free DNA to monitor the course of disease in patients with head and neck squamous cell carcinoma treated with primary radiochemotherapy

Franz Joachim Hilke (Inst. f. Medical Genetics and Applied Genomics, Uni. Tübingen)

With the growing success of implementing next-generation-sequencing in cancer diagnostics it is now feasible to observe changes in the genetic composition of a tumor and its cell free DNA (ctDNA) by so called "liquid biopsy". Here we present this approach in a patient cohort with advanced HNSCC.

Risk demonstrators for progression of Non-Ischemic Cardiomyopathy - approaches of personalised treatment in Heart Failure (NICE-HF)

Elena Ionesi (Internal Medicine III, University Hospital Tübingen)

The aim of the integrated project will be to investigate novel risk demonstrators including biomarkers, biosignals, cardiac imaging and genetic determinants in NICMP to identify patients at risk and to control disease progression on an individualized aspect.

iVacPortal:A Web-based Portal for the Design of Individualized Epitope-based Vaccines

Christopher Mohr (Applied Bioinformatics, University Tübingen)

Therapeutic vaccines are one active area of research in cancer immunotherapy. Vaccines based on tumor specific mutations can be designed for individual patients on the basis of their genomic data. We present iVacPortal, a web-based workbench for the design of patient specific epitope-based vaccines.

Personalized multi-peptide vaccination induces immune responses associated with long term survival in a patient with metastatic intrahepatic cholangiocarcinoma

Markus Löffler (Dept. of Immunology, University Tübingen)

We report the case of a patient diagnosed in 2010 who was treated with a personalized peptide vaccine. Over the course of 3 years, the primary tumor, locally recurrent tumors on two instances as well as a pulmonary metastasis were resected and analyzed. Based on HLA-ligandomics and transcriptome sequencing, a vaccine cocktail containing seven peptides was administered 27 months after initial diagnosis.

Characterisation of the gut microbial community of obese patients undergoing a weight-loss diet intervention using whole genome shotgun metagenomic sequencing

Rewati Mukund Tappu (Dep. of Computer Science, Center for Bioinformatics Tübingen)

Dysbiosis of the gut microbiome has been implicated in several diseases like obesity, metabolic syndrome and non-alcoholic fatty liver disease. In this study we characterized the gut microbiome composition of 16 obese patients who took part in a multidisciplinary weight loss program.

Simultaneous multiparametric F-18-FDG-PET/MRI in the evaluation of breast cancer: initial results

Heike Preibsch (Diagnostische und Interventionelle Radiologie, Universitätskl. Tübingen)

To evaluate the feasibility of simultaneous FDG-PET/MRI in breast cancer. PET/MR in breast cancer is feasible and provides excellent image quality and good alignment quality of PET and MRI. The used 4-channel breast coil currently leads to artifacts in PET which might impair the detection of small lesions in PET.

Automated Data Analysis in Cancer Genomics

Hans-Joachim Ruscheweyh (D-BSSE; ETH Zurich)

We present a fully automated analysis pipeline for Exome, Whole Genome and Transcriptome data in the context of cancer genomics. The pipeline integrates 18 tools such as aligners, quality control and variant callers. The pipeline can additionally be integrated in the data management system openBIS.

Interleukin-6 gene polymorphisms: a key in personalized cancer patients' treatments

Yolande Saab (Pharmaceutical Sciences, Lebanese American University)

Recent advances in chemotherapy and targeted therapy have helped to improve the clinical outcomes in only a subset of cancer patients. Interleukin-6 (IL-6) is involved in the host immune defense mechanism. The gene encoding for IL-6 is highly polymorphic. The objective of the study is to investigate the role of IL-6 gene polymorphisms in personalized cancer treatments.

DrugTargetInspector: An assistance tool for patient treatment stratification

Lara Schneider (Center for Bioinformatics, Saarland University)

DTI is an assistance tool for treatment stratification that analyzes genomic and transcriptomic datasets to provide information on deregulated drug targets, enriched biological pathways and deregulated subnetworks, as well as mutations and their potential effects on drugs and drug targets.

A custom bioinformatics analysis pipeline for the stratification of admixed populations and prioritization of rare single nucleotide variants

Nada Salem (King Abdulaziz University, Center of Excellence in Genomic Medicine Research)

Exome sequencing has become an emerging technique in the identification of SNVs that harbor deleterious impact and possible health risk. In this study we utilized a customized principle component analysis (PCA) tool to classify a cohort of whole-exomes data derived from cases from the western region of the Kingdom of Saudi Arabia; a region known to be inhabited by an admixed and poorly genetically characterized population.

Personalized Vaccine Design for Cancer Immunotherapy

Benjamin Schubert (Applied Bioinformatics, University Tübingen)

Tumor-specific antigen vaccination has become a promising approach for cancer therapy. The design heavily relies on bioinformatics. Here we present a flexible framework that covers all major steps of the design process and incorporates patient-specific information to increase potency.

The Application of Multi-gene Panel in Detection of Mutations in Women with Hereditary Breast and/or Ovarian Cancer

Ilnaz Sepahi (Inst. f. Medical Genetics and Applied Genomics, Uni. Tübingen)

Multi-gene panel testing for hereditary breast and ovarian cancer is broadly used recently in diagnostic laboratories. Here we present data from 505 patients with family history suspicious for HBOC. Our data suggests that pathogenic mutations can be found in genes other than standard diagnostic genes and that these mutations may be of relevant to the families.

CURETINA: Personalised medicine for hereditary retinal distrophies

Katarina Stingl (Center for Ophthalmology, University of Tübingen)

Hereditary retinal distrophies are a very heterogeneous disease. At present no effective therapy exists. With the help of molecular and multi-modal diagnostic tools inclusively modern imaging technologies the phenotypic and genotypic diverse disease can be stratified very accurately. Several preclinical proof-of-concept studies could show the efficacy of individualized gene replacement therapy in this disease.

Onctopus: A New Model for the Reconstruction of the Clonal and Subclonal Composition of Cancer Samples

Linda K. Sundermann (Inst. for Bioinformatics, Bielefeld University, Germany)

Recently, several methods that attempt to infer the genotype of subpopulations using CNVs, SSMs, or both have been published. Here, we present Onctopus , a new approach to jointly model and reconstruct the subclonal composition of a bulk tumor sample utilizing SSMs and CNVs.

The role of MGMT, MLH1, MSH2, MSH6, PARP-1 and PMS-2 genes in cytotoxicity of Temozolomide of cell lines and tumour cells of primary patients with Glioblastoma.

Mehmet Taspinar (Yuzuncu Yil Univ., Faculty of Medicine, Dep. Medical Biology, Van Turkey)

Glioblastoma (GB), the most lethal brain tumor type in humans. One of the greatest challenges in the treatment is the development of chemotherapy resistance. The aim of the study is to investigate the expression and methylation pattern of candidate genes in primary cell culture of patients with GB and cell lines.

Hypoxia image guided radiation dose escalation in patients with head and neck cancer: Results of a planned interim-analysis of a randomized phase II trial.

Daniela Thorwarth (Sec. f. Biomedical Physics, Uni. Hospital f. Radiation Oncology, Tübingen)

The aim of this phase II study was to evaluate feasibility and toxicity of hypoxia imaging guided radiation dose escalation (DE) in locally advanced head and neck squamous cell carcinoma (HNSCC) and to investigate the prognostic value of hypoxia PET imaging using [18F]-FMISO.

ImMiGeNe - Implementation of a Pipeline Integrating Gut Metagenome Data, Host Immunogenetics, and Clinical Biomarkers for Stratified Clinical Management

Alexander Weber (Interfaculty Institute of Cell Biology, Dep. of Immunology, Tübingen)

The gut microbiota, is believed to play a pivotal role in human health. In a discovery cohort of children undergoing stem cell transplantation (SCT) we want to identify defined and stratifiable host and microbial biomarkers that can be directly used to anticipate and reduce graft-versus-host disease (GvHD) and infection-related complications in childhood and adult SCT patients.

Integrated PET/MR imaging of tumor response to fractionated irradiation in xenograft models of human HNSCC –a feasibility study

René Winter (University Hospital Tübingen, Radiation Oncology, Sect. f. Biomedical Physics)

Hypoxia is an important prognostic marker for radiotherapy response, particularly for head and neck tumors and measured by using dedicated PET-tracers such as 18F-FMISO. Our hypothesis is that a suitable combination of different parameters derived from PET and functional MR would allow a better prediction.

Personalised postoperative radiochemotherapy in patients with head and neck cancer

Kerstin Zwirner (Radiation Oncology, University Hospital Tübingen)

The purpose of this demonstrator project in the Centre for Personalised Medicine Tübingen is to develop a multi-scale prediction model for radiotherapy outcome based on quantitative functional imaging, NGS and DNA repair capacity data in patients with head and neck cancer.