Evolution of coding structures
Genotype-phenotype mapping: Coding structure

3 questions/answers:

**Given code – > which evolutionary dynamics?**
eg RNA folding: punctuated evolution etc.

**Given problem – > how to code?**
expectation: smooth, non-redundant;
found intertwining neutral paths

**Given evolutionary dynamics – > which code?**
towards robustness, hence evolvability
RNA secondary structure as paradigm for genotype-phenotype mapping computable??

A. globiformis, Anabaena sp., A. tumefaciens, B. japonicum, E. coli B. subtilis, T. thermoph, Pir. marina, Rb. sphaero

alternative basins of attraction: replicator in nonMFE state

FIGURE 13. Structures and base pairing density plots for the native structure and the metastable conformation of the Gβi variant SY11. The secondary structures and their free energies are shown in the upper part. In the lower half we show the matrix of base pair probabilities as obtained from the thermodynamic partition function (McCaskill, 1990; Holzäcker et al., 1994) (left) and from kinetic trajectories (right).

FIGURE 13. Fraction of folding paths visiting local minima in the Gβi variant SY11. The majority of paths visits the local minima in the basin of the metastable structure where the paths get trapped. Only about 15% reach the ground state.
Elucidate evolutionary properties
JUST RNA?
or even just by wrongly computed (and 2 D) folding?

percolating neutral path; innovations
 evolution toward robustness

NO......

similar (mutatis mutandis) properties in

Gene regulatory networks ( A Wagner 2007a,b)
Protein folding A Wagner 2010
Metabolic networks (A.Wagner 2012)

see also books by A. Wagner
From paradigm systems to general conclusions

vs

Studying “all” cases

NK landscapes (Kauffman):
Class of models to study impact of GP mapping on evolutionary dynamics.

N: number of properties (e.g. sequence length)
K: number of “epistatic’ interactions
most often 2 states per position

Fitness contribution of each $N \cdot 2^K$ states
chosen randomly. Fitness is sum of those

Calculate e.g. pathlength to local peak
height of optima reached (etc.)

NO percolating, intercalating neutral paths
and its evolutionary consequences

later versions have included neutrality
Evolution of coding structure:
Evolution of multiple coding in RNA’s

doing more with less

Evolve towards target == set of (25) RNA structures .
ALL other structures (Shapiro) TOXIC

define possible interaction of RNA’s:
adaptors (=single hairpin)
can bind to other RNA
bound (modified) nucl not ’available’
for folding

fitness of cell: set of struct.
cells compete in space

How to cope with high mutation rates?

de Boer & H. PLOS-One 2012
High mutation rate - short genome - same functionality
one adaptor used by all sequences
many adaptors used by 1 sequence
Conclusion: multiple coding

RNA even more an “ideal evolvable molecule”

information threshold shapes coding structure
multiple coding arises and alleviates information threshold

information threshold does not (necessarily) limit functionality

(Similar effects seen with alternative (non-minimal energy) foldings)

Also in this case:
local competition in space helps!
Conclusions

Coding structure adapts to mutation rate
Coding length, selection strength

Result:

Evolution converges to being

Close to Information Threshold