

## Use of Constraint Based Methods for Analysis of Senescence

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#### Senescent Cells

Unable to replicate anymore.

Associated with aging.

Caused by different types of internal or external stress.

Telomere shortening is one common senescence cause.

Have a multi-component senescenceassociated secretory phenotype(SASP).

Phenotype is dynamic and depends on cell and stress type.

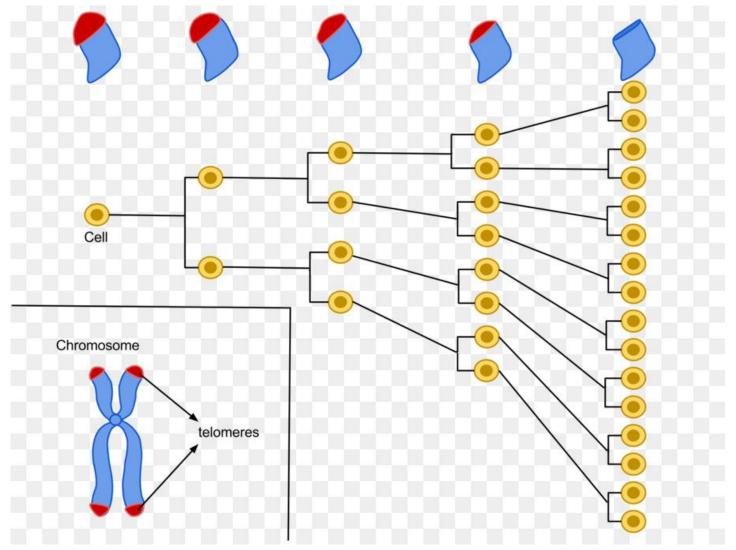


Figure 1: Telomere shortening as a common cause of senescence. Retrieved from: https://en.wikipedia.org/wiki/Cellular\_senescence

Wiley, C., & Campisi, J. (2016). From Ancient Pathways to Aging Cells—Connecting Metabolism and Cellular Senescence. Cell Metabolism, 23(6), 1013-1021. doi: 10.1016/j.cmet.2016.05.010

#### Benefits:

Protection of Organisms from cancer.

Improvement of specific biological processes (wound healing, embryonic structure formation)

#### Detriments:

Senescence-associated secretory phenotype(SASP) has a detrimental effect on surrounding cells.

Linked to age-related diseases

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### Benefits and Detriments of Senescence

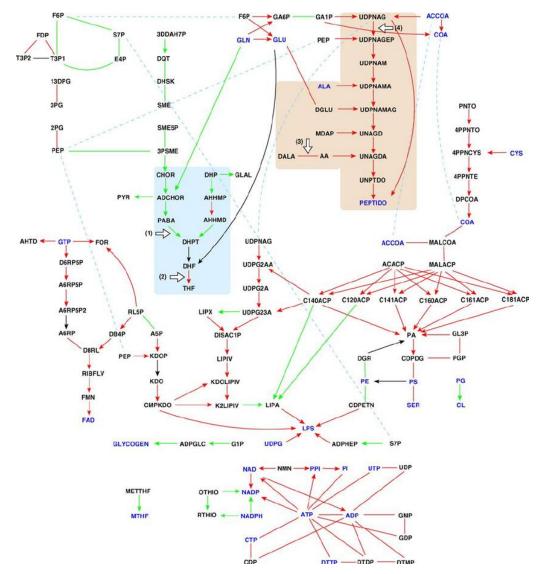


Figure 2: Metabolic Core of E.Coli. Retrieved from: https://journals.plos.org/ploscompbiol/article/figure?id=10.1371/journal.pcbi.0010068.g002

### Metabolic model

Senescence can be analyzed through metabolic models.

Metabolic models: describe interactions of different metabolites through their different reactions.

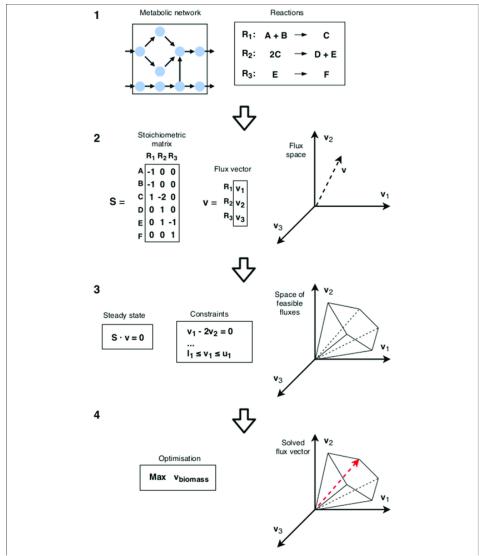


Figure 3: Visualization of Flux Balance Analysis. Retrieved from: https://www.frontiersin.org/articles/10.3389/fams.2019.00018/full

#### **COBRA**

Constraint-Based Reconstruction and Analysis (COBRA) methods can be used to analyze the metabolic models of non-senescent and radiation-induced senescent human diploid fibroblast cells (WI-38).

COBRA imposes a steady-state mass balance constraint which keeps the concentration of all the metabolites constant.

These constraints mathematically describe a multidimensional solution space of the possibly steady-state flux distributions of the model.

# Monte Carlo Sampling

Commonly used COBRA method.

Whole flux space is sampled in a uniform fashion yielding a big number of flux vectors that collectively map out a solution space.

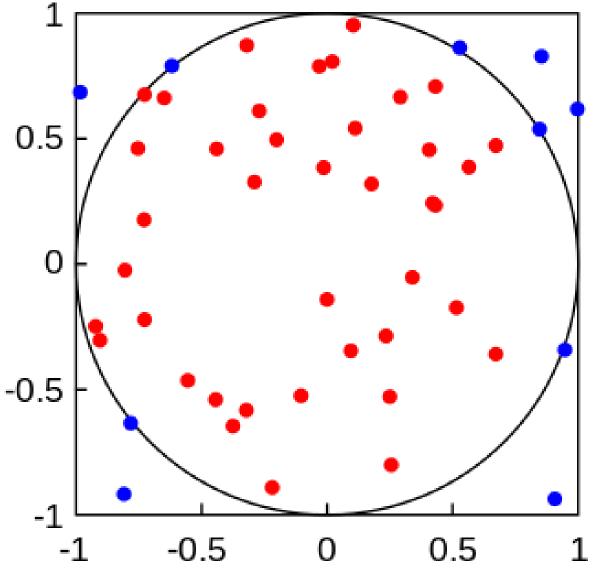


Figure 4: Visualization of Monte Carlo Sampling. Retrieved from: https://en.wikipedia.org/wiki/Monte\_Carlo\_integration

Barrett, C., Herrgard, M., & Palsson, B. (2009). Decomposing complex reaction networks using random sampling, principal component analysis, and basis rotation. BMC Systems Biology, 3(1), 30. doi: 10.1186/1752-0509-3-30

## Expectation Propagation

Is a similar method to Flux Space Sampling which is based on Expectation Propagation(EP) equations and provides a probability distribution for each reaction flux.

EP provides an analytical approximation to Monte Carlo Sampling.

EP has much lower computation time and yields similar results to Monte Carlo Sampling.

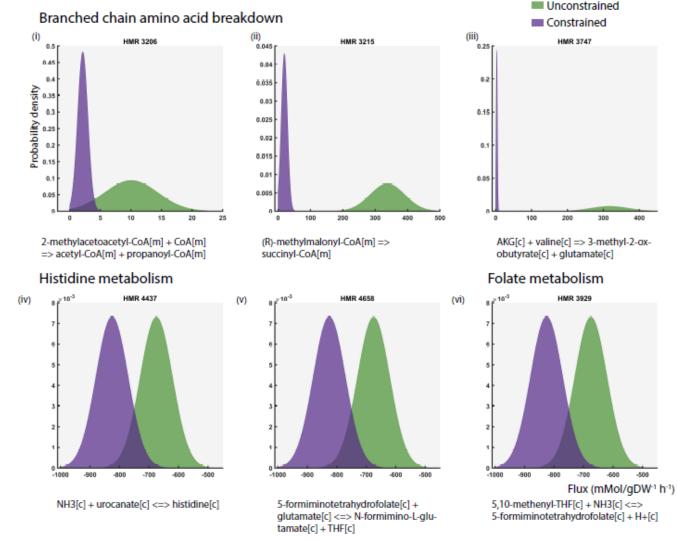


Figure 5: Probability distribution of reaction flux of different reactions. Retrieved from: https://www.biorxiv.org/content/10.1101/2020.09.14.296145v1

Braunstein, A., Muntoni, A., & Pagnani, A. (2017). An analytic approximation of the feasible space of metabolic networks. Nature Communications, 8(1). doi: 10.1038/ncomms14915

#### ComMet

ComMet is a method to compare metabolic states between metabolic networks.

ComMet uses EP for sampling which means it can be used to analyze flux rates of the metabolic model of non-senescent and radiation-induced senescent human diploid fibroblast cells (WI-38).

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