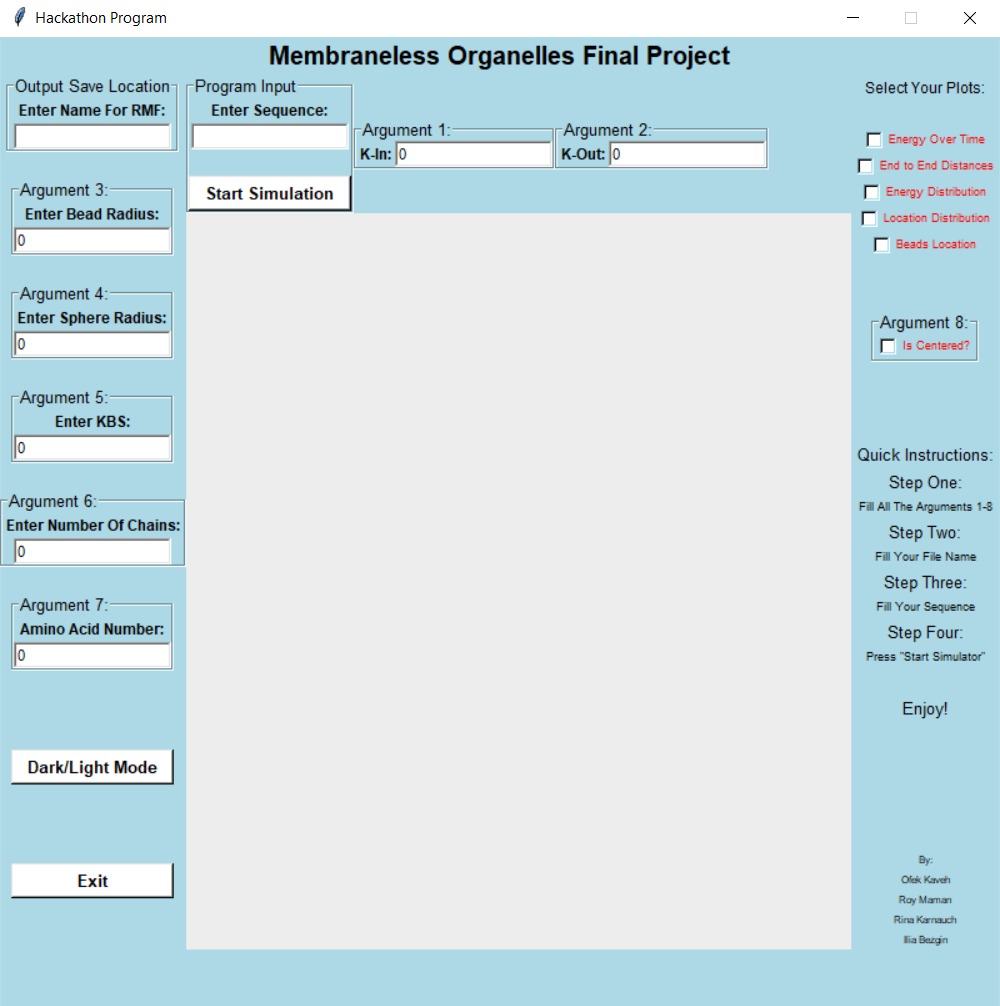
**User manual**

**Output save location:** full path for final RMF file simulation (a visual movie of the entire simulation)

**Program input:** A sequence of amino acids (for instance, "MSDQSQEPT")

**Arg 1 (k-In):** A parameter to set the harmonic coupling between beads of the same string. K-In of 5 is a good choice for well coupled strings.

**Arg 2 (k-Out):** A parameter to set the harmonic coupling between beads of different strings. K-Out values smaller than 1 works well for spontaneous binding and unbinding of adjacent strings.

**Arg 3 (Bead Radius):** The spatial radius of every bead. We worked with 10.

**Arg 4 (Sphere Radius):** The spatial radius of the bounding sphere. Defines the molecular concentration.

**Arg 5 (KBS):** A parameter to set the harmonic coupling between the bounding sphere and the strings. We worked with 0.1.

**Arg 6 (Number of Chains):** how many copies of the chain to simulate.

**Arg 7 (Amino Acid Number):** number of amino acids per bead.

**Arg 8 (Is centered):** sets the initial values. if checked, the strings are all located in 0 point at time 0 (not recommended for large K-Out values or for simulation of many strings). Else, every string starts in a unique random point.