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Medizinische Universität Graz

D&F Institut für Humangenetik
Diagnostik & Forschungszentrum für Molekulare BioMedizin
Neue Stiftingtalstr. 6, A-8010 Graz

Das **D&F Institut für Humangenetik** lädt herzlich zu folgendem Seminar ein:

Dr. Johannes G. Reiter

Assistant Professor, Canary Center for Cancer Early Detection,
Stanford University, Palo Alto (USA)

Genetic heterogeneity in untreated cancers and implications for cancer early detection

Donnerstag 09. Mai 2019 um 11:15 Uhr
MC1.G.01.005 (SR 01); Med Campus

Prof. Reiter (Stanford University) focuses on the stochastic biological processes underlying cancer evolution with the goal to improve the detection and treatment of tumors. He develops computational methods and designs mathematical models to generate novel hypotheses and explain observations on a mechanistic level. For example, his recently developed model demonstrated why a single biopsy is typically sufficient to capture the essential information for initial therapeutic decision-making.

The abstract of the lecture: Genetic intratumoral heterogeneity is a natural consequence of imperfect DNA replication. Any two randomly selected cells, whether normal or cancerous, are therefore genetically different. I will discuss the extent of genetic heterogeneity within untreated cancers with particular regard to its clinical relevance. While genomic heterogeneity within primary tumors is associated with relapse, heterogeneity among treatment-naïve metastases has not been comprehensively assessed. We analyzed sequencing data for 76 untreated metastases from 20 patients and inferred cancer phylogenies for breast, colorectal, endometrial, gastric, lung, melanoma, pancreatic, and prostate cancers. We found that within individual patients a large majority of driver gene mutations are common to all metastases. Further analysis revealed that the driver gene mutations that were not shared by all metastases are unlikely to have functional consequences. A mathematical model of tumor evolution and metastasis formation provides an explanation for the observed driver gene homogeneity. These data indicate that malignant cells are genetically homogeneous with respect to functional driver gene mutations. A mathematical model of ctDNA secretion suggests that this homogeneity can be exploited to detect a substantial fraction of tumors earlier.