

**Software 2. Molecular-mechanical model of the dynamic microtubule.**  
(Zakharov et al., 2015)

**Programming language:** C++, OpenMP library.

**Files:** Constants.h, MT.cpp, Protofilament.cpp

**Compilation** (using Microsoft Intel compiler): `icc -openmp MT.cpp Protofilament.cpp Constants.h -o MT`.

**Input parameters** are all in the Constants.h file in order as they appear in the Table 1 (Model Parameters) with comments describing what each parameter means.

**Output files:** Position of  $i^{\text{th}}$  monomer in  $j^{\text{th}}$  protofilament is defined by three coordinates  $(x^{ij}, y^{ij}, \tau^{ij})$  as described in the paper. Coordinates are written in one line in MT\_coords.txt file and nucleotide states of corresponding monomers are saved in Type\_mon.txt file (0 for “D”-monomers, 1 for “T”- monomers and -1 for absent subunits ). Each line in both files represents one time moment. Default time period between saving is 14 ms.

One line in MT\_coords.txt file consists of coordinates ordered as follows:  $\{x^{i1}\}, \{y^{i1}\}, \{\tau^{i1}\}, \{x^{i2}\}, \{y^{i2}\}, \{\tau^{i2}\}, \dots, \{x^{ij}\}, \{y^{ij}\}, \{\tau^{ij}\}, \dots, \{x^{iN}\}, \{y^{iN}\}, \{\tau^{iN}\}$ , where  $\{a^{i1}\} \equiv \{a^{i1}\}_{i=1,2,\dots,50}$ . Corresponding line in the Type\_mon.txt file consists of nucleotide states  $\{f^{i1}\}, \{f^{i2}\}, \dots, \{f^{iN}\}$ . Here  $N=13$ ;  $i=1,2,\dots,49,50$ .