Geometry,
Integrability
and
Quantization

SYMMETRY PROPERTIES OF THE MEMBRANE SHAPE EQUATION

VLADIMIR PULOV, EDY CHACAROV[†], MARIANA HADZHILAZOVA[‡] and IVAÏLO MLADENOV[‡]

Department of Physics, Technical University of Varna, Studentska Str. 1, 9010 Varna, Bulgaria

[†] *Department of Computer Science, Varna Free University, Chaika Resort, 9007 Varna, Bulgaria*

[‡] *Institute of Biophysics, Bulgarian Academy of Science, Acad. G. Bonchev Str. Bl. 21, 1113 Sofia, Bulgaria*

Abstract. Here we consider the Helfrich's membrane shape model from a group-theoretical viewpoint. By making use of the conformal metric on the associated surface the model is represented by a system of four second order nonlinear partial differential equations. In order to construct the determining system for the symmetries of the metric we rely on the previously developed package *LieSymm-PDE* within Mathematica®. In this way we have obtained the determining system consisting of 206 equations. Using the above mentioned programs we have solved the equations in a semi-automatic way. As a result we end up with an infinite dimensional symmetry Lie algebra of the Helfrich's model in conformal metric representation which we present here in explicit form.

1. Helfrich's Membrane Shape Model

The Helfrich's model of fluid membranes (biomembranes) is based on the equilibrium shape equation [1, 3]

$$\Delta H + 2(H^2 + \mathbb{h}H - K)(H - \mathbb{h}) - \frac{2\lambda H}{k} + \frac{p}{k} = 0 \qquad (1)$$

often referred to as the general **membrane shape equation** or the **Helfrich's equation**. The Helfrich's equation (1) serves to describe the equilibrium forms of the simplest closed biological membrane structures – lipid vesicles. A lipid vesicle is