

## **Bern Seminar Series for Precision Medicine**

### **Prof. Jean-Pierre Hubaux**

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### **Title: Data Protection for Personalized Health**

**Tuesday October 15 at 12 noon, room H810 (top floor), MEM Murtenstrasse 35  
(Sandwiches will be provided)**

Host: Prof. Dr. Mark Rubin, Director Bern Center for Precision Medicine (BCPM)



Jean-Pierre Hubaux is a full professor at EPFL. Through his research, he contributes to laying the foundations and developing the tools for protecting privacy in tomorrow's hyper-connected world. He has pioneered the areas of privacy and security in mobile/wireless networks and in personalized health.

He is the academic director of Center for Digital Trust (c4dt.org). He leads the ETH-funded project Data Protection in Personalized Health (DPPH) and is a co-chair of the Data Security Work Stream of the Global Alliance for Genomics and Health (GA4GH). He is a Fellow of both IEEE (2008) and ACM (2010). He is among the most cited researchers in privacy protection and in information security.

<https://people.epfl.ch/jean-pierre.hubaux?lang=en>

#### **Abstract:**

My talk will focus on how to leverage thousands of functional genomics datasets to deeply annotate the disease genome and perform data mining to discover disease-associated regulators and variations.

First, I will introduce our computational efforts to perform large-scale integration to accurately define distal and proximal regulatory elements (MatchedFilter) and then show how our extended gene annotation allows us to place oncogenic transformations in the context of a broad cell space; here, many normal-to-tumor transitions move towards a stem-like state, while oncogene knockdowns show an opposing trend.

Second, I will look at our comprehensive regulatory networks of both transcription factors and RNA-binding proteins (TFs and RBPs). I will showcase their value by highlighting how SUB1, a previously uncharacterized RBP, drives aberrant tumor expression and amplifies the effect of the well-known oncogenic TF MYC.

Third, I will introduce a workflow to prioritize key elements and variants. I will showcase the application of this prioritization to somatic burdening, cancer differential expression and GWAS (LARVA, MOAT & uORF tools). Targeted validations of the prioritized regulators, elements and variants demonstrate the value of our annotation resource.

Finally, I will put all these methods together through application to kidney and prostate cancers.