Normal mode calculations with the QM/MM full Hessian and the Mobile Block Hessian (MBH) method

An Ghysels[1], *Lee H. Woodcock*[2], *Yihan Shao*[3], *Bernard R. Brooks*[2], *Veronique Van Speybroeck*[1], *Dimitri Van Neck*[1], *Michel Waroquier*[1]
1. Center for Molecular Modeling, Ghent University, Belgium
2. Laboratory of Computational Biology, National Heart, Lung and Blood Institute, National Institutes of Health, Bethesda, Maryland
3. Q-Chem, Inc, Pittsburgh, Pennsylvania
Email: an.ghysels@ugent.be

We have implemented the full Hessian evaluation in QM/MM simulations, as well as the approximate Mobile Block Hessian (MBH). The Hessian is the *3Nx3N* matrix containing the second derivatives of the potential energy surface with respect to the *3N* nuclear coordinates, and needs to be diagonalized when calculating the frequencies and normal modes. In extended systems, however, its calculation, storage and diagonalization is an expensive computational task. Note that even in case of a small QM region, the numerous derivatives of the QM/MM interaction terms still form a bottleneck in the frequency calculation.
Recently, the Mobile Block Hessian (MBH) method was developed in order to reduce the dimensionality of the Hessian. The main concept is the introduction of blocks, which move as rigid bodies during the vibrational analysis. The blocks can also be linear or have atoms in common (leading to adjoined blocks). This block concept is now combined with the QM/MM scheme. The reduced computational cost opens the path to a broad range of applications of normal mode analysis.