

# Computational efficiency and Amdahl's law for the adaptive resolution simulation technique



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## ABSTRACT

We discuss the computational performance of the adaptive resolution technique in molecular simulation when it is compared with equivalent full coarse-grained and full atomistic simulations. We show that an estimate of its efficiency, within 10%–15% accuracy, is given by the Amdahl's Law adapted to the specific quantities involved in the problem. The derivation of the predictive formula is general enough that it may be applied to the general case of molecular dynamics approaches where a reduction of degrees of freedom in a multiscale fashion occurs.

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## 1. Introduction

Adaptive Resolution Simulation (AdResS) [1,2] falls in the category of “concurrent” multiscale methods where “concurrent” means that a system is treated at different molecular resolutions according to the position of molecules in space. In this scenario, there is a region where molecules are represented with high resolution (e.g. full atomistic), while at the same time, in the rest of the system molecules are treated at lower resolution (e.g. coarse-grained/simple spheres). The main characteristic of AdResS is that the exchange of particles between different regions takes place “on-the-fly” from one resolution to another; the technical advantage is that for some molecular systems, the region where the important process is taking place, can be described in full detail (with all the explicit degrees of freedom), while the region far away from it, not relevant for the process of interest, can be described in less detail (coarse-grained models). A typical example is the solvation of a molecule in water; the molecule as well as the solvent in the first solvation shell can be treated using all the explicit degrees of freedom (atomistic resolution), while far away from the molecule, the solvent can be studied with satisfied accuracy using coarse-grained models. This partitioning in regions of different molecular resolutions has two advantages, one conceptual, that is the systematic identification of the essential degrees of freedom involved in a given process, and one practical, that is the drastically

reduced number of degrees of freedom implies a computational gain compared to a full atomistic simulation. In this paper we will treat the second aspect, that is we will show the computational performance of AdResS w.r.t. the full atomistic and full coarse grained simulations. The paper is organized in two sections: In the first section, we provide an upper bound to the computational efficiency of AdResS based on its computational scaling properties. We show that the scaling properties follow the so called Amdahl's law of computational science. We will show results for the case of the AdResS code implemented in GROMACS [3], however the upper bound of efficiency is general. We generalize the formula for the upper bound of AdResS simulations with finite size of atomistic and coarse-grained regions. Thus, we have a generic formula to derive the computational gain (or, equivalently called “speedup”) associated with AdResS simulations compared to full-atomistic simulations. In the second section, we perform the numerical verification of the formula of efficiency and discuss the actual computational gain one obtains with AdResS simulations relative to full-atomistic simulations.

### 1.1. Adaptive Resolution Simulation (AdResS)

In AdResS, the simulation box is divided into three regions, one is represented by atomistic resolution, another one is represented by coarse-grained resolution and in between, there is a third region where molecules have a mixed resolution, where both atomistic and coarse-grained degrees of freedom are present (see Fig. 1). The resolution of the molecules in different regions is defined by a weighting function  $w(x)$ . The most common weighting function

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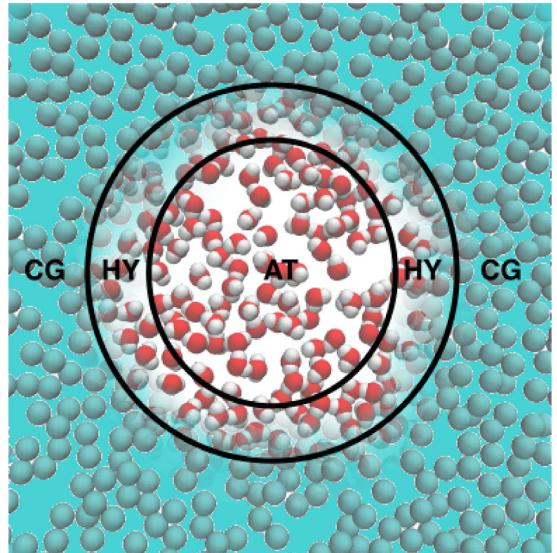
that has been used in AdResS is:

$$w(x) = \begin{cases} 1 & x < d_{AT} \\ \cos^2 \left[ \frac{\pi}{2(d_{\Delta})}(x - d_{AT}) \right] & d_{AT} < x < d_{AT} + d_{\Delta} \\ 0 & d_{AT} + d_{\Delta} < x \end{cases}$$

where,  $d_{AT}$  and  $d_{\Delta}$  are size of atomistic and hybrid regions respectively and  $x$  is the  $x$ -coordinate of the center of mass of the molecule. The weighting function smoothly goes from 0 to 1 in the transition region, where a coarse-grained molecule transforms into an atomistic molecule and vice versa. The molecules in atomistic and coarse-grained resolutions are coupled via an interpolation of the forces.

$$F_{\alpha\beta} = w(X_{\alpha})w(X_{\beta})F_{\alpha\beta}^{atom} + [1 - w(X_{\alpha})w(X_{\beta})]F_{\alpha\beta}^{cg} \quad (1)$$

where  $\alpha$  and  $\beta$  indicate two molecules, and  $w(X_{\alpha})$  and  $w(X_{\beta})$  are the weighting functions characterizing these two molecules.  $F_{\alpha\beta}^{atom}$  is the force in the atomistic region, which is derived from atomistic interactions,  $F_{\alpha\beta}^{cg}$  is the force in the coarse-grained region, which is derived from coarse-grained potential. Thus, two molecules within the atomistic region interact via atomistic force, while the two molecules within the coarse-grained region interact via coarse-grained force. The rest of the molecules interact via space-dependent force equation according to the weighting function of two molecules. The consequence is that as the molecule moves from the atomistic region to the coarse-grained region, the atomistic forces start diminishing, and the coarse-grained forces between the center of mass of the molecules start to be dominating. Finally, the equilibrium between the different regions is maintained via a global thermostat which takes care of extra energy that has to be added/removed while a molecule moves from the atomistic to coarse-grained region and vice versa. The above approach was shown to reproduce structural and thermodynamic properties of a wide variety of liquids within an error of 5%–10%. For higher accuracy, the concept of thermodynamic force which acts on the center of mass of molecule in the hybrid region, was introduced. It was formulated in terms of difference of chemical potential [4] characterizing the atomistic region, and hybrid and coarse-grained regions. This approach improved the accuracy, however, it proved to be computationally expensive. The thermodynamic force was reformulated in terms of difference of grand potential [5,6] characterizing the atomistic and coarse-grained regions and was the first step in the formulation of Grand-Canonical like Adaptive Resolution simulations (GC-AdResS), where there is an exact Hamiltonian for the molecules contained in the atomistic region, while the hybrid and coarse-grained region act as reservoir of energy and particles. In Ref. [7], it was shown that the atomistic region samples the space in a grand-canonical fashion, and necessary conditions were derived for the probability distributions to be correct up to a desired order. One of the most important feature of GC-AdResS is that there is no restriction on the coarse-grained model; this can be just a liquid of spheres interacting via a generic potential. This was validated in Ref. [8], where GC-AdResS was used to calculate the chemical potential for various liquids and mixtures and further confirmed by more elaborate and rigorous theoretical models [9]. In practice the calculation of the thermodynamic force corresponds to the equilibration of the system before the production run is initiated and it has been shown that there are rather efficient and fast ways to calculate it for a prototype system and then this same calculated force can be reused every time a system with similar characteristics is simulated [8,10]. Anyway, regarding the focus of this paper, one must consider the fact that this force introduces an additional calculation in the hybrid region and this makes the method computationally less efficient; however its application (for higher accuracy) is useful only when the hybrid region is small compared to the atomistic and to the coarse-grained region,



**Fig. 1.** Pictorial representation of the AdResS scheme with a generic molecule; CG indicates the coarse-grained region, HY the hybrid region where atomistic and coarse-grained forces are interpolated via a space-dependent, slowly varying, function  $w(x)$  and AT the atomistic region (that is the region of interest).

and thus the cost of its application is computationally negligible, otherwise the standard original AdResS is more convenient. For the reasons given above, in this paper we do not treat cases where the thermodynamic force is applied.

## 2. Amdahl's law

Amdahl's law [11] in computer science predicts the overall speed up of a process, when only part of the computing process is improved. In a nutshell, if one part of a process can have a speed up due to parallelization, the overall speed up will be limited by the parts which have not gained a speed up factor from parallelization. As an example let us consider a process in which 90% can be sped up infinitely, but 10% stays untouched and hence the maximum speed up is a factor 10 due to the fact that tenth of the overall runtime is remaining. In the case of AdResS the force calculation can be sped up easily, but the remaining parts cannot, we will use such similarity for a systematic estimate of the speed up (compared to a full atomistic simulation) of AdResS.

### 2.1. Computational analysis

For AdResS we will not consider absolute times, but use the time of a full atomistic simulation,  $t_{AT}$  as a reference. In general, the running time accumulated in Molecular Dynamics (MD) simulations can be divided into two parts: The first part is the time needed to calculate the forces,  $t_F$ , which usually goes as  $N^2$  ( $N$  here indicates the number of atoms) for long range interactions and  $NN_{Neighbors}$  for short range interactions. The second part,  $t_{NF}$ , is the time needed for performing all the other operations, such as neighbor list rebuilds, communication I/O, and even bonded interactions; this part scales with  $N$ .

#### 2.1.1. Coarse-grained simulations

The coarse-grained simulation can be seen as the upper bound for speeding up a simulation. This is due to the fact that an AdResS simulation with vanishing atomistic region is equivalent to a coarse-grained simulation. In fact the number of atoms per molecule is reduced by clustering multiple atoms into one coarse-grained bead. In coarse-grained simulations one can reach longer

time scales since the intrinsic dynamics is faster (faster equilibration), larger time steps can be used due to softer interactions, and the equations of motion of a reduced number of particles need to be integrated. Here we will not consider the first two aspects in the following calculations and limit ourselves to the speed up due to decreased number of particles (thus this is a sort of “worst case scenario” estimate). For a single component system, where  $P$  atoms are replaced by 1 coarse-grained bead, the running time will be:

$$t_{CG} = t_{F,AT}/P^2 + t_{NF,AT}/P. \quad (2)$$

This results from the fact that two beads interact with 1 instead of  $P^2$  interactions, so  $t_{F,AT}$  is reduced by a factor  $P^2$  and  $t_{NF,AT}$  is reduced by a factor  $P$  due to the decreased number of particles. For a typical simulation, for example SPC/E water, where  $P = 3$  and  $t_F = 0.75t_{AT}$ , one calculates:

$$t_{CG} = 0.75t_{AT}/9 + 0.25t_{AT}/3 = 0.167t_{AT} = t_{AT}/6, \quad (3)$$

which means a maximum speed up factor (i.e.  $\frac{t_{AT}}{t_{CG}}$ ) of 6, compared to the performance of a full atomistic simulation. This calculation is only approximate as in real implementations, the water molecules interact with 10 (9 Coulomb and 1 Lennard-Jones) interactions instead of 9 and the coarse-grained interaction is tabulated instead of *hard-coded*, which also implies a slow down factor of 50%; thus a more realistic value might be 4. It must be noticed that the formula provided above is rather general and it is not restricted to the coarse-grain mapping of one molecule to one molecule. For example, when mapping multiple molecules into a single coarse-grained bead the same formula can be used provided that the scaling factor  $P$  is replaced by  $PK$ , where  $K$  is the number of molecules mapped on a single interaction site. Furthermore, the process of bundling and unbundling of multiple molecules in AdResS also implies some computational cost; this cost, although it may not be sizable, must anyway be taken into account. In actual simulations, this procedure is still a topic of recent research and its computational optimization has not been fully developed yet [12,13]. Similarly to the case of multiple mapping discussed above, in the Path Integral formulation of MD the factor  $1/P^2$  has to be replaced by  $1/QP^2$ , due to the fact that atoms are treated as polymer rings and in such a case the  $Q$  beads of a polymer ring of one atom interact only with the corresponding  $Q$  beads of the polymer ring of another atom (see e.g. [10]).

### 2.1.2. AdResS simulations

The upper bound in the computational performance of AdResS can be made more accurate by considering that the system is composed of an atomistic, a hybrid and a coarse-grained zone. In the hybrid zone, coarse-grained as well as atomistic interactions have to be calculated. We assume that the volume is proportional to the average number of molecules at a given (averaged) density and it follows that:

$$t_{AdResS} = \frac{V_{CG} + V_{HY}}{V_{Tot}} t_{CG} + \frac{V_{AT} + V_{HY}}{V_{Tot}} t_{AT}. \quad (4)$$

Note that the above equation assumes uniform density throughout the system, which is always the case in AdResS simulations. For  $V_{CG}$  being much larger than  $V_{HY}$  and  $V_{AT}$ , we again obtain  $t_{CG}$  as an upper bound.

### 2.1.3. Implementations

In all implementations in GROMACS and Espresso, which currently exist, the atomistic representation is actually not removed in the coarse-grained region [14]. For the moment, until a better technical solution will be found, this is done mainly to avoid the reinsertion of the atomistic structure, which is an expensive operation from the point of view of memory. This also allows to maintain the integration of the internal degree of freedom, which

otherwise would have to be re-initialized whenever a molecule re-enters the hybrid zone. For the calculation of the speed up factor this implies that  $t_{CG}$  must be corrected to:

$$t'_{CG} = t_{F,AT}/P^2 + t_{NF,AT}, \quad (5)$$

which becomes the new upper bound (for the above SPC/E system, the speedup will be 3). This implies that even for very large molecules ( $P \gg 1$ ):

$$t'_{CG} = t_{NF,AT} \quad (6)$$

which is equivalent to Amdahl's law discussed in the previous section. For most systems  $t_{NF,AT}$  is about 25% of the total running time, so the maximum speedup will be 4. It is important to note that this bound applies in a strict manner to the so called H-AdResS [15], while in other version of AdResS (GC-AdResS), as underlined above, after proper redesign of the code, it can be avoided to keep the atomistic resolution in the coarse-grained region and hence  $t_{NF,AT}$  can be significantly reduced. In fact, for H-AdResS, the internal degrees of freedom cannot be removed as they explicitly appear in the Hamiltonian and hence even in theory (with the best implementation possible)  $t_{NF,AT}$  does not scale with  $P$ . Additionally  $t'_{CG}$  increases due to the use of virtual sites as coarse-grained particles (usually something of the order of 10% for SPC/E water and up to 25% for toluene). This, of course, limits the speed up even more:

$$t''_{CG} = t_{NF,AT} + \frac{t_{NF,AT}}{t_{AT}} t_{vs}, \quad (7)$$

(assuming  $t_{vs}$  contributes equally to  $t_{NF,AT}$  and  $t_{F,AT}$ ). For the above SPC/E system, the speedup would be lowered to  $4/1.1 = 3.6$ . For toluene ( $P = 15$ ), where  $t_{F,AT} = 0.74t_{AT}$  and  $t_{vs} = 0.25t_{AT}$ , the speed up will reduced from 3.84 to  $3.84/1.25 = 3.07$ , which is in very good agreement with the numbers (obtained from simulations) reported in [16].

#### 2.1.4. Performance efficiency/speed-up

We can generalize Eqs. (4), (5) to AdResS systems with finite size of atomistic region and hybrid region and define the computational gain one obtains when performing AdResS simulations compared to atomistic simulations. If we combine Eq. (4) with Eq. (5), then we get

$$t_{AdResS} = \frac{V_{CG} + V_{HY}}{V_{Tot}} (t_{F,AT}/P^2 + t_{NF,AT}) + \frac{V_{AT} + V_{HY}}{V_{Tot}} t_{AT} \quad (8)$$

and,

$$t_{AdResS}/t_{AT} = v + \left(1 + \frac{V_{HY}}{V_{Tot}} - v\right) (\%_{F,AT}/P^2 + 1 - \%_{F,AT}), \quad (9)$$

where  $v = (V_{AT} + V_{HY})/V_{Tot}$  and  $\%_{F,AT} = t_{F,AT}/t_{AT}$ . The inverse of  $t_{AdResS}/t_{AT}$  is often referred to as the speedup  $s$ . In conclusion the speed up factor as a function of the size of the atomic region will have the functional form of  $s(v) = 1/(a(1+b) + v(1-a))$ . It should be noted here that the difference between a standard full-atomistic simulation and the full atomistic representation in AdResS simulation is the introduction of an additional (virtual site) in the atomistic molecule in order to couple the coarse-grained representation to the full-atomistic one. As a consequence a virtual size correction must be added from Eq. (7); i.e. scaling  $1 - \%_{F,AT}$  by  $1 + \%_{vs}$ . However, there is no way of determining *a priori* the cost of the virtual site correction, thus, we would need to perform the full atomistic calculation with an extra virtual site kept at the center-of-mass of the molecule, i.e. atomistic simulations within AdResS framework. This site does not interact with any molecules and would change once the position and momenta of all the atoms in the molecule are updated; therefore, in this work, we have

not considered this correction. Instead, we also report the “actual speed up”, that is the speed up calculated by direct comparison between an AdResS simulation and a standard full atomistic simulation. This represents a further term of comparison and a more direct practical estimate that complements the theoretical analysis of Eq. (9). As we will see, the formula of Eq. (9) predicts always an upper bound for the “actual speed up”. It must be clarified that in general, there exist two approaches to study the scaling behavior of AdResS: strong scaling and weak scaling. In the former the speed up (over full-atomistic) is measured for a system of constant size varying the size of the atomistic region only. For the latter the atomistic region is kept constant and the total size of the system is varied. The results reported in the next section concern the strong scaling approach as we believe that this approach provides a better use case for common AdResS simulation, where a full-atomistic simulation is possible but is slow. The weak scaling analysis and its results are instead particularly interesting for system where a very large buffer region or reservoir is needed, e.g. grand-canonical simulations [7–9]. Recently strong scaling results have been reported in [17] looking at the force contribution only, neglecting the non-parallelized part of the code, which is the main focus of this paper.

### 2.1.5. Case of mixtures

In the case of mixture  $t_{F,AT}$  has to be split into the contributions from the different species of molecules. If we consider a mixture with two types of molecules A and B, then  $t_{F,AT}$  can be written in terms of contribution of different types of interactions.

$$\frac{t_{F,AT}}{t_{AT}} = \%_{F,AT,AA} + \%_{F,AT,AB} + \%_{F,AT,BB} \quad (10)$$

where  $t_{AT}$  is the time for the full-atomistic simulation,  $\%_{F,AT,AA}$  is the % time spent in force calculation when only A-A interactions are switched on and rest of the interactions are switched off. Similarly, one can define  $\%_{F,AT,AB}$  and  $\%_{F,AT,BB}$ . Since there is no direct procedure to calculate the individual percentages, we first calculate  $\%_{F,AT,mix}$ , i.e., % time spent in force calculation in A-B mixture, which can be obtained directly from GROMACS output. We then calculate  $\%_{F,AT,AA}$ ,  $\%_{F,AT,AB}$  and  $\%_{F,AT,BB}$  by considering the number of interactions of specific type in the system. Suppose there are X number of interactions of type A-A, Y number of interactions of type A-B and Z number of interactions of type B-B, then

$$\%_{F,AT,AA} = \frac{X}{X+Y+Z} \%_{F,AT,mix} \quad (11)$$

$$\%_{F,AT,AB} = \frac{Y}{X+Y+Z} \%_{F,AT,mix} \quad (12)$$

$$\%_{F,AT,BB} = \frac{Z}{X+Y+Z} \%_{F,AT,mix} \quad (13)$$

To obtain the coarse-grained time, these contributions need to be scaled by the number of atoms which are coarse-grained:

$$\frac{t_{F,CG}}{t_{AT}} = \left( \frac{\%_{F,AT,AA}}{P_A^2} + \frac{\%_{F,AT,AB}}{P_A P_B} + \frac{\%_{F,AT,BB}}{P_B^2} \right) \quad (14)$$

where  $P_A$  is the number of atoms coarse-grained in molecule A and  $P_B$  is the number of atoms coarse-grained in molecule B.

## 2.2. Numerical results

We compare the computational gain obtained using Eq. (9) with the actual gain obtained from AdResS simulations compared to the full-atomistic simulation. We treated five different systems in this work: liquid water, hexane, butanol, DMSO and TBA/DMSO mixture. The technical details of these systems as well as simulations details are reported in Appendix. All the simulations are performed on a single processor Intel Xeon CPU E31245 machine, since the load balancing in AdResS and atomistic simulations works

**Table 1**

Estimate of %time spent in force calculation in a full atomistic simulation of various systems studied in this work. It must be noticed that this information is given by the code in terms of generic time required for the calculation of forces. In reality given the complexity of the computational architecture and the entanglement between overlapping operations the real time for force calculations may be smaller. In fact the factor of 10%–15% of disagreement between the theoretical estimate and the numerical results carries in part the uncertainty of %time spent in force calculation. In any case, we assume to be in an ideal condition where the time printed by the code is indeed the time of force calculations only. Such an assumption implies that our theoretical estimate can be viewed always as an indication (within 10%–15%) of the best performance (upper bound) of the real computational calculation.

System	$\%_{F,AT}$
TIP5P water	63
Butanol	58
Hexane	46
DMSO	55
TBA-DMSO mixture	57

**Table 2**

Comparison of speed up for TIP5P water using IBI potential [18] with pressure correction in the coarse-grained region, calculated using Eq. (9) and from AdResS simulation. “AT” refers to the size of the atomistic region,  $v = (V_{AT} + V_{HY})/V_{Tot}$ , the third column reports the quantity  $\frac{t_{AT}}{t_{AdResS}}$  from the formula and the fourth column reports the quantity  $\frac{t_{AT}}{t_{AdResS}}$  from simulation; the same convention is used in all the following tables.

AT (nm)	$v$	Equation	Simulation
0.0	0.0	2.53	2.94
0.5	0.0136	2.45	2.69
0.9	0.0284	2.37	2.47
1.3	0.0511	2.26	2.17
1.7	0.0835	2.13	1.88
2.1	0.127	1.98	1.60

**Table 3**

Actual speed up  $\frac{t_{AT}}{t_{AdResS}}$  for TIP5P water using IBI potential with pressure correction in the coarse-grained region. “AT” refers to the size of the atomistic region.

AT (nm)	Actual speedup
0.0	2.45
0.5	2.24
0.9	2.05
1.3	1.81
1.7	1.56
2.1	1.33

**Table 4**

Comparison of speed up for liquid butanol using IBI potential with pressure correction in the coarse-grained region, calculated using Eq. (9) and from AdResS simulation.

AT (nm)	$v$	Equation	Simulation
0.0	0.0	2.28	2.07
0.5	0.0127	2.22	1.98
1.0	0.0265	2.16	1.92
1.3	0.0476	2.08	1.82
1.7	0.0779	1.97	1.71
2.1	0.118	1.85	1.56

differently. Table 1 shows the percentage of time that is spent in force calculation ( $\%_{F,AT}$ ) for the above mentioned systems and Tables 2, 4, 6, 8 and 10 show the speed up obtained with AdResS simulations of these systems relative to atomistic systems within AdResS framework (i.e. with an additional virtual site). Tables 3, 5, 7, 9 and 11 show the actual speedup obtained with AdResS simulations relative to full-atomistic simulations. Since there is no additional cost of virtual site involved, the actual speedup is lower. We have used TIP5P model for water; the reason for this choice was made in order to make a consistent comparison between the

**Table 5**

Actual speed up  $\frac{t_{\text{AT}}}{t_{\text{AdResS}}}$  for liquid butanol using IBI potential with pressure correction in the coarse-grained region. “AT” refers to the size of the atomistic region.

AT (nm)	Actual speedup
0.0	2.02
0.5	1.93
0.9	1.87
1.3	1.77
1.7	1.66
2.1	1.52

**Table 6**

Comparison of speed up for liquid DMSO using IBI potential with pressure correction in the coarse-grained region, calculated using Eq. (9) and from AdResS simulation.

AT (nm)	$v$	Equation	Simulation
0.0	0.0	2.06	1.88
0.5	0.0167	2.00	1.78
0.9	0.0348	1.93	1.70
1.3	0.0627	1.85	1.60
1.7	0.102	1.74	1.46
2.1	0.156	1.62	1.33

**Table 7**

Actual speed up  $\frac{t_{\text{AT}}}{t_{\text{AdResS}}}$  for liquid DMSO using IBI potential with pressure correction in the coarse-grained region. “AT” refers to the size of the atomistic region.

AT (nm)	Actual speedup
0.0	1.66
0.5	1.57
0.9	1.50
1.3	1.41
1.7	1.28
2.1	1.17

**Table 8**

Comparison of speed up for liquid hexane using IBI potential with pressure correction in the coarse-grained region, calculated using Eq. (9) and from AdResS simulation.

AT (nm)	$v$	Equation	Simulation
0.0	0.0	1.8	2.06
0.5	0.0113	1.76	2.00
0.9	0.0236	1.73	1.93
1.3	0.0425	1.68	1.85
1.7	0.0694	1.63	1.73
2.1	0.105	1.56	1.62

**Table 9**

Actual speed up  $\frac{t_{\text{AT}}}{t_{\text{AdResS}}}$  for liquid hexane using IBI potential with pressure correction in the coarse-grained region. “AT” refers to the size of the atomistic region.

AT (nm)	Actual speedup
0.0	1.45
0.5	1.41
0.9	1.36
1.3	1.30
1.7	1.22
2.1	1.14

performance of AdResS and that of a full atomistic simulation. In fact the full-atomistic simulations for standard water models such as SPC, SPC/E in GROMACS are highly optimized, while AdResS in GROMACS, for the moment, is not equivalently optimized for such models. It must be noted here that we have only varied the size of the atomistic region, while keeping the thickness of the hybrid region fixed. While the overall trend of the numerical results follows the theoretical prediction of Amdahl's law, it can be seen that the maximum discrepancy between the predicted

**Table 10**

Comparison of speed up for TBA/DMSO mixture using IBI potential with pressure correction in the coarse-grained region, calculated using Eq. (9) and from AdResS simulation.

AT (nm)	$v$	Equation	Simulation
0.0	0.0	2.17	2.16
0.9	0.0166	2.10	2.01
1.3	0.0298	2.05	1.96
1.7	0.0488	1.98	1.88
2.1	0.0744	1.91	1.76
2.5	0.107	1.82	1.65

**Table 11**

Actual speed up  $\frac{t_{\text{AT}}}{t_{\text{AdResS}}}$  for TBA/DMSO mixture using IBI potential with pressure correction in the coarse-grained region. “AT” refers to the size of the atomistic region.

AT (nm)	Actual speedup
0.0	1.56
0.9	1.45
1.3	1.41
1.7	1.35
2.1	1.27
2.5	1.19

speedup and the speed up obtained from the simulations is 15% (but in some cases, e.g. hexane, the maximum discrepancy is less than 10%). One of the reasons of such a discrepancy is the use of coarse-grained potential (obtained with the Iterative Boltzmann Inversion (IBI) technique with pressure correction) in the coarse-grained region. In fact, Eq. (9) assumes that the (average) density is uniform across the atomistic, hybrid and coarse-grained region, however, it has been reported (and discussed) that the density in the hybrid region is not perfectly uniform and presents a systematic discrepancy of 5% w.r.t. the reference density of the full-atomistic simulation; this leads to the fact that the particle density in the atomistic and coarse-grained regions is not the same as that of target (i.e. that of the full-atomistic simulation of reference). Although the discrepancy regarding the density is small, and it does not affect the structural and thermodynamic properties, this difference could affect the “ideal” performance (of Amdahl's Law) that one may expect from an AdResS simulation. As underlined before, from the technical point of view the introduction of the thermodynamic force removes the problem of non homogeneous density, but also implies an additional force calculation in the hybrid region. This extra calculation is not massive and in principle can be neglected, for relatively small hybrid regions, in the estimate of the performance. However we prefer to remain within the “worst case scenario” of non uniform density in order to estimate the maximum discrepancy of the numerical results compared to the theoretical prediction of Amdahl's formula. Additionally it is important to remember that the IBI potentials are tabulated potentials, while the full-atomistic simulation uses Lennard-Jones type potential and there is a certain level of penalty (5%) for using those. On the other hand for some of the atomistic systems (e.g. TIP5P), Coulomb interactions need to be calculated as well; this aspect has not been explicitly considered but it is assumed that the interactions between two atoms (beads in CG simulation) lead to the same order of calculation time. Finally, the additional virtual site adds additional overhead to the AdResS simulation in comparison to the full atomistic simulation. Thus, we can use the formula of Amdahl's law to estimate the upper bound for the gain in computational efficiency of AdResS compared to an equivalent full atomistic simulation but must keep in mind an uncertainty of about 10%–15%. However, we must also keep in mind that the estimate formula suggested here regards the “worst scenario” case of computational implementation of AdResS, i.e. the only part affected is in the calculation of the forces. In practice,

there are several aspects where the computational architecture can be improved and further efficiency improvements can be added to the one discussed in this work.

### 3. Conclusions

We have developed a model to predict the upper bound of the speedup which can be achieved in adaptive resolution simulations and look at the particular case of AdResS. First, it is obvious that a full coarse-grained simulation is the maximum speedup possible. Second, assuming that all the code implementations of the AdResS method are not ideal, that is, only the force calculation is optimized, the upper bound for the speed up is controlled within a limit imposed by Amdahl's law and hence even if the force calculation would not have a cost, which is nearly true for large molecules, a maximum speedup inversely proportional to the non-force calculation part of the full-atomistic simulation is imposed. We have tested this hypothesis on multiple systems and confirmed the performance model within 15% accuracy, which is reasonable considering the broad range of systems and the simplicity of the performance model (this latter does not incorporate any correction terms related to the inhomogeneous density, and other different interaction types used in the full-atomistic simulation). Finally, from the various calculations it can be seen that for reasonable sizes of the atomistic region (at fixed coarse-grained region) one can have a gain factor of about 1.5–2.0. While for small systems this is not relevant, for large systems it may represent a sizable gain, for example in the path integral based AdResS [8,19] such a gain allows for treating systems otherwise at the limit of the computational capability of standard resources. In this perspective, a formula as the one proposed here allows researchers to estimate the gain they would have if they treat the system of interest using AdResS. To decide whether or not to use AdResS, if the aim is to save computational time, can be made practical by our proposal.

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### Appendix. Technical details

All the simulations are performed with Gromacs-4.6.7. A spherical atomistic and transition region is used in all the AdResS simulations. The time step used in all the simulations is 2 fs. For each system, the size of the atomistic region is varied while the size of

**Table 12**

Technical details of the various systems studied in this work.

System	$N_{atom}$	System size (nm <sup>3</sup> )
TIP5P water	30 000	9.77 × 9.77 × 9.77
butanol	6530	10.01 × 10.01 × 10.01
Hexane	4700	10.39 × 10.39 × 10.39
DMSO	6020	9.12 × 9.12 × 9.12
TBA/DMSO	2500/10 000	11.69 × 11.69 × 11.69

the transition region (0.95 nm) is kept fixed. We use a Langevin thermostat with inverse friction coefficient 0.1 ps in all the simulations, and the temperature is maintained at 300 K. The reaction-field method is used to treat the electrostatic interactions, while the cut-off method is used to treat the van der Waals interactions. We use TIP5P model for water molecule and the parameters are taken from OPLSAA force field. The parameters for Liquid Hexane, butanol and DMSO are taken from GROMOS53A6 parameter set. For all the systems, a cut-off radius of 0.9 nm was used for van der Waals and Coulomb interactions. To obtain the initial trajectory to be used in AdResS simulations, we performed an equilibration run under NPT conditions for 1 ns. To obtain the coarse-grained potential, we used Iterative Boltzmann Inversion in conjunction with pressure correction, which ensures that the coarse-grained region has the same pressure as the atomistic region. Table 12 lists the specific details of the systems studied in this work.

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