

Lie group structure and Markov invariants for the strand symmetric model [– an adventure in invariant theory]

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Phylomania, November 2011



Conformal supermultiplets without superpartners

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(Dated: June 2011)

We consider polynomial deformations of Lie superalgebras and their representations. For the class $A(n-1, 0) \cong sl(n/1)$, we identify families of superalgebras of quadratic and cubic type, consistent with Jacobi identities. For such deformed superalgebras we point out the possibility of *zero step* supermultiplets, carried on a single, irreducible representation of the even (Lie) subalgebra. For the conformal group $SU(2, 2)$ in 1+3-dimensional spacetime, such irreducible (unitary) representations correspond to standard conformal fields $(j_1, j_2; d)$, where (j_1, j_2) is the spin and d the conformal dimension; in the massless class $j_1 j_2 = 0$, and $d = j_1 + j_2 + 1$. We show that these representations are zero step supermultiplets for the superalgebra $SU_{(2)}(2, 2/1)$, the quadratic deformation of conformal supersymmetry $SU(2, 2/1)$. We propose to elevate $SU_{(2)}(2, 2/1)$ to a symmetry of the S -matrix. Under this scenario, low-energy standard model matter fields (leptons, quarks, Higgs scalars and gauge fields) descended from such conformal supermultiplets are not accompanied by superpartners.

I. INTRODUCTION

The concept of supersymmetry as an extended relativistic invariance principle for the fundamental particles and their interactions confronts severe experimental con-

II. POLYNOMIAL $gl(n)$ SUPERALGEBRAS

The method consists simply in postulating generalised structure constants for the bracket relations of the generators of these algebras, which give the standard relations, plus (including deformation parameters), terms 'nonlinear' in the generators (quadratic and higher polynomials



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Quantum dissipative systems - new and extended models

Quantum dissipative systems (QDS) are essential tools for investigating how quantum systems behave in complex environments, with wide-ranging applications from quantum computation and nanodevices to the molecular behaviour of biological systems. We have recently extended the library of such dissipative systems by revealing the intricate structure of the bosonised elliptic spin-1/2 Kondo model, and by introducing a new three-level QDS via bosonisation of an anisotropic Coqblin-Schrieffer model.

The scattering data of both models can be parameterised by R -matrices satisfying the Yang-Baxter equation for exact solvability, confirming the utility of the models in exposing system behaviour, as well as the potential for new applications. The structure revealed for the extended two-level system indicates that such systems could provide new examples of continuous-time quantum random walks. Bath-mediated transitions between the two levels occur, and potentially provide a new way of assessing the influence of the bath on the quantum system – or on the walker's performance. For the case of the new three-level QDS, the multitude of potential applications includes three-level quantum dots, qutrit states, tritonic triple well potentials (such as ammonia) and Bose-Einstein condensate atomic transistors, which have a three well structure.

The development of these QDS proceeds by careful re-examination of the well-known method of constructive bosonisation and unitary transformation, which has previously been used to establish a mapping between the standard, spin-1/2 anisotropic Kondo model and the spin-boson model (the simplest possible QDS of a two-level system with ohmic coupling to an oscillator bath). The method itself may in the future be applied to other Fermi-gas Hamiltonians in the search for still more QDS, but the range of applications associated with the current exactly solvable QDS firmly establishes the significance of these models in re-assessing the behaviour of quantum systems in complex environments. Evaluation of quantitative aspects of these models will require examination of the associated Bethe Ansatz equations and their solution in terms of the physics of the dissipative system. Furthermore, entanglement relations may be studied in detail, with the associated implications for quantum information and the role of decoherence in a system-environment model.

This work was originally published in *J. Phys. A: Math. Theor.* 44 115003 and *J. Phys. A: Math. Theor.* 43 255305.



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About the author

Sol H Jacobsen recently completed her PhD entitled 'Entanglement and the Quantum-Classical Transition' at the University of Tasmania as a Commonwealth Endeavour Scholar. Peter D Jarvis is currently associate professor at the University of Tasmania, leading their theoretical physics group.



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Proc. Natl. Acad. Sci. USA
Vol. 95, pp. 987–992, February 1998
Biochemistry

A supersymmetric model for the evolution of the genetic code

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Edited by Yuval Ne'eman, Tel-Aviv University, Ramat Aviv, Israel, and approved November 13, 1997 (received for review March 6, 1997)

ABSTRACT A model is presented for the structure and evolution of the eukaryotic and vertebrate mitochondrial genetic codes, based on the representation theory of the Lie superalgebra $A(5,0) = sl(6/1)$. A key role is played by pyrimidine and purine exchange symmetries in codon quartets.

The application of group theoretical methods to spectroscopy is today part of the accepted set of techniques for the analysis

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Quantum dissipative systems - new and extended models

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The scattering data of both models can be parameterised by R-matrices satisfying the Yang-Baxter equation for exact solvability, confirming the utility of the models in exposing system behaviour, as well as the potential for new applications. The structure revealed for the extended two-level system indicates that such systems could provide new examples of continuous-time quantum random walks. Bath-mediated transitions between the two levels occur, and potentially provide a new way of assessing the influence of the bath on the quantum system – or on the walker's performance. For the case of the new three-level QDS, the multitude of potential applications includes three-level quantum dots, qutrit states, tritonic triple well potentials (such as ammonia) and Bose-Einstein condensate atomic transitions, which have a three well structure.

The development of these QDS proceeds by careful re-examination of the well-known method of constructive bosonisation and unitary transformation, which has previously been used to establish a mapping between the standard, spin-1/2 anisotropic Kondo model and the spin-boson model (the simplest possible QDS of a two-level system with ohmic coupling to an oscillator bath). The method itself may in the future be applied to other Fermi-gas Hamiltonians in the search for still more QDS, but the range of applications associated with the current exactly solvable QDS firmly establishes the significance of these models in re-assessing the behaviour of quantum systems in the formation of the associated Bethe Ansatz entanglement relations may be studied in a system-environment model.

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What is the *strand symmetric* model?

- A model of base mutations which addresses DNA double-strandedness:
- Allows different parameters for probabilities of base transitions and base transversions, as in K3ST;
- Instead of being symmetric, Markov matrix keeps track of base pairing, by equating $X \rightarrow Y$ with $\bar{X} \rightarrow \bar{Y}$ where X, \bar{X} and Y, \bar{Y} are canonical (Crick-Watson) base pairs.
- Markov matrix is

$$m = \begin{pmatrix} m_{AA} & m_{AC} & m_{AG} & m_{AT} \\ m_{CA} & m_{CC} & m_{CG} & m_{CT} \\ m_{GA} & m_{GC} & m_{GG} & m_{GT} \\ m_{TA} & m_{TC} & m_{TG} & m_{TT} \end{pmatrix} = \begin{pmatrix} a & b & c & d \\ e & f & g & h \\ h & g & f & e \\ d & c & b & a \end{pmatrix}$$

- May be biologically interesting in situations with reading and transcription on both DNA strands?



What is the *strand symmetric* model? -II

- Theoretically, it sits in a nested sequence of models:
 $GMM \supset SSM \supset K3ST$.
- Introduced by Casanellas and Sullivant, who developed phylogenetic invariants for it.
- Markov matrices have the property that for different parameter sets a, b, c, \dots , and a', b', c', \dots , there are parameters a'', b'', c'', \dots such that $mm' = m''$, namely

$$\begin{pmatrix} a & b & c & d \\ e & f & g & h \\ h & g & f & e \\ d & c & b & a \end{pmatrix} \begin{pmatrix} a' & b' & c' & d' \\ e' & f' & g' & h' \\ h' & g' & f' & e' \\ d' & c' & b' & a' \end{pmatrix} = \begin{pmatrix} a'' & b'' & c'' & d'' \\ e'' & f'' & g'' & h'' \\ h'' & g'' & f'' & e'' \\ d'' & c'' & b'' & a'' \end{pmatrix}$$

- This *multiplicative closure* is very important!
- The SSM has 6 parameters, a, b, c, d, e, f, g, h with two constraints $a + b + c + d = 1$, and $e + f + g + h = 1$.



Rate matrices

- Extend the parametrization to include matrix *inverses*, i.e. consider the associated matrix Lie group, a subgroup $G_{\text{SSM}} \triangleleft GL_1(4) \triangleleft GL(4)$;



Rate matrices

- Extend the parametrization to include matrix *inverses*, i.e. consider the associated matrix Lie group, a subgroup $G_{\text{SSM}} \triangleleft GL_1(4) \triangleleft GL(4)$;
- Standard definitions yield 6D Lie algebra, with generators

$$S_1 = \begin{pmatrix} \bar{1} & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 1 & \bar{1} \end{pmatrix}, \quad S_2 = \begin{pmatrix} \bar{1} & 0 & 1 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & \bar{1} \end{pmatrix}, \quad S_3 = \begin{pmatrix} \bar{1} & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & \bar{1} \end{pmatrix},$$
$$T_1 = \begin{pmatrix} 0 & 0 & 0 & 0 \\ 1 & \bar{1} & 0 & 0 \\ 0 & 0 & \bar{1} & 1 \\ 0 & 0 & 0 & 0 \end{pmatrix}, \quad T_2 = \begin{pmatrix} 0 & 0 & 0 & 0 \\ 0 & \bar{1} & 1 & 0 \\ 0 & 1 & \bar{1} & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}, \quad T_3 = \begin{pmatrix} 0 & 0 & 0 & 0 \\ 0 & \bar{1} & 0 & 1 \\ 1 & 0 & \bar{1} & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix}.$$

- In a continuous time formulation, the Markov matrices become matrix exponentials $m = \exp(tQ)$ for rate matrices Q , and edge time t , &

$$Q = \alpha_1 S_1 + \alpha_2 S_2 + \alpha_3 S_3 + \beta_1 T_1 + \beta_2 T_2 + \beta_3 T_3$$

for 'suitable' rate parameters $\alpha_1, \alpha_2, \alpha_3, \beta_1, \beta_2, \beta_3$ (e.g., all ≥ 0).

Structure of the Lie algebra - I

Theorem The Lie algebra $L(G_{\text{SSM}})$ of the strand symmetric model is isomorphic to a direct sum $sl_2 + g_1 + g_1 \times \mathbb{C}$ where sl_2 is the standard simple 3D Lie algebra ($\cong A_1$), g_1 is a 1D abelian Lie algebra ($\cong \mathbb{C}$) and $g_1 \times \mathbb{C}$ is the 2D shift algebra equivalent to GMM_2 .



Structure of the Lie algebra - I

Theorem The Lie algebra $L(G_{\text{SSM}})$ of the strand symmetric model is isomorphic to a direct sum $s\mathfrak{l}_2 + \mathfrak{g}\mathfrak{l}_1 + \mathfrak{g}\mathfrak{l}_1 \times \mathbb{C}$ where $s\mathfrak{l}_2$ is the standard simple 3D Lie algebra ($\cong A_1$), $\mathfrak{g}\mathfrak{l}_1$ is a 1D abelian Lie algebra ($\cong \mathbb{C}$) and $\mathfrak{g}\mathfrak{l}_1 \times \mathbb{C}$ is the 2D shift algebra equivalent to GMM_2 .

The 4×4 generator matrices adapted to the above decomposition are the combinations

$$K_0 = -\frac{1}{4}(S_3 - T_2), \quad K_+ = \frac{1}{2}(S_1 - S_2), \quad K_- = \frac{1}{2}(T_1 - T_3);$$

$$R = \frac{1}{2}(S_3 + T_2);$$

$$X = \frac{1}{4}(S_1 + S_2 + T_1 + T_3),$$

$$Y = \frac{1}{4}(-S_1 - S_2 + S_3 + T_1 - T_2 + T_3).$$

and nonzero Lie brackets (commutation relations)

$$[K_0, K_{\pm}] = \pm K_{\pm}, \quad [K_+, K_-] = 2K_0,$$

$$[X, Y] = Y$$



Structure of the Lie algebra - II

– explicitly, these combinations of rate matrices are

$$K_0 = \frac{1}{4} \begin{pmatrix} 1 & 0 & 0 & \bar{1} \\ 0 & \bar{1} & 1 & 0 \\ 0 & 1 & \bar{1} & 0 \\ \bar{1} & 0 & 0 & 1 \end{pmatrix}, \quad K_+ = \frac{1}{2} \begin{pmatrix} 0 & 1 & \bar{1} & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & \bar{1} & 1 & 0 \end{pmatrix}, \quad K_- = \frac{1}{2} \begin{pmatrix} 0 & 0 & 0 & 0 \\ 1 & 0 & 0 & \bar{1} \\ \bar{1} & 0 & 0 & 1 \\ 0 & 0 & 0 & 0 \end{pmatrix};$$

$$R = \frac{1}{2} \begin{pmatrix} \bar{1} & 0 & 0 & 1 \\ 0 & \bar{1} & 1 & 0 \\ 0 & 1 & \bar{1} & 0 \\ 1 & 0 & 0 & \bar{1} \end{pmatrix};$$

$$X = \frac{1}{4} \begin{pmatrix} \bar{2} & 1 & 1 & 0 \\ 1 & \bar{2} & 0 & 1 \\ 1 & 0 & \bar{2} & 1 \\ 0 & 1 & 1 & \bar{2} \end{pmatrix}, \quad Y = \frac{1}{4} \begin{pmatrix} 1 & \bar{1} & \bar{1} & 1 \\ 1 & \bar{1} & \bar{1} & 1 \\ 1 & \bar{1} & \bar{1} & 1 \\ 1 & \bar{1} & \bar{1} & 1 \end{pmatrix}.$$



Structure of the nucleotide character states

- We are at liberty to choose effective nucleotide character 'states' which reflect the symmetry transformation structure more closely (that is, use a special basis!)
- Define the special vectors

$$\mathbf{e}_0 = \begin{pmatrix} 1 \\ 0 \\ 0 \\ \bar{1} \end{pmatrix}, \quad \mathbf{e}_1 = \begin{pmatrix} 0 \\ 1 \\ \bar{1} \\ 0 \end{pmatrix}, \quad \mathbf{u}_0 = \begin{pmatrix} 1 \\ 0 \\ 0 \\ 1 \end{pmatrix}, \quad \mathbf{u}_1 = \begin{pmatrix} 0 \\ 1 \\ 1 \\ 0 \end{pmatrix},$$

- Then $\mathbf{e}_0, \mathbf{e}_1$ transform only under K_0, K_{\pm} (as a doublet, with R eigenvalue -1), and w.r.t. $\mathbf{u}_0, \mathbf{u}_1$, the generators X, Y are equivalent to the binary GMM,

$$X = \begin{pmatrix} \bar{1} & 1 \\ 0 & 0 \end{pmatrix}, \quad Y = \begin{pmatrix} 1 & \bar{1} \\ 1 & \bar{1} \end{pmatrix}, \quad \left[X+Y \equiv \begin{pmatrix} 0 & 0 \\ 1 & \bar{1} \end{pmatrix} \right]$$



Markov invariants - abstract

- Consider some phylogenetic group $G \triangleleft GL_1(4)$ and L taxa. Then phylogenetic pattern frequencies $P_{i_1 i_2 \dots i_L}$ evolve under the product group $\times^L G = G \times G \times \dots \times G$ (by matrix multiplication),

$$P \rightarrow P' = m_1 \times m_2 \times \dots \times m_L \cdot P$$

- We look for polynomials $I(P)$ of degree D which form one-dimensional representations, i.e. which change only up to a scalar factor under phylogenetic evolution:

$$I(P') = \det(m_1)^{w_1} \det(m_2)^{w_2} \dots \det(m_L)^{w_L} I(P)$$

– we call such objects *Markov invariants* (of weight (w_1, w_2, \dots, w_L)).



Markov invariants – algorithm

- In the following, we require partitions $\sigma \vdash D$, $\sigma = (\sigma_1, \sigma_2, \dots, \sigma_\ell)$ with $\sigma_1 \geq \sigma_2 \geq \dots \geq \sigma_\ell$, $|\sigma| := \sum_i \sigma_i \equiv D$, in their guise as representations of the symmetric group \mathfrak{S}_D .
- For example (D) is a one part partition, and $(1, 1, \dots, 1) \equiv (1^D)$ is a D part partition
- *Inner product* $\rho * \sigma = \sum_{\tau} g_{\rho, \sigma}^{\tau} \tau$ derives from reduction of Kronecker product of representations in \mathfrak{S}_D , iterated version

$$\sigma_1 * \sigma_2 * \dots * \sigma_L = \sum_{\tau} g_{\sigma_1, \sigma_2, \dots, \sigma_L}^{\tau} \tau$$

- We also need the notion of plethysm (symmetrised Kronecker power, Schur functor) of a representation, written $\rho \underline{\otimes} \sigma$



Markov invariants – algorithm II

- For simplicity call $\mathbf{4}$ the 4×4 representation of G afforded by nucleic acid base states.
To enumerate Markov invariants at degree D , carry out the following steps:



Markov invariants – algorithm II

- For simplicity call $\mathbf{4}$ the 4×4 representation of G afforded by nucleic acid base states.

To enumerate Markov invariants at degree D , carry out the following steps:

- 1 For $\sigma \vdash D$, compute the number of one-dimensional representations f_σ occurring in the decomposition of $\mathbf{4}^{\otimes \sigma}$
- 2 The number of Markov invariants at degree D is

$$n_D = \sum_{\sigma_1, \sigma_2, \dots, \sigma_L, \sigma_i \vdash D} g_{\sigma_1, \sigma_2, \dots, \sigma_L}^{(D)} f_{\sigma_1} f_{\sigma_2} \cdots f_{\sigma_L}$$



Markov invariants – strand symmetric case

- We label representations by dimension; w.r.t. $sl_2 + GMM_2 + gl_1$, we have

$$4 \rightarrow (2 \times 1)_{-1} + (1 \times 2)_0$$

where the subscript is the weight of the gl_1 generator R .



Markov invariants – strand symmetric case

- We label representations by dimension; w.r.t. $sl_2 + \text{GMM}_2 + gl_1$, we have

$$\mathbf{4} \rightarrow (\mathbf{2} \times \mathbf{1})_{-1} + (\mathbf{1} \times \mathbf{2})_0$$

where the subscript is the weight of the gl_1 generator R .

- Use $(A + B) \underline{\otimes} \sigma = \sum_{\alpha} [(A \underline{\otimes} \alpha) \cdot (B \underline{\otimes} \sigma / \alpha)]$ where ρ / σ is the operation of skew, (dual to outer product).
- Then

$$\mathbf{4} \underline{\otimes} \sigma \rightarrow \sum_{\alpha} [(\mathbf{2} \underline{\otimes} \alpha) \times (\mathbf{2} \underline{\otimes} \sigma / \alpha)]_{-|\alpha|}$$

- Really, since “**2**” is the defining representation for both factors, the “ $\mathbf{2} \underline{\otimes} \alpha$ ” are simply polynomial representations of gl_2 .
- One dimensional representations occur whenever α is of shape (m, m) and σ / α is of shape $(r, r + s)$ so we require $D = 2m + 2r + s$, and f_{σ} is the total number of such pairs $\alpha, \sigma / \alpha$.



Markov invariants – examples for strand symmetric case

- Linear invariants, $D = 1$: $\mathbf{4} \rightarrow (\mathbf{2} \times \mathbf{1})_{-1} + (\mathbf{1} \times \mathbf{2})_0$ is equivalent to

$$\mathbf{4} \otimes (1) \rightarrow (\mathbf{2} \otimes (1)) \times (\mathbf{2} \otimes (0))_{-1} + (\mathbf{2} \otimes (0)) \times (\mathbf{2} \otimes (1))_0$$

and in the second term, the partition (1) is of the form $(r + s, r)$ so contains a 1D representation (the probability mass). Hence there is a single linear invariant (for any L).

- Quadratic invariants, $D = 2$:

$$\mathbf{4} \otimes (2) \rightarrow \mathbf{2} \otimes (2) \times \mathbf{2} \otimes (0)_{-2} + \mathbf{2} \otimes (1) \times \mathbf{2} \otimes (1)_{-1} + \mathbf{2} \otimes (0) \times \mathbf{2} \otimes (2)_0;$$

$$\mathbf{4} \otimes (1^2) \rightarrow \mathbf{2} \otimes (1^2) \times \mathbf{2} \otimes (0)_{-2} + \mathbf{2} \otimes (1) \times \mathbf{2} \otimes (1)_{-1} + \mathbf{2} \otimes (0) \times \mathbf{2} \otimes (1^2)_0.$$

Thus as $(2) * (2) = (2)$, $(1^2) * (1^2) = (2)$, $(1^2) * (1^2) * (1^2) = (1^2)$, etc,

$$n_2 = \begin{cases} 2^2 + 1 = 5, & L = 2; \\ 3 \times 2^2 + 1 = 13, & L = 3; \\ 2^4 + 6 \times 2^2 + 1 = 41, & L = 4 \\ \dots\dots\dots, & \dots \end{cases}$$

- ... and many more at degrees $D \geq 3$!!



THAT'S ALL FOLKS
thanks for your attention!



<http://www-theory.phys.utas.edu.au/>





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