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Applications of Taylor's Theorem in Biology

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Taylor series is a function of an infinite sum of terms in increasing order of degree. Taylor series of polynomial functions is also a polynomial. It is used to evaluate the value of a whole function in each point if the functional values and derivatives are identified at a single point.

$$f(x) = f(a)\frac{f'(a)}{1!}(x-a) + \frac{f''(a)}{2!}(x-a)^2 + \frac{f^{(3)}(a)}{3!}(x-a)^3 + \dots.$$

Also, when the function is centered at a zero point; this is a special case called as Maclaurin series . i.e when, if a=0

Where will we use this ?

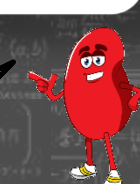
Cell fate determination is an important aspect of normal development and disease. It directly affects tissues human health. So, we have proposed a polynomial model to predict cell fate based on Taylor series.

Since there are many genes, we used two types of trait selection methods, i.e. correlation-based and apoptosis-pathway-based. Then, polynomials of varying degrees were used to refine the cell fate prediction function.

But where and how will we use this in biology?

No worries! I will explain you how we take advantage of Taylor's Theorem in Medical Science.

So, to build a model to predict cell fate based on single-cell gene expression data, where a function is used to demonstrate their relationship, consider cell fate as the probability of cell death. We now express it as a Taylor series under the condition of being infinitely differentiable at a fixed point; we applied this theory and directly used different degree polynomials to fit the cell fate prediction function



Now that is Smart!

Method

Suppose we are given three cell fate related genes *A*, *B*, and *C*, with the corresponding expression levels of x_A, x_B, and x_C, respectively. Suppose that the three genes are independent of each other, then *P* can be represented as:

$$P = f(x_A) + g(x_B) + h(x_C),$$

Where *f*, *g*, and *h* are three arbitrary functions. If $f(x_A)$ is infinitely differentiable at *a*, we can expand $f(x_A)$ with Taylor series as follows:

$$\sum_{n=0}^{\infty} \frac{f^{(n)}(a)}{n!}(x_A - a)^n = f(a) + \frac{f'(a)}{1!}(x_A - a) + \frac{f''(a)}{2!}(x_A - a)^2 + \cdots.$$

Here, $f^{(n)}(a)$ denotes the *n*-th derivative of $f(x_A)$ at *a*. Similarly, $g(x_B)$ and $h(x_C)$ can be represented with Taylor series, respectively.

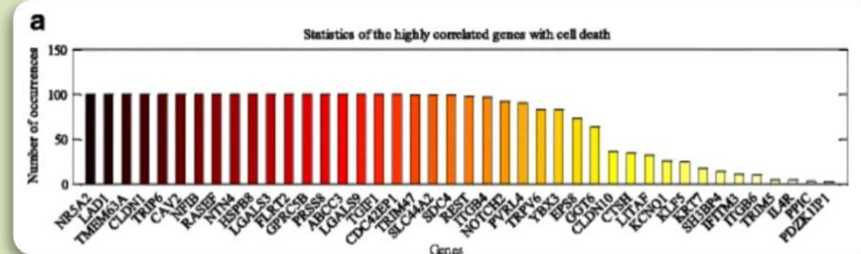
As such, *P* can be rewritten as:

$$P = \sum_{n=0}^{\infty} \left(k_{An}x_A^n + k_{Bn}x_B^n + k_{Cn}x_C^n\right)$$
$$= \sum_{n=1}^{\infty} \left(k_{An}x_A^n + k_{Bn}x_B^n + k_{Cn}x_C^n\right) + b,$$

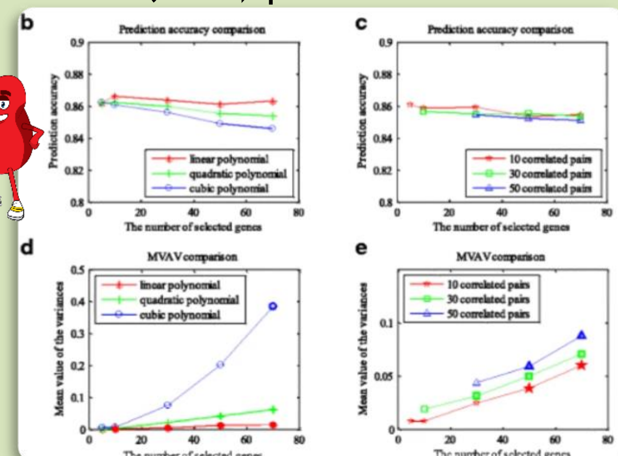
where k_{An}, k_{Bn} and k_{Cn} are polynomial coefficients, and *b* is a constant.

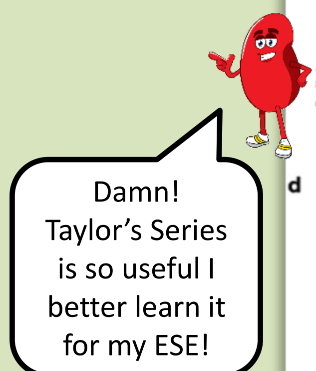
Results

Cell fate prediction based on genes selected by correlation analysis



Prediction accuracies of cell death by using different degree polynomial models (linear, quadratic and cubic polynomials)





References

[Byjus-Taylor-Series]

[Taylor's theorem – Wikipedia]

[A polynomial based model for cell fate prediction in human diseases | BMC Systems Biology | Full Text (biomedcentral.com)]