Research interests

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Research theme 1: The applications of Artificial intelligence in human health: ANALYSIS OF PUBLIC DATABASES

Artificial Intelligence (AI), is the process of imparting a machine with an 'Intelligence' often called 'models', such that it can make its own decisions or draw conclusions from given data. AI models have multiple applications in broad areas of society, including breakthrough applications in modern medicine for the diagnosis, detection, and management of various diseases. Machine learning (ML) is a subset of AI that is broadly utilized in the field of health sciences.

There are numerous publicly available health databases from both worldwide sources and national sources. For example, at the local level, the National Database (NDB) of Japan, Japan Medical Data Center (JMDC), National Health and Wellness Survey, etc. that can be utilized to perform data analysis to identify new risk factors, disease associations, and predictors.

Multidisciplinary topics of interest include the followings:

1) Lifestyle and environmental factors associated with cancer
2) Nutritional indicators and chronic diseases in the elderly, including diabetes, dementia, and cardiovascular diseases
3) Metabolic serum markers and cancer incidence
4) Serum markers and the risk of allergies and autoimmune diseases

Methods: Standard statistical analysis and Artificial intelligence (AI) tools, especially machine learning (ML) for data analysis (Figure 1).
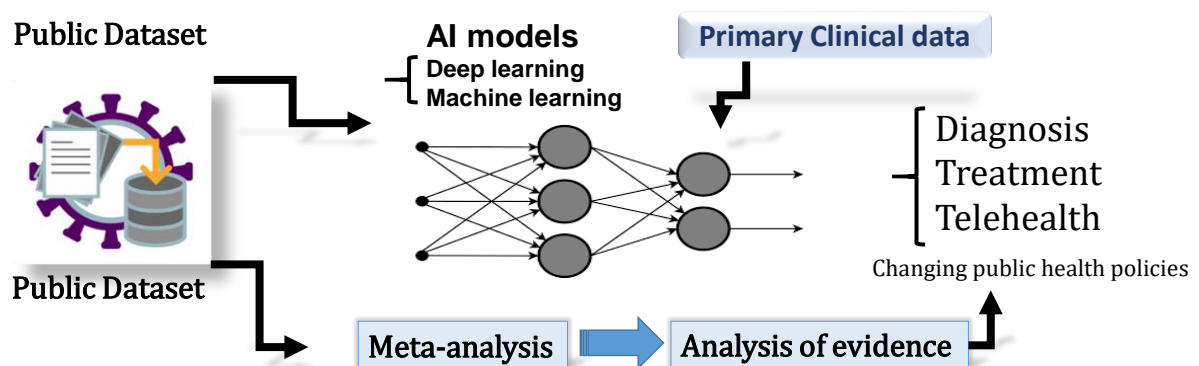
Types of studies conducted: 1) Re-analysis of primary data; 2) Systematic reviews and meta-analysis; 3) Reanalysis of clinical trials, 4) Dataset analysis using; 5) Machine learning for in deep analysis of the evidence.

Research Theme 2:

1) Coupling artificial Intelligence with high throughput screening for studying anti-cancer and immune modulatory agents

Using ML models it is possible to predict correlations between gene expression and drug response and ultimately drug-target prediction. Coupling ML-based drug-target prediction with cell culture experiments, followed by cell response studies, including gene expression and protein expression assays, it is possible to based

This approach is used in throughput screening studies for the identification of health-promoting properties and potential molecular targets of food-derived compounds. This include the identification of antiviral agents, immunomodulatory agents, and bioactive compounds with anticancer properties (**Figure 2**).

This model has practical application not only for the identification of novel bioactive compounds with therapeutic potential but also has the potential to identify the cell target that interact with the compounds of interest and eventually could lead to significant advances in personalized medicine.
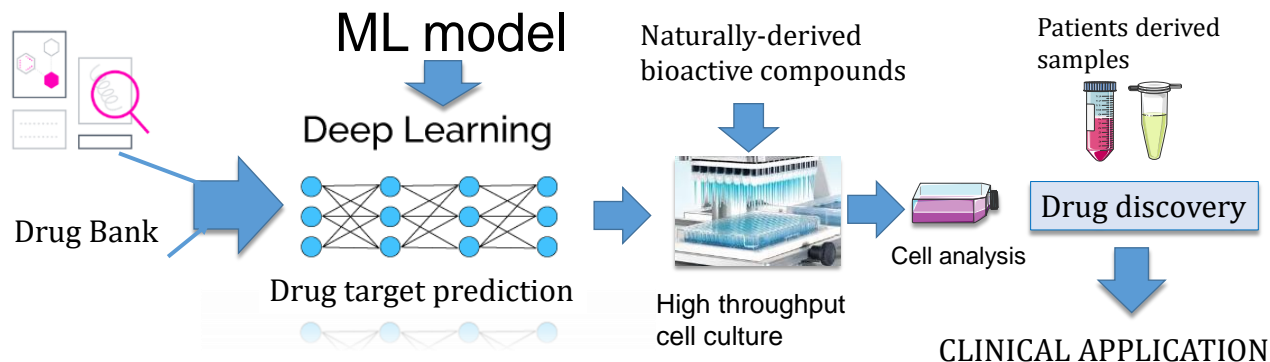
Figure 2: *ML models are used to predict potential targets of naturally-derived compounds based on the predicted gene expression profiles of cell lines exposed to bioactive compounds. Candidate compounds with the most stronger correlations are selected for further analysis and corroborated in cell analysis for the identification of health-promoting properties.*