An Approach To Screening For Drugs/Therapeutics To Treat Covid-19 And Other Viral Pandemics

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TECHNOLOGY DESCRIPTION

Coronavirus Disease 2019 (Covid-19) continues to rapidly claim lives and challenge the limits of our knowledge and our healthcare system. Therapy currently consists of supportive care, while several FDA-approved drugs are being rapidly investigated in clinical trials with the hope of repurposing them. Even during outbreaks such as this, investigational approaches should be guided by sound rationale and rigorous and unbiased scientific vetting.

Here is presented a unique approach to understand the emerging features of COVID-19 and use those insights gained to precisely tailor disease management and inform drug discovery. The approach involves the use of a fundamental and powerful mathematical principle, i.e., Boolean Equivalent Correlated Clusters (BECC) to sift through human transcriptomic datasets and extract a universal (invariant) gene expression **signature** that is associated with acute CoV infection which resolves during convalescence.

ADVANTAGES

An approach was developed that is geared to overcome the above-mentioned challenges using a few in-built features: (i) *Unbiased and rigorous*; it uses an informatics approach to sift through > 50,000 datasets to identify insightful and actionable patterns/signatures from 'big' data; (ii) *Precise*, because it uses a quantitative criteria, set by mathematical logic and statistical cutoffs; (iii) *Rationalized*, because it not only takes into consideration how SARS-CoV-2 breaches the host cell, but also the host immune response that is mounted in response to such a breach. (iv) *Targeted,* because the approach first formulates a precise therapeutic goal before screening for drugs that can achieve such goal; (v) *Predictive*, of whether or not any targeted intervention takes us towards or farther from the desirable therapeutic goal; and (vi) *Rapidly translatable*, because when used in conjunction with *in vitro* human screening platforms as Phase '0' models, it can interpret and validate drug efficacy. This approach has not only allowed pinpointing predisposing conditions and vetting beneficial *vs.* harmful diets and drugs, but also objectively weighing in on ongoing controversies, pinpointing high priority drugs, and predicting prospectively the outcome of several ongoing and planned clinical trials.

INTELLECTUAL PROPERTY INFO

This technology is available for non-exclusive licensing.

CONTACT
University of California, San Diego
Office of Innovation and Commercialization
innovation@ucsd.edu
tel: 858.534.5815.

OTHER INFORMATION

CATEGORIZED AS
- Biotechnology
  - Bioinformatics
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University of California, San Diego
Office of Innovation and Commercialization
9500 Gilman Drive, MC 0910, ,
La Jolla,CA 92093-0910

Tel: 858.534.5815
innovation@ucsd.edu
https://innovation.ucsd.edu
Fax: 858.534.7345

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