# Supplementary Information: Small and large scale conformational changes of adenylate kinase: a molecular dynamics study of the subdomain motion and mechanics

Francesco Pontiggia , Andrea Zen and Cristian Micheletti
Statistical and Biological Physics Sector,
International School for Advanced Studies
and CNR-INFM Democritos,
Trieste, Italy

August 27, 2008

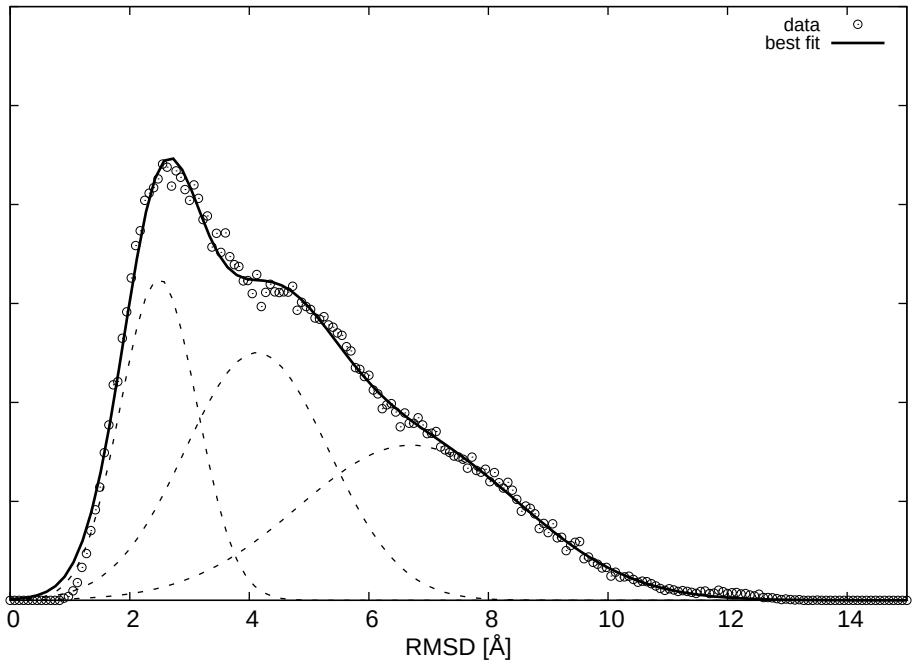



Figure 1: Distribution of RMSD distances of each pair of conformers of the simulation started from the open crystallographic structure (circles). The data are well fitted by a sum of three gaussian functions (solid line). The three gaussian are shown as dashed lines. The lowest peak ($\sim$ 2.5 Å) provides a measure of the tipical intra-basin distance of the structures, while the broader background distribution is a measure of the distances between structures belonging to distinct substates.

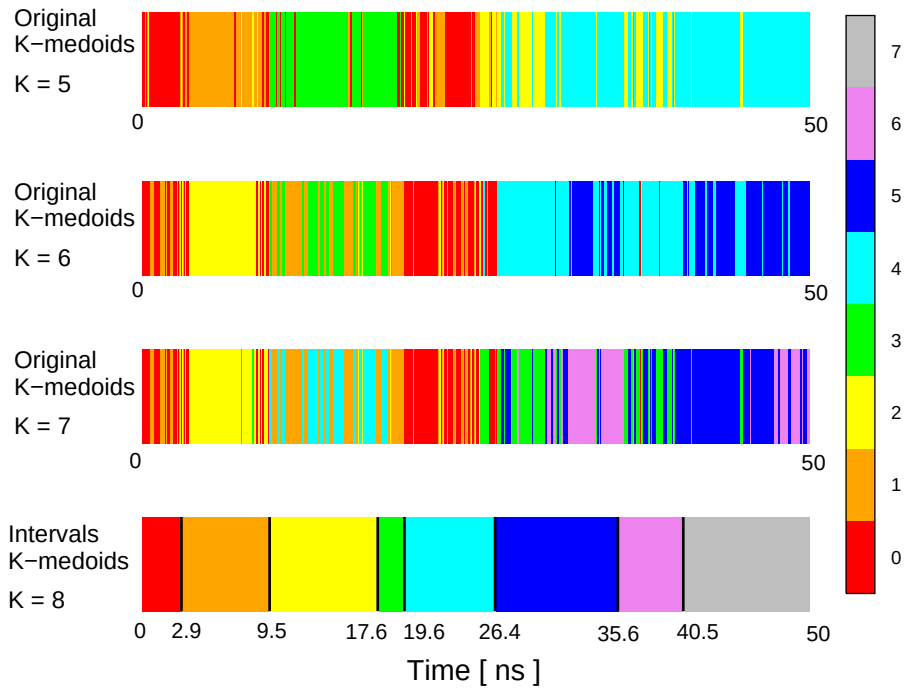
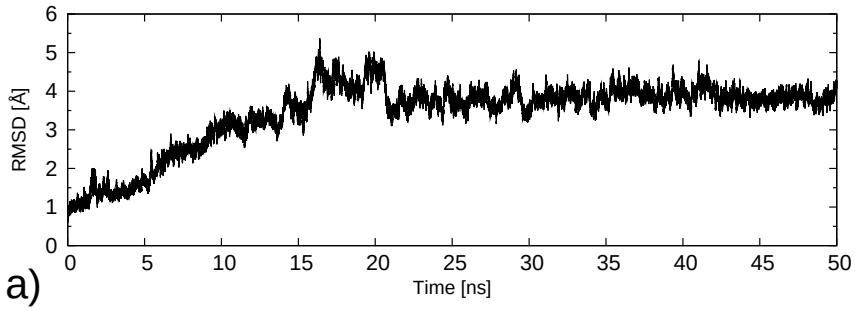
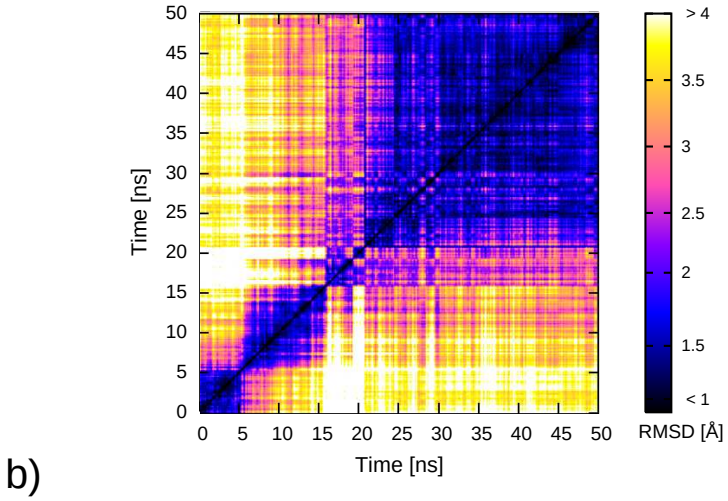



Figure 2: Partitioning of the trajectory started from the open conformation in different conformational basins (frames belonging to different clusters are represented as lines of different colors). The grouping has been performed with the standard K-medoids algorithm with several values of K (here we show only results for K=5,6,7), and with a modified version of the algorithm that requires the elements of each group to span an uninterrupted time interval (lower panel).



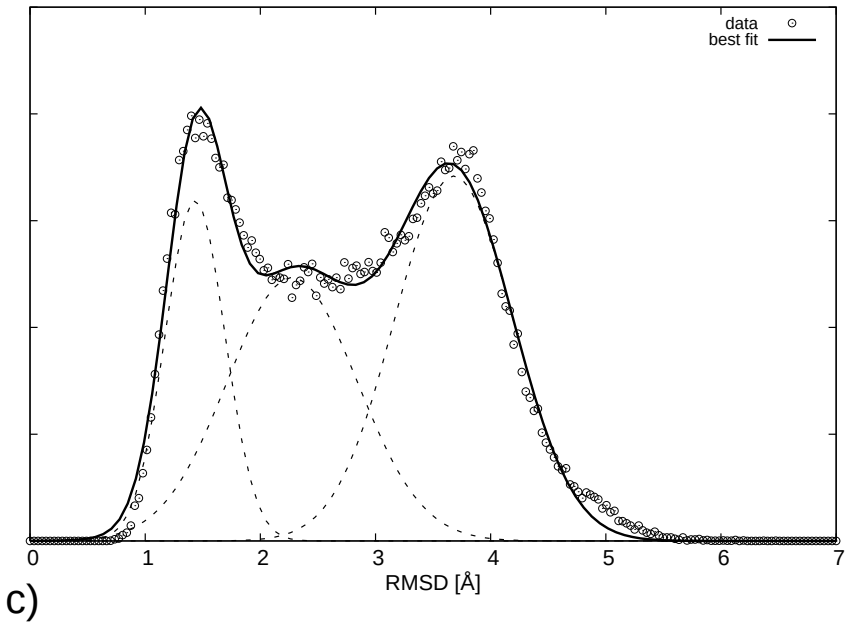




Figure 3: Analysis of the structural heterogeneity of the conformations sampled in the simulation started from the closed structure: RMSD pairwise distances (a) between each trajectory frame and the initial conformation, and (b) between each pair of trajectory frames. As in the case of the simulation started from the open conformation the block character of the matrix of pairwise distances is clear. From the inspection of the clearly multimodal distribution of RMSD values (c) is apparent that during the simulation the system has visited different conformations, even if the overall structural deformation is less pronunciated than in the other simulation.

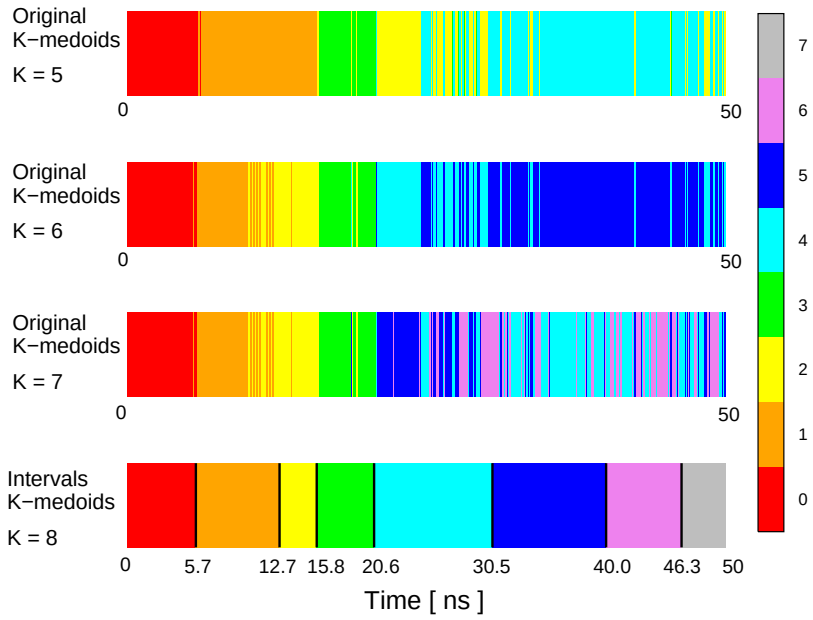



Figure 4: Partitioning of the trajectory started from the closed conformation in different conformational basins (frames belonging to different clusters are represented as lines of different colors). The grouping has been performed with the standard K-medoids algorithm with several values of K (her we show only results for K=5,6,7), and with a modified version of the algorithm that requires the element of each group to span an uninterrupted time interval (lower panel).

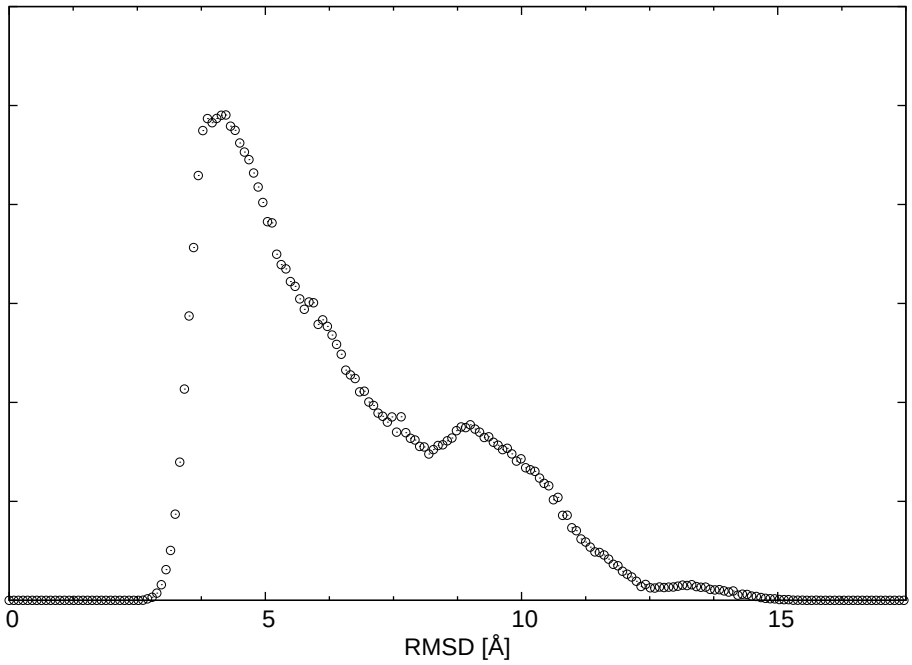



Figure 5: Distribution of RMSD values between pairs of conformations belonging to the two different trajectories. It's interesting to notice that there are structures belonging tho the different ensembles that differs as low as $\sim$ 2.5 Å

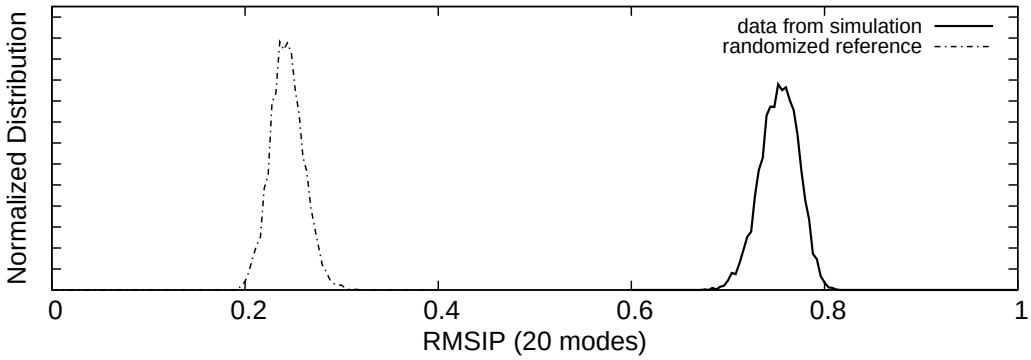



Figure 6: Distribution of RMSIP values computed on the top 20 essential dynamical spaces from pairs of 0.5ns-long intervals (see Fig 7b of main paper) is shown with a solid curve. The dashed curve shows the distribution of RMSIP values obtained by randomizing (in a way which preserves the mobility profiles of the amino acids) the original EDS.