Using fuzzy logic algorithm and gene expression database ONCOMINE in COPD outcome forecasting
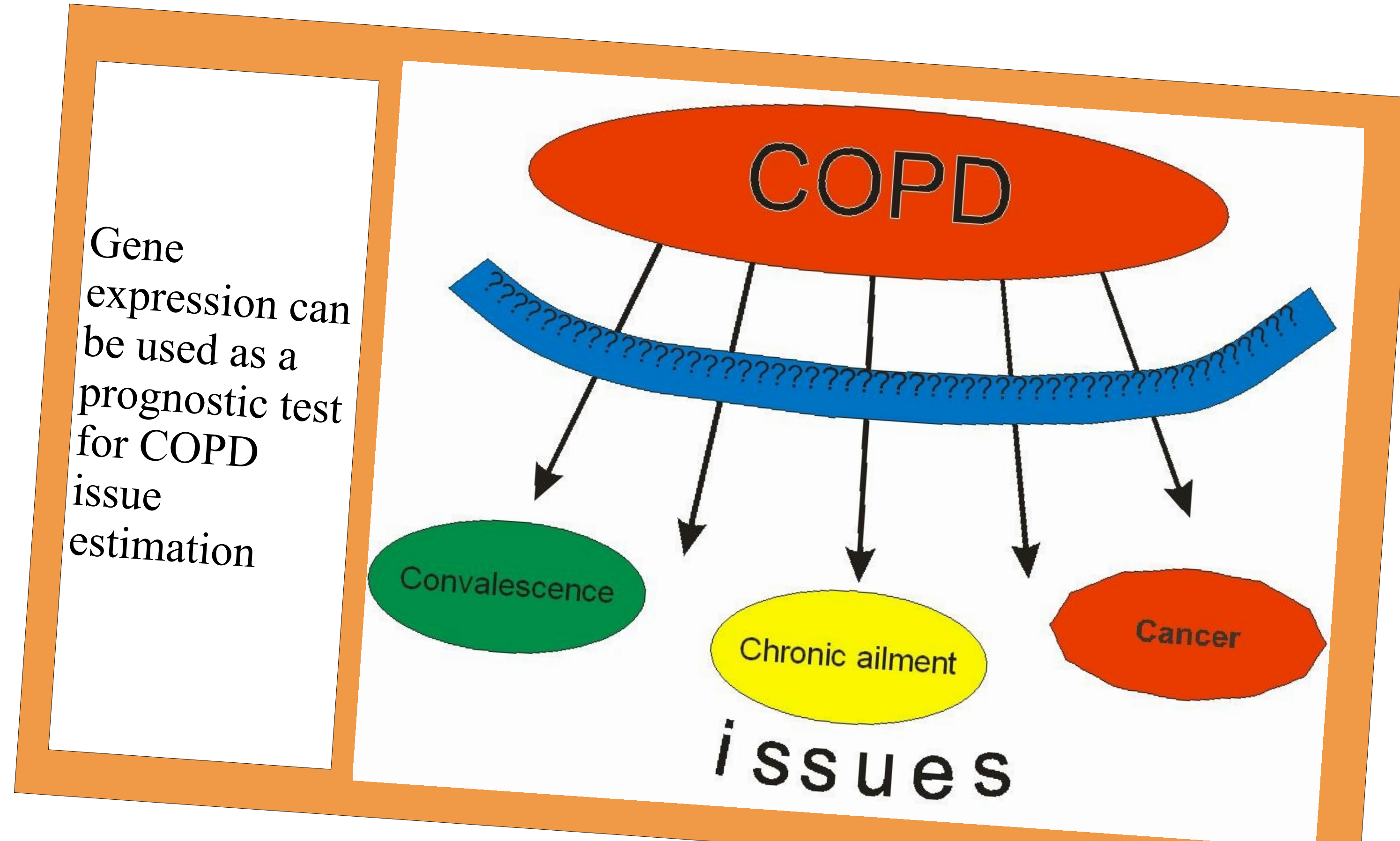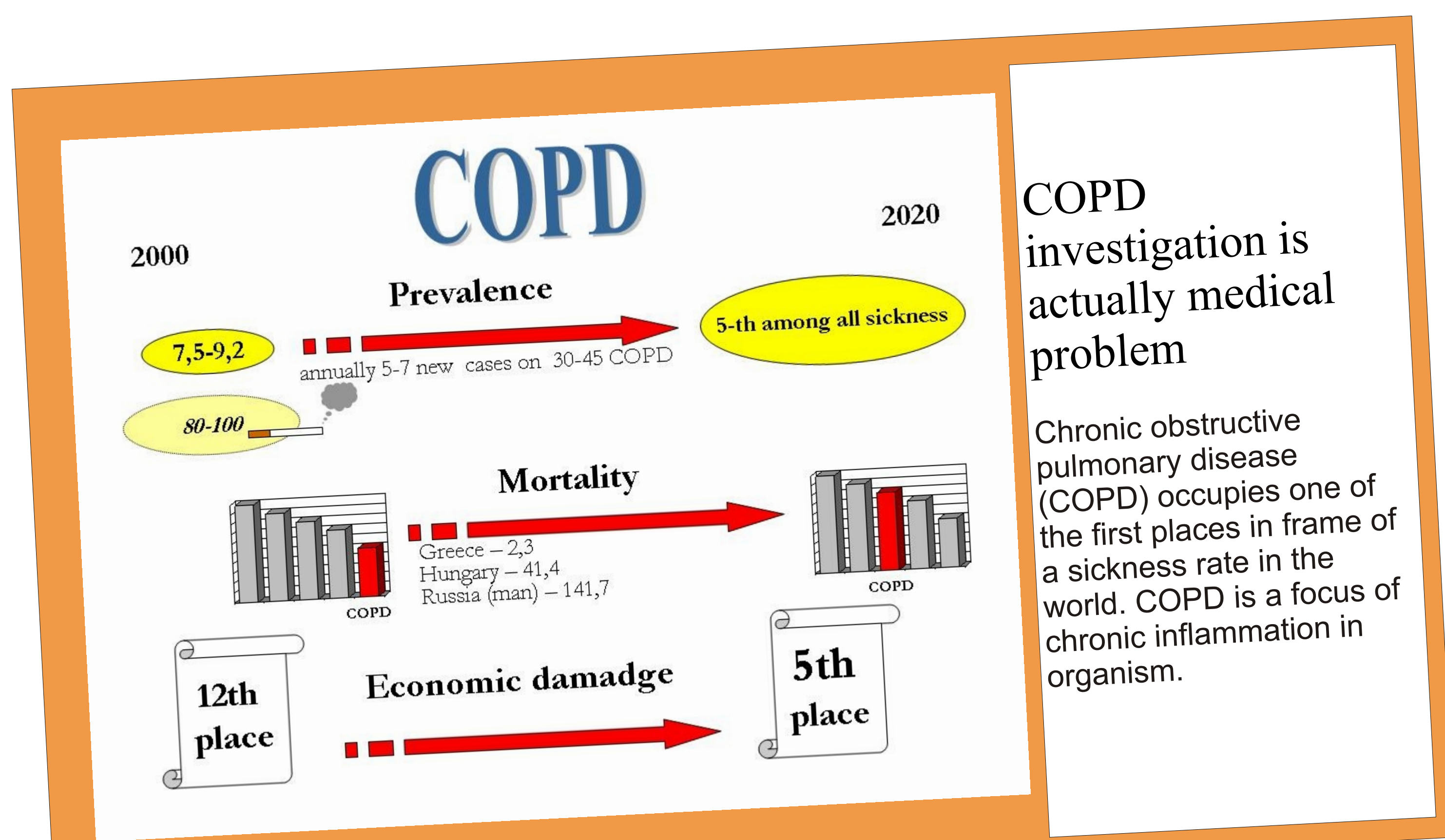
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COPD investigation is actually medical problem

Chronic obstructive pulmonary disease (COPD) occupies one of the first places in frame of a sickness rate in the world. COPD is a focus of chronic inflammation in organism.

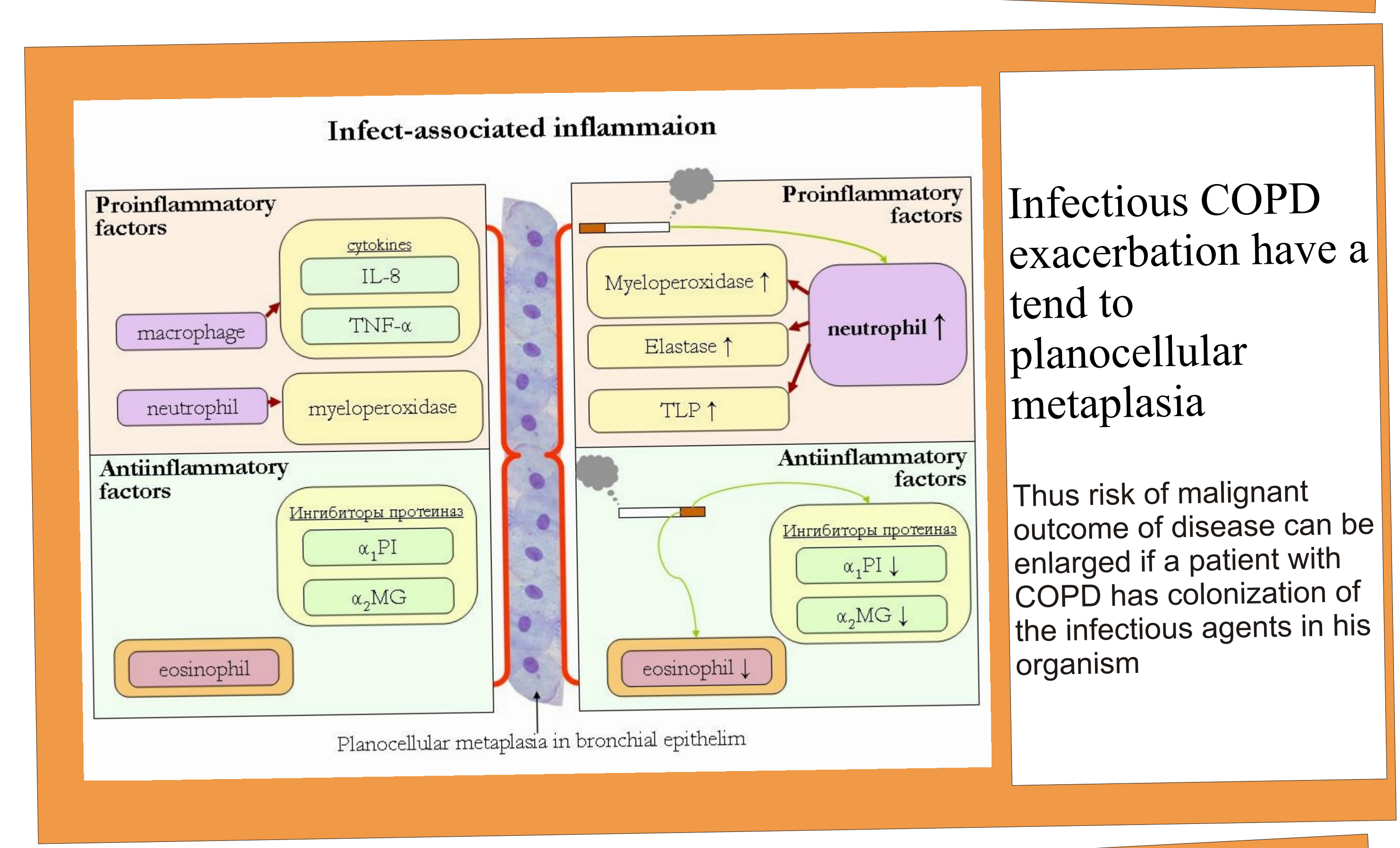**Gene expression can be used as a prognostic test for COPD issue estimation**

Mainly of COPD-cases is an infectious genesis

Chronic inflammation and its local repeated stress have long been known to be risk factors for cancer. Moreover risk of carcinogenesis increases under influence infectious pathogen. Examples include: (a) Helicobacter pylor bacterial infection and gastric adenocarcinoma; (b) hepatitis B virus and hepato-cellular carcinoma; (c) chronic bowel disease and colon carcinoma; (d) EBV and nasopharyngeal carcinoma in humans.

Proved:

-Basics of COPD pathogenesis is pathological (abnormal) inflammation response

-Main cause of COPD exacerbation (**50-60%**) is infectious agents:
  - *S. pneumoniae*
  - *H. influenzae*
  - *M. catarrhalis*

-**Viruses** as COPD exacirbation cause mainly with other bacterium

ONCOMINE, a cancer microarray database and web-based data-mining platform aimed at facilitating discovery from genome-wide expression analyses for elucidation state of indicated genes expression in patients with squamous cell methaplasia

Infectious COPD exacerbation have a tend to planocellular metaplasia

Thus risk of malignant outcome of disease can be enlarged if a patient with COPD has colonization of the infectious agents in his organism

Fuzzy logic is an algorithm drawn from engineering and other applied sciences to control systems as diverse as washing machines to autofocus cameras. It provides a way to transform precise numbers, into qualitative descriptors in a process called "fuzzification." Although other techniques can be used to change precise values into discrete descriptors, fuzzy logic provides a systematic and unbiased way to perform this transformation, thereby removing the need for expert knowledge about the system. When dealing with gene expression data, the problem is even more complicated, because no expert exists to determine what defines a "normal" expression level. Using fuzzy logic, the full range of expression data is first measured and is then broken into discrete subsections based on the observed data. These discrete subsections then provide a qualitative description of the data. Once transformed, this qualitative data can be analyzed using heuristic rules, which in turn generate fuzzy solutions. There are three main reward of applying fuzzy logic to the analysis of gene expression data. First, fuzzy logic accounts for noise in the data because it extracts trends, not precise values. Second, in contrast to other automated decision making algorithms, such as neural networks, algorithms in fuzzy logic are cast in the same language used in routine conversation. As a result, predictions made using fuzzy logic are easily interpretable and can be extrapolated in predictable ways. Third, fuzzy logic techniques are computationally efficient and can be scaled to include an unlimited number of components. Thus they are able to recognize a large number of biologically important patterns what are a given data about genes expression.

Reserve cells in G_2 from brush-biopsy of COPD patients with high level of plan cells