Keynote Forum

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CureMatch Inc, USA

Cancer treatment in the era of precision medicine

Traditional approach to cancer treatment generally involves "one-size-fits-all" treatments and procedures (e.g., chemotherapy, radiation therapy, and surgery), which is focused largely at fighting a particular type of cancer (e.g., liver, lung, colorectal). However, this approach ignores the unique nature of an individual patient's cancer, despite the fact that the complex genotypic and phenotypic heterogeneity of an individual patient's cancer/tumor has a profound influence on the clinical responses to targeted anticancer therapies. Genetic sequencing of tumors is conducted for only a small number of patients (~2%), and the large number (>4.5 M) of options and potential for drug-drug interactions have precluded widespread adoption of combination therapies. Current approach to treatment response planning and assessment also lacks an efficient method to consolidate biomarker changes into a holistic understanding of treatment response.

Major goals of successful combination therapy include the ability to: (a) cover most of the patient's aberrations with a minimal number of drugs, (b) achieve enhanced effectiveness through drug synergy, (c) reduce the frequency and severity of adverse events (AEs) and (d) minimize the potential to develop drug resistance. While the majority of research on chemotherapies focus on cellular and genetic mechanisms of resistance, there are numerous patient-specific and tumor-specific measures that contribute to treatment response. Development of effective combination therapy is also challenging because many cancer drugs act on intersecting signaling pathways and thus can potentially interfere or antagonize each other. One approach to identify effective combinations is by precise targeting of synergistic combinations, which exhibit enhanced therapeutic efficacy when combined at lower doses. However, identification of synergistic drug combinations is often a labor- and resource-intensive process. We developed a precise, multimodal computational model that can leverage clinically-available measurements to optimize treatment selection and schedules for patients.

Biography

Igor F Tsigelny is an expert in structural biology, molecular modeling, bioinformatics, structure-based drug design and personalized cancer medicine. He published >200 articles, 4 scientific books and around 15 patents. The book 'Protein Structure Prediction: Bioinformatic Approach' that he edited has been called 'The Bible of all current prediction techniques' by BioPlanet Bioinformatics Forums. His computational study of molecular mechanisms of Parkinson's disease was included in the US Department of Energy publication 'Decade of Discovery' where the best computational studies of the decade 1999–2009 have been described. He is a Professor in the UC San Diego and CSO of CureMatch Inc. (San Diego).

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Ondrej Slaby

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Translational potential of non-coding RNAs in oncology

For many years, central dogma of molecular biology has been that RNA functions mainly as an informational intermediate between DNA sequence and its encoded protein. One of the great surprises of modern biology was discovery that protein-coding genes represent less than 2% of total genome sequence, and subsequently that almost 90% of human genome is actively transcribed. Thus, human transcriptome was found to be more complex than collection of protein-coding gene transcripts and their splice variants. Recent evidences have clearly shown that non-coding RNAs (ncRNAs) play major biological roles in cellular development, physiology and pathologies. NcRNAs are grouped into two major classes based on transcript size; small ncRNAs and long ncRNAs. Each of these classes can be further divided, whereas novel subclasses are still being discovered and characterized. In last ten years, class of small ncRNAs called microRNAs was studied most intensively with more than fifty thousand hits at PubMed database. Huge amount of evidence has been accumulated to describe molecular mechanisms of novel RNA species functioning, providing insight into their functional roles in cellular biology and in human disease, especially in cancer. Knowledge regarding ncRNAs functioning in cancer biology and their translational potential to serve as disease biomarkers and novel therapeutic targets in cancer will be summarized and demonstrated on several examples based on our recent observations.

Biography

Ondrej Slaby is a Professor of Medical Biochemistry at the the 1st Faculty of Medicine at Charles University in Prague, Czech Republic. He works as Research Group Leader at the Department of Molecular Medicine, Central European Institute of Technology (CEITEC), Masaryk University (Brno, Czech Republic) and as a Scientific Secretary at the Masaryk Memorial Cancer Institute in Brno. He has published extensively in the field of non-coding RNAs and solid cancer with special focus on their translational potential in diagnostics and as the therapeutic targets (h-index 31, Sum of the times cited without auto-citations > 3500. Since 2018, he is a chair of Czechoslovak Biological Society. In 2010 and 2012, he received Award of Czech Society for Oncology, in 2016 an Award of Czech Medical Society and 2014 and 2016 Award for Medical Research of Czech Minister of Health, Novartis Discovery Award 2017.

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From a public health point of view to investigate the control of obesity, diabetes, and cardiovascular risk via nutrition and exercise (GH-Method: math-physical medicine)

Introduction:In 2017, public health data revealed that the United States had 2 million deaths which included diabetes, heart diseases, stroke, and nephrosis that occupied 45% (~907,000) of this number. Furthermore, >85% of type 2 diabetes (T2D) patients are overweight and >50% are obese.

Methods: The author spent 23,000 hours during the past 8.5 years using math-physical medicine to conduct his research. He has collected and processed ~1.5 million data, including ~300,000 medical conditions, and ~1.2 million lifestyle details. He then utilized the GH-Method: math-physical medicine (MPM) which involves advanced mathematics, optical physics, signal processing, energy and wave theories, statistics, big data analytics, machine learning, artificial intelligence to develop five prediction models, including weight, FPG, PPG, adjusted glucose, and HbA1C.

Results: His clinical case studies have offered the following results:

(1) BMI reduction from 32 (obese) to 24.7 (normal)

(2) FPG reduction from ~200 mg/dL to ~105 mg/dL; PPG from 279 mg/dL to 119 mg/dL; Daily average glucose from >250 mg/dL to ~116 mg/dL; HbA1C from 10% to <6.5%

(3) Risk reduction of having cardiovascular diseases and stroke from 74% prior to 2010 (suffered 5 cardiac episodes) to 26.4% in 2017.

(4) Averaged carbs/sugar intake amounts (38% contribution on PPG): 14.5 gram/meal and ~60 grams/day (low carb diet). Exercise amount (41% contribution on PPG): 4,300 steps/meal and 18,000 steps/day.

Conclusion: His MPM methodology and prediction models (>99% accuracy) are proven to be effective tools on controlling T2D. His flow diagram can also provide an effective guidance to patients to control and improve their conditions on obesity, diabetes, and heart problems. These technology-based prediction and prevention models can be used as educational tools to help diabetes patients through public-health platforms, channels and programs.

Biography

The author received an honourable PhD in mathematics and majored in engineering at MIT. He attended different universities over 17 years and studied seven academic disciplines. He has spent 20,000 hours in T2D research. First, he studied six metabolic diseases and food nutrition during 2010 to 2013, then conducted his own diabetes research during 2014 to 2018. His approach is “quantitative medicine” based on mathematics, physics, optical and electronics physics, engineering modelling, signal processing, computer science, big data analytics, statistics, machine learning, and artificial intelligence. His main focus is on preventive medicine using prediction tools. He believes that the better the prediction, the more control you have.

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Health Examination Record	2010	2017	No
C (<6.4%)	10	6.1	
days Average Glucose (<120 mg/dL)	279	113	
R (<30)	116.4	12.3	
glyceride (<150)	1161	67	
L (>40)	24	48	
L (<130)	174	74	
al Cholesterol (<200)	253	118	
od Pressuire Index M3 (<1.0)	1.2	0.7	
II (<25.0)	31.0	24.7	
ight (lbs)	210	167	
istline (inch)	44	32	
tabolism Index (MI / GHSU: <73.5%)	140% / 103%	49% / 55%	
art episodes (1994 - 2006)			5 tin
liney			Ye
der			Ye
t Ulcer			Ye

Figure 1: Health Exam Results Comparison

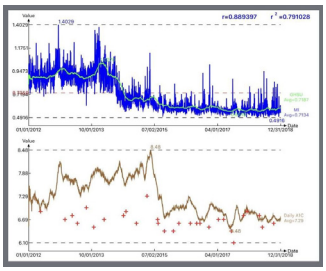

Figure 2: Metabolism Index and HbA1C

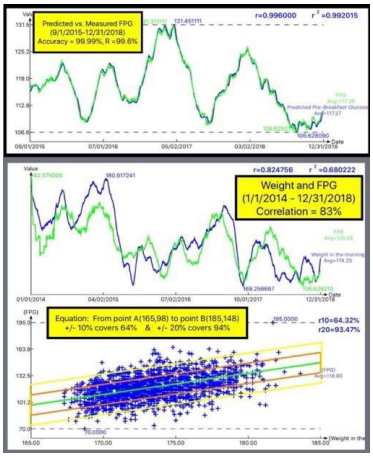

Figure 3: FPG

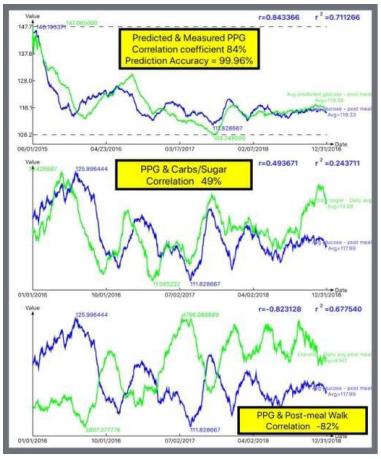

Figure 4: PPG

Year	Probability MI	Probability Medical	Probability Lifestyle	Year Averaged
2000		74%	83%	79%
2012	74%	62%	70%	69%
2013	77%	38%	66%	60%
2014	59%	42%	54%	51%
2015	43%	39%	44%	42%
2016	36%	31%	38%	35%
2017	34%	26%	33%	31%
2018	33%	31%	33%	32%
7-Years	52%	34%	34%	40%

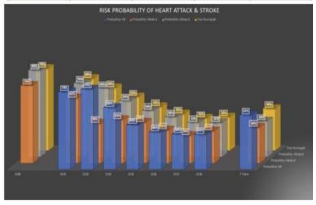

Figure 5: Risk Probability of CVD & Stroke

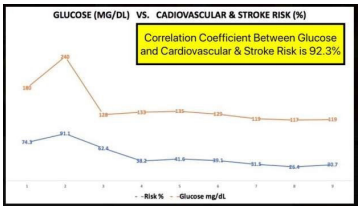

Figure 6: Correlation between Glucose and CVD Risk

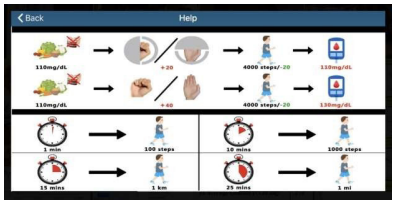

Figure 7: Nursing Guide of T2D Control

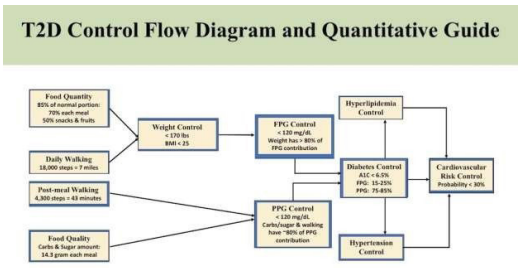

Figure 8: T2D Control Flow Diagram