

novel cost-effective technology to extract gold from these tailings and also from low grade ore (extraction grade less than 3 g/t).

Use of plants to extract metals from ore is called phytomining. The uptake of gold by plants has fascinated scientists for over 100 years but no hyper-accumulator-species for this metal has been reliably reported. This is due to gold's low solubility in a soil environment. Induced hyper-accumulation of gold by plants was first reported⁴ in 1998. Preliminary research conducted in our laboratory also proved that some of the terrestrial wild cultivars of local plants are the best candidates for this purpose and accumulate high amounts of gold up to 30–40 mg/kg of plant dry weight (unpublished data) in the presence of a known chelating agent which increases the availability of gold to plant roots.

The concentration of gold that can be induced into a plant is dependent upon the gold concentration in the soil on which a plant is growing⁵. Experimental results showed that plants will accumulate approximately 20% of the total amount of gold available within a root zone based on any

one treatment by different chosen chelating agents⁶. The 20% recovery rule was proved to be true for many tested plant species. Anderson and his coworkers showed that approximately 2 mg of gold per kg of soil is needed by considering a soil profile of 20 cm depth to achieve 100 mg/kg of plant dry biomass. The model also assumes a harvested biomass of 10 tonnes/ha and a gold concentration of 100 mg/kg of plant dry weight. This will yield 1 kg of gold per hectare. It has been proved that the conventional solvent extraction method to recover gold from 1 tonne of ash obtained by incinerating 10 tonnes of dry plant material, is an economically viable option.

A study was conducted at the Fazenda Brasileiro Gold Mines⁶, north of Salvador, Brazil during April–July 2003. The extraction grade of ore was approximately 1.5 g/t. The plants *Brassica* sp. and *Zea mays* were used as hyper-accumulator plants and the results proved that the phytomining technology is a cost-effective promising technology. There is an urgent need to conduct some field experiments and optimize this technology in KGF soil using ore tailings and fresh ore sample to develop some economic models. If a proper

approach is given to address this problem using phytomining technology, the city of gold will regain its glitter soon.

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Systems biology is all noise

Old age is generally characterized by a set of debilitating health conditions. The symptom-free and the disease-free definitions of old age are unpopular. Likewise, a perturbation-free description of gene expression is uncommon, i.e. the gene expression profile is usually defined in relation to changes in environmental conditions, both external and internal.

Michael Elowitz¹ and his colleagues showed that genes do not *talk* they actually *chatter*, i.e. the gene expression flux varies significantly during transcription. Cells heuristically guide transcriptional machinery towards an optimized output while retaining the noisy expression profile in the background. To understand the gene network dynamics, it may be intuitive to follow the 'conversation', but studies hint that 'chatter' may be equally or even more important^{2–5}. Thus a complete understanding of the system would emerge by taking into account the optimal trajectories of gene expression, the range within which genes express themselves and the

underlying reason of chosen trajectories. Thus, the key to understanding gene behaviour in a multi-component and hierarchical network lies in the ability to systematically capture, manage and analyse gene expression noise, while following the optimal solution temporally. Here I discuss various aspects of noise dynamics and try to build a case for 'noisome'—a perturbation-free, time-correlated, background gene expression profile under normal physiological conditions. Since the expression data can be temporally sampled in a controlled environment using defined genes, promoters and environment, it is experimentally feasible to build a module-centric, network-centric or cell-centric noisome. Noisome can serve as a reference point for understanding the mechanistic basis of perturbation-induced variations with their corresponding phenotypic outcomes.

What are the raw materials and challenges in building 'noisome'? At the component level, the primary requirement is

the availability of a reproducible time-series expression data⁶. At the network level, it is the availability of expression data of at least a pair of interacting genes. Due to experimental limitations and prohibitive lab costs, it is unfeasible to cover all the desirable time points. To overcome this limitation, computational modelling can be used to fill-in the missing data points between any two experimentally derived data points. Of various qualitative and quantitative methods of animating gene expression *in-silico*, stochastic approach gives the most accurate solution. However, both stochastic and spatio-temporal algorithms impose the immense computational burden and are painfully slow. On the other hand, Tau–Leap methods, hybrid algorithms and parallel algorithms are among the fastest simulation algorithms, but are less rigorous. A good compromise is offered by Stochsim and Gibson algorithms, which increase the speed of simulation without sacrificing the accuracy of solutions⁷.

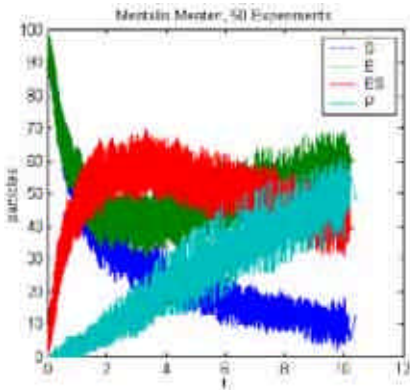


Figure 1. Computer generated stochastic simulation showing how noise accompanies the evolution of an optimal solution.

What is the biological value of building noise? Among the very first users would be people trying to understand the dynamics of gene regulatory networks *vis-à-vis* the existence of noise *smear* over the network. A number of unsolved questions can be addressed through noise. For example: Do gene families with a particular noise pattern exist? What mechanisms ensure that genes or a category of genes always function within a specific noise threshold? What happens when the cells cross the optimal noise boundary conditions? Are biological complexity and emergence a function of noise? How do activators and inhibitors impact noise levels in a given network space? Does noise play a role in speciation and phylogenetic evolution of gene networks? The answer to all these questions is: We simply do not know.

Noisome may help genome engineers to make use of noise signatures and design novel genomes finely tuned to specific noise patterns. A less noisy gene would be energetically more favourable to operate and maintain than a noisier gene. The additive/subtractive property of noise can be used to create synthetic networks with a specific noise profile. We do not know if network phenotype is determined by the ratio of low-noise and pure high-noise genes, maintained at a certain equilibrium state. How do pure low-noise and pure high-noise gene families behave in isolation? We have no idea. It would be interesting to investigate the behaviour of low-noise and high-noise genes connected serially and in parallel. This has application in synthetic biology where the sole aim is to create novel and unnatural cell circuits *in-vivo* for biological and clinical applications.

The emergence of noise may also address a number of questions of fundamental importance. For example, is genome 'compartmentalized' into various noise domains? If yes, are gene communities topologically ordered on the basis of their noise patterns? Do cells use local and/or global noise thresholds as built-in memory primitives? What is the effect of adding noise (strong promoter, gene knock-in) or decreasing noise (weak promoter, gene knock-out) on cell circuits? Is cancer an outcome of mismanaged network noise dynamics? Do chromosomal translocations or deletions push cells beyond an allowable noise threshold? What fea-

tures and combination of noise patterns make a cell fragile/robust to external conditions? It is obvious that a number of interesting unsolved problems in biology can be addressed through noise. Transcriptomics and metabolomics only reveal a part of the cell story. Noisomics, the systems biology of noise and a *subspecies* of transcriptomics may turn out to be a *genus* in itself.

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Ethics in science: On the selective suppression of inconvenient data

In a recent article¹, Narlikar has recounted the circumstances behind Eddington's claim to have provided convincing proof of Einstein's theory of general relativity. This was based on the famous 1919 experiments performed by Eddington and Crommelin during a total solar eclipse. However, recent research by science-historians has given an entirely different perspective on the whole affair². It transpires that Eddington had resorted to unethical means to substantiate his claim. The details of the 1919 experiments have now been fully exposed in a book by John Waller².

When light from a distant star passes close to the sun, it gets deviated by a minute fraction of a degree because of the gravitational warp of space. This deviation should be about 1.7 arcsec if Einstein's theory was correct. On the other hand, if the light ray followed the existing Newtonian laws, the deviation should be only around 0.8 arcsec. In 1919, Eddington planned to set out on an expedition to regions where the solar eclipse would be clearly visible, and to set up experiments to measure the deviation of the stellar light in the vicinity of the sun. This was certainly

an ambitious aim. The problem of accurately measuring such minute displacements with the available instruments was further compounded by several others: if the light rays did not pass almost along the edge of the sun during the eclipse, but farther away, the gravitational effect would be smaller and so the deviation would be still less; atmospheric turbulence as well as variations in temperature during the measurements would contribute to the distortion and would have to be adjusted for. Such adjustments could only be carried out if proper statistical tech-