Towards Cross-Modeling between Life and Solid State Physics

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Abstract. We develop a hierarchical model for an organism which is primarily based on structural scale. This is then compared with the Kronig-Penney model for electron propagation in a crystal. Both models exhibit similar multi-level structure, where the levels are separated by complex or forbidden regions. We conclude that cross-modeling between natural hierarchy and electron band structures may help in formulating future models of biological systems.

Keywords: scale, hierarchy, hyperscale, life, Kronig-Penney.

1 Introduction

There have been many and varied attempts to provide models of living systems or organisms. Possibly the two most well-known are due to James Grier Miller (1978) and Robert Rosen (1991). Miller proposed that living systems form 8 levels of complexity, from biological cells up to supranational organizations, each depending on the same 20 essential subsystems in order to survive. Rosen developed his (M,R) representation of an organism by internalizing efficient cause. Unfortunately, neither of these successfully describes a multi-scalar organism: Miller's model takes no account of inter-scalar coupling, and Rosen's makes no attempt to deal with scale (Cottam et al., 2007).

In this paper we will develop a model of a living system – or organism – which is primarily based on structural scale. A major characteristic of the model is the way in which scales are coupled together through complex fractal regions, and this leads us in the direction of another different model. Arguably, the most developed model of a physical domain is that of solid state physics, through its application to the development of integrated circuits and computer processors. Fascinatingly, this model itself presents a number of different energetic levels similarly separated by 'forbidden zones'. Our central thesis is that it may be possible to develop better models of life by crossover between the two very different representations. An immediate objection which comes to mind is that the solid state physics of informatics applications is based on the long-range atomic order of perfect crystals, which is absent from living entities. However, many of the constituent chemicals which go to make up living tissue present an almost crystal-like appearance – for example the lipid pdmpg, or

even DNA. We do not propose that simplistic solid state physical models can be directly applied to organisms, merely that it should be instructive to compare them with models of life.

2 Scale

Different systems or systemic sub-units exhibit different bandwidths in the way that they relate to their surroundings. In the theoretical extreme, these could range from sensitivity to *all* sizes to sensitivity to only *one* size (Figure 1(a), 1(b)). Practically, however, these extremes never exist, and real bandwidths range from large-but-finite to small-but-finite extents (Figure 1(c), 1(d)). Individual bandwidths start to become interesting when their owners are combined into more complicated systems.

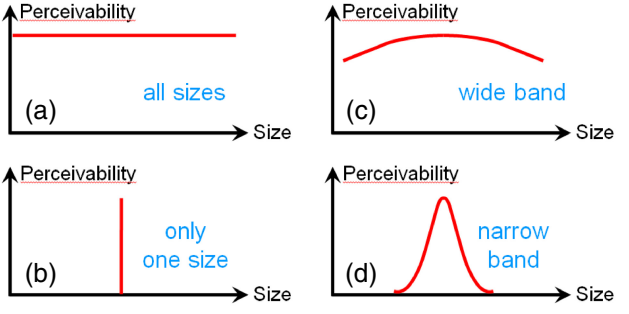

Fig. 1. System sub-unit bandwidths: (a) and (b) theoretical extremes; (c) and (d) realistic limits.

In the case of the theoretical extremes, if all sub-units possessed infinite sensitivities, then the individual sub-units would have no relevance at all (Figure 2(a)); and if all possessed sensitivities to just one size there would be no inter-unit coupling (Figure 2(b)).

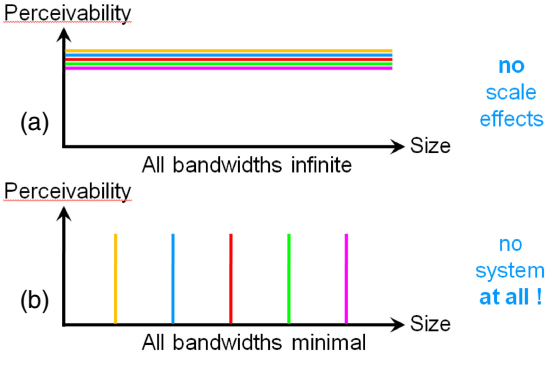

Fig. 2. Theoretical extremes of sub-unit bandwidth combinations.

More pragmatically, combining differently-'scaled' sub-units with wide bandwidths results in a global system which exhibits hardly any effects of scale – as in the case of a crystal (Figure 3(a)) – while combining sub-units with narrow but still overlapping bandwidths results in a system which exhibits complex inter-scalar properties – as in the case of an organism (Figure 3(b)).

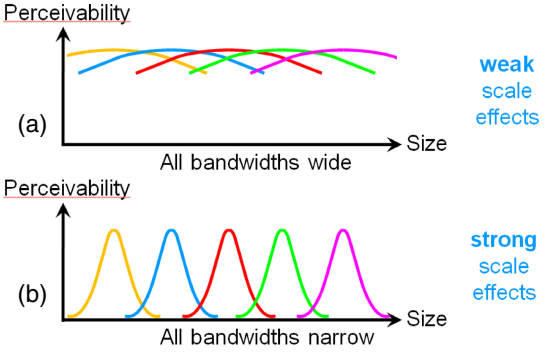

Fig. 3. Realistic limits of sub-unit bandwidth combinations

Given a system consisting of a number of different interacting scalar levels, then the ease or difficulty of transiting between any pair of adjacent levels depends on the similarity or diversity of their internal representations. Figure 4 presents an example of such a set of model-levels: those used to represent an electronic diode.

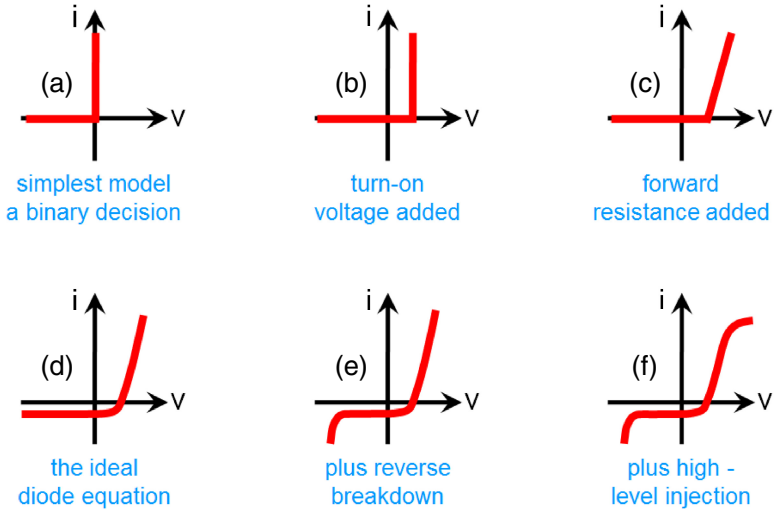

Fig. 4. A sequential set of models of an electronic diode.

The first, simplest model 4(a) corresponds to zero electronic current i for reverse (negative) voltage V, but a positive electronic current for forward (positive) voltage. The next, 4(b) adds in a zero-offset (the 'turn-on' voltage). Model 4(c) adds a linear slope to the forward current characteristic. All three of these – 4(a), 4(b) and 4(c) – are related piecewise linear models. The fourth model, 4(d) is radically different, being based on an exponential evaluation of electronic flow – the 'ideal diode equation'. Model five 4(e) adds in the result of 'reverse breakdown' of the diode, and model six 4(f) adds in the result of 'high-level injection'. None of these models is universally 'the best' – each of them relates best to a specific set of environmental conditions, mainly in terms of the applied voltage. This in itself is a valid generalization of all model sets for a specific parameter or phenomenon: a long-standing model is rarely 'wrong', but usually badly adapted to newly occurring or discovered environmental conditions. Transit between levels 4(a), 4(b) and 4(c) or between 4(d), 4(e) and 4(f) is comparatively easy, but certainly not between 4(c) and 4(d), where the models' derivations are completely different.

This question of inter-scalar transit is fundamental to the way multi-scalar systems operate. Each scalar level must be partially independent – or 'closed' – to maintain itself, while partially communicating with its neighbors – or 'open' – to maintain system unification. A good example of the problems involved in going from lower to higher scales of a system is the equation 1 + 1 = 2. This is far more complex than initially appears. The first thing we should notice is that there is no generally applicable manner of combining two entities to make one. The equation itself belongs in a completely abstract mathematical domain where its meaning and result are predefined. The problem is that between the left hand side and the right hand side of the equation there is a loss of degrees of freedom – a loss of information! In reality, one apple plus one apple does not give one bigger apple. And if it did, would that apple be two times the volume, or two times the width, or two times the height, or … This is a basic difficulty for the progressive evolution of multiple scales… at each level of development information is lost.

A place we expect to find scale, where in fact there is none, is in large complicated digital information processors. A computer has a physical nature, and as such there may/will be some aspects of spatial scale depending on the construction of its components. However, in its role as a digital information processor the individual processing gate operations are absolutely isolated from each other by the system clock, which ensures that all of the gates have settled down to their pre-ordained states before they are connected or re-connected for a short period. In essence, the only global properties of such an information processor *were* in the head of the computer designer or programmer, or *are* in the head of its user. Consequently, any attempt to create global-dependent phenomena in a digital computer – whether 'intelligence' or 'consciousness' – is doomed to failure.

In passing, this raises another, more general question: that of *information*. Information depends on interpretation. Habitually, the concept of information is closely tied to the work of Shannon (1948) on communication channels. Unfortunately, Shannon effectively maintains that information exists not only in 'the sender' and 'the receiver', but also within the intervening channel (Schroeder, 2011). This is unreasonable.

As we pointed out, information depends on interpretation – it is a combination of data and context, whose correlation is absent from the communication channel, where data and context are indistinguishable[1].

The principal function of a computer clock, therefore, is to isolate local from global. A result of this is that a computer cannot provide output until it has waited for the outputs of each and every one of its gates (it is no defense to maintain that many gates are eliminated by 'if-then' clauses; in terms of the current computation these gates do not exist!). Consequently, the bigger you make a processing structure, the slower the computer will be (for the same clock speed): lower 'levels' run faster than higher ones. This is fundamentally different from a biological multi-scalar system, where the bigger the scalar assembly, the faster it can run in responding to external stimuli: higher levels run faster than lower ones!

3 Hierarchy

Hierarchy is nominally "a human abstraction"[2]. Traditionally, only two types of hierarchy are recognized:

a *scalar* hierarchy, e.g. atoms – molecules – cells – organisms - …

a *specification* hierarchy, e.g. physics – chemistry – biology – society - …

However, natural systems are better represented by a *model* hierarchy, similar to that described in Figure 4, which resembles a specification hierarchy that has been constructed in terms of scale. Conventionally, the highest level of a hierarchy is supposed to be dominant, but in a model hierarchy this is not the case; any model level can be the most suitable in a specific context.

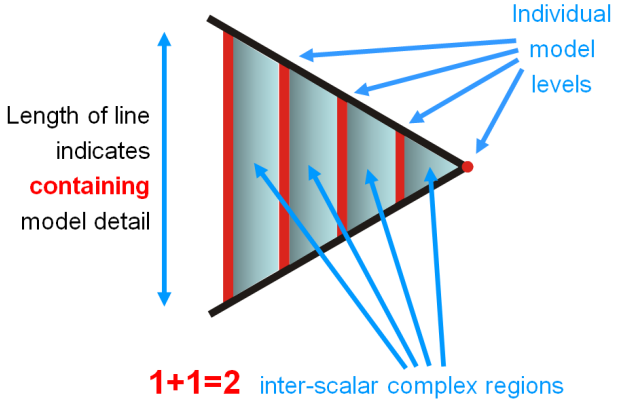

Fig. 5. A general representation of a natural multi-scalar hierarchy.

[1] Clearly, in the case that both are transmitted as binary digits there is no distinction between them.
[2] A quotation from Stan Salthe.

To indicate this difference we will draw our hierarchy turned on its side (Figure 5), with the 'highest' level[3] at the right hand side. In Figure 5, each scalar level is represented by a vertical line, where the length of the line indicates how much information is needed to define that level. Between each pair of levels is a complex region which corresponds to the difficulty in generalizing the loss of degrees of freedom on transiting upscale[3].

The complexity we refer to here is not the Kolmogorov complexity related to digital systems, it is equivalent to Robert Rosen's definition:

> "*A system is simple if all its models are simulable. A system that is not simple, and that accordingly must have a nonsimulable model, is complex*." (Rosen, 1991)

More generally, for our purposes, we can suggest that:

> *simple* implies 'easy to compute',
> *complicated* implies 'more of the same',
> *complex* implies 'only imprecisely computable, if that!'

The logistic plot of $x_{i+1} = -Kx_i\,(1-x_i)$ has the same form as this representation of a natural hierarchy (Figure 6), with scaled simple discrete solutions separated by regions of complexity[4]. This suggests that this general nature of scale sets and complex coupling may be more widespread than at first appears.

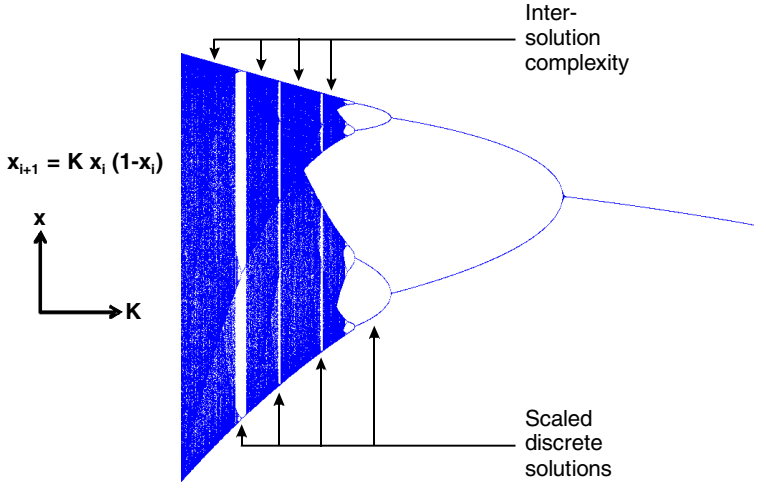

Fig. 6. The form of the logistic plot is similar to that of the natural hierarchy.

[3] The 'higher' the level, the more descriptive information has been lost (c.f. 1+1=2).
[4] Note that here the complexity is not naturally Rosennean, it is created by temporal incomputability.

Natural multi-scalar systems, like organisms, are unified. However, unification cannot be imposed from outside – it is the result of inter-scalar correlations. It is important to note again that individual scalar levels are partially 'enclosed' – shut off from their neighbors – and therefore can only be approximately observed from outside. In essence, any specific level can 'decide' what it communicates and what it withholds (in the way that a biological cell does with respect to its neighbors).

The result of this cross-scalar-set correlation is a systemic identity referred to as *hyperscale* – an approximate reproduction of the scalar set but one which is transparent to inter-scalar transit (Figure 7). Hyperscale is the real nature of the system, whether it is observed from inside or from outside. To the extent that we can, we create a hyperscalar image of everything we encounter – even of ourselves! Any lack of 'correct' information is filled in subconsciously with un-validated images, convenient but outdated models, etc.[5]

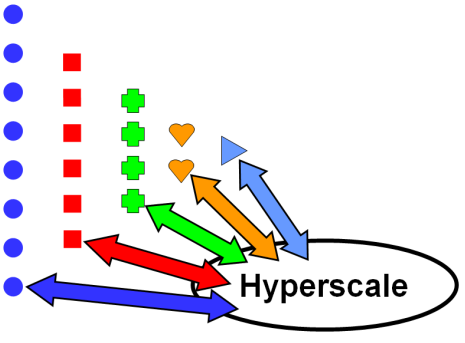

Fig. 7. Integration of the scales of a unified natural hierarchy into its *hyperscalar* identity.

The central premise of this paper is that the establishment of this kind of natural hierarchy is sufficient to create life. Such a hierarchical framework appears to be the basic building block of nature. Ergo, life is unavoidable. In searching for a mathematical formulation to represent biology this is an important guide; we should look for mathematical structures which naturally generate this kind of complexity-coupled multi-layer framework.

4 Electron Properties in the Solid State

We can refer to electrons in crystals either as particles or as waves.

In free space, the motion of electrons as particles can be characterized by

$$Energy\ E = \frac{1}{2}mv^2$$ where m is electron mass, and v is its velocity

[5] For example, it is convenient when using satellite navigation (GPS) to re-assume that the earth is flat!

$$Momentum\ p = mv$$

$$Energy\ E = (1/2m)p^2$$

In a crystal, solution of Schrödinger's equation injects Dirac's constant $h/2\pi$:

$$Energy\ E = \left(h^2/8\pi^2\, m^*\right)p^2$$

where m^* is the electron's effective mass[6]

This yields the parabola of *Energy E* plotted against *p* shown in Figure 8.

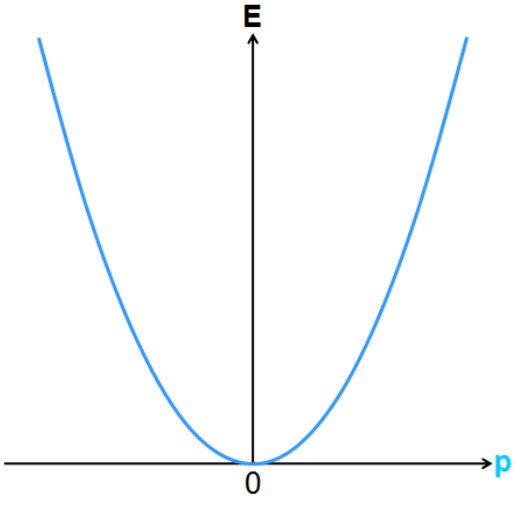

Fig. 8. Energy *E* versus momentum *p* for a particulate electron in a crystal

In a crystal with atomic separation *a*, and an electron characterized as a wave with wavelength λ, discontinuities in wave propagation will occur when $\lambda/2 = a$. Using the De Broglie relation $p = h/\lambda$ these will occur on the p-axis of Figure 8 at values of $n\pi$, where *n* is any integer.

Kronig and Penney (1930) proposed that the energy potential associated with each atom in a crystal, which causes these discontinuities, could be represented by a rectangular profile of width *w* and height V_0. Solutions for the electron wave propagation are then derived from the global equation

$$\cos ka = (R/\alpha a)\sin \alpha a + \cos \alpha a$$

where

$$k = 2\pi/\lambda$$

$$\alpha = (2\pi/h)\sqrt{2Em^*}$$

$$R = V_0 w(4\pi^2 m^* a/h^2)$$

[6] In a crystal, an electron appears to have a different mass from its free space value, called the effective mass m^*.

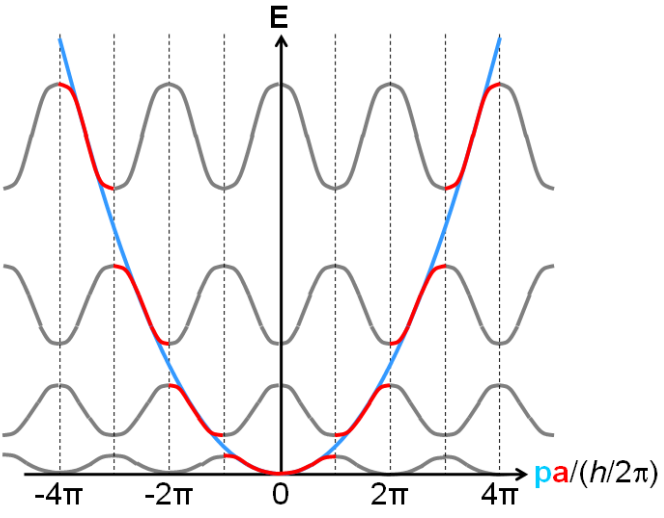

Fig. 9. Solutions of the Kronig-Penney equation. Valid portions are those closest to the parabola.

This yields the set of sinusoidal solutions shown superimposed on the parabola in Figure 9.

Restriction of the solutions to real values of sin/cos between -1 and 1 retains only the parts of the solutions which are closeto the parabola (Figure 10).

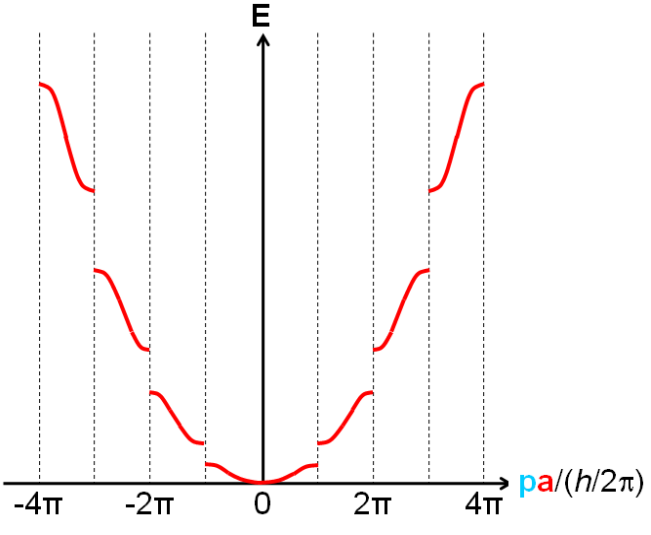

Fig. 10. Remaining *real* solutions to the Kronig-Penney equation

Regions of these solutions which are far from values of $n\pi$ in the plot coincide with the free-space parabola[7], but there are distortions from the parabola at values of $n\pi$. The repeated occurrence of discontinuities with $n\pi$ means that the individual sections of the plot can be folded in on themselves until everything lies between $-\pi$ and $+\pi$ (Figure 11). This gives us the normal way in which the electron *energy bands* are portrayed.

As indicated in Figure 11, we now have a set of permitted regions for electron occupancy which are separated by *forbidden gaps*: precisely the form we were looking for to represent the scale-set of a natural hierarchy.

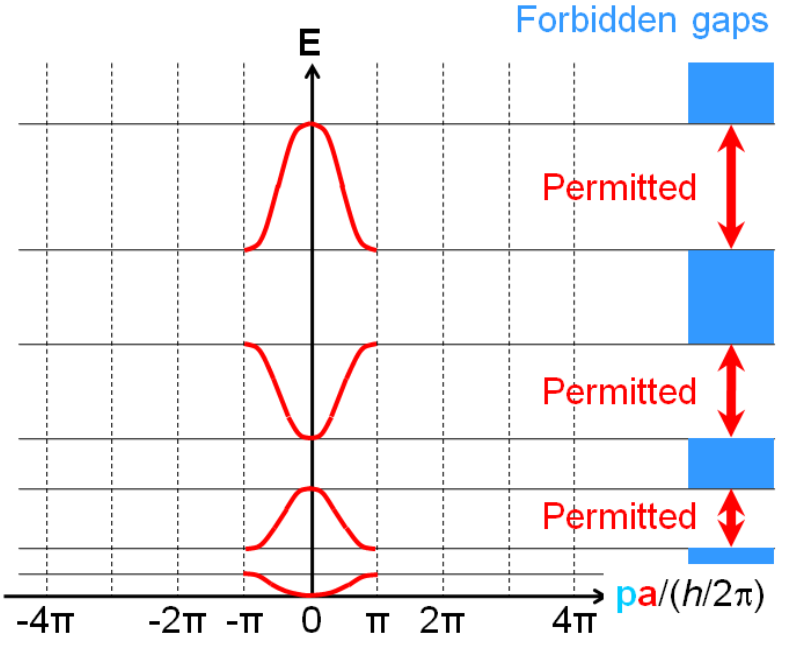

Fig. 11. Real solutions to the Kronig-Penney equation folded in to the region $-\pi$ to $+\pi$.

In addition, the folding in of the different energy bands to the central region closely resembles the generation of *hyperscale* in the multiscalar representation of a living system.

5 Conclusion

The mathematics of solid state physics does indeed present us with a possible mathematical route towards representing the scale-set of a natural hierarchy. As we commented earlier, a clear restriction is the lack of precise long-range order in a biological

[7] … except for the modified value of electron mass m^*.

system when compared to a crystal, and it would be fatuous to suggest that the comparison between natural hierarchy and electron energy bands is sufficient to apply the mathematics we have presented directly to living systems. However, it may be that the fuzziness of biochemical and cellular order, which would correspond to a fuzziness in any comparison, indicates that the hierarchical model we have presented is itself far too precise. It remains to be seen whether cross-modeling between these two very different organizations may directly or indirectly lead to more successful models of biological systems.

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