The need for accuracy and smoothness in numerical simulations

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Introduction

This is not a talk about, say,

1. computational speed
2. parallelism
3. energy efficency

This is a talk about

the relevance of the numbers returned by our simulations

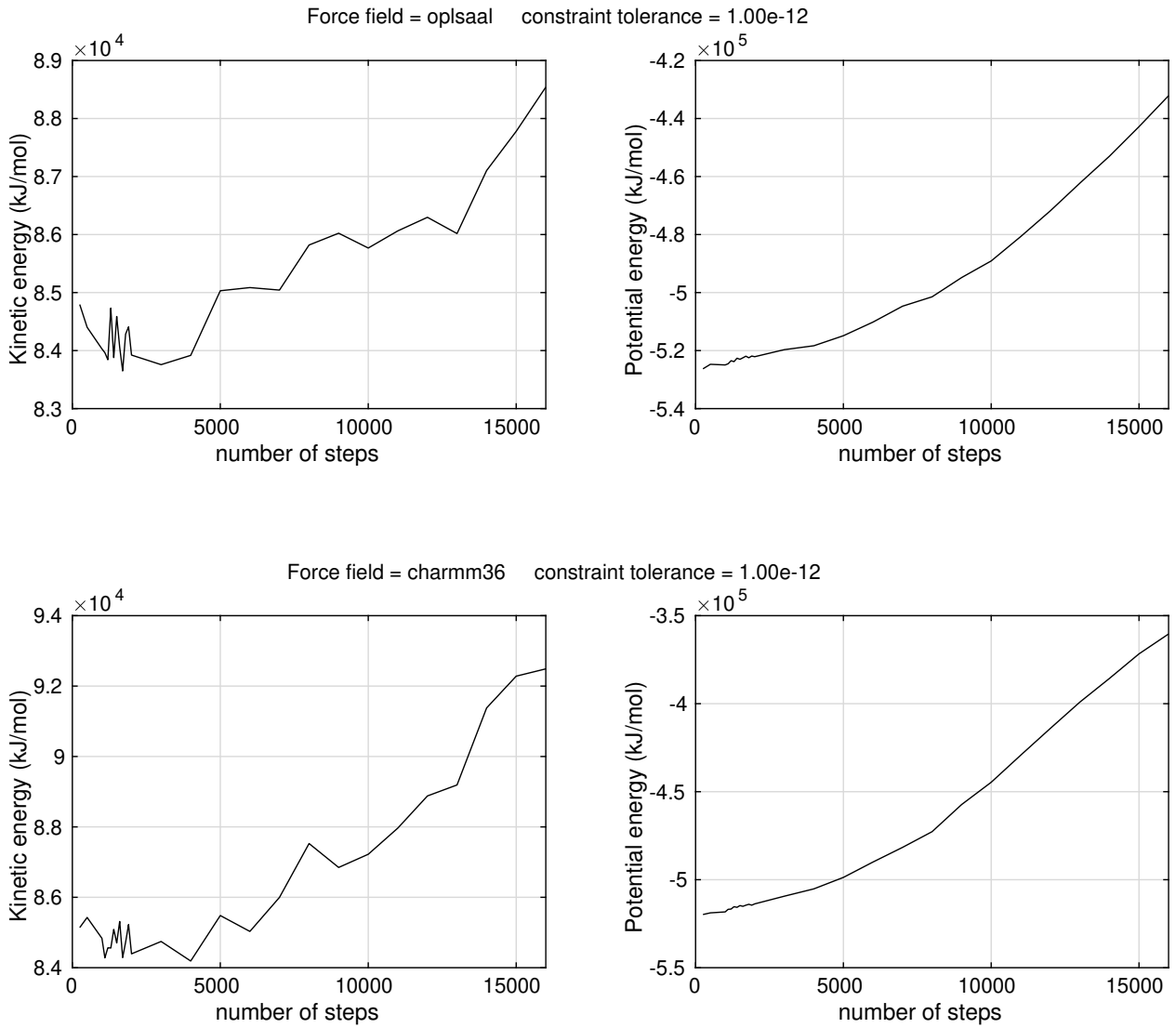
Warning: Disturbing pictures to follow

We did two sets of simulations of a molecule in water

1. fixed real time
2. two different force-fields: `charmm36`, `oopsaal`
3. identical initial conditions

and tracked the energy as a function of the number of steps.

Warning: Disturbing pictures below



Molecular dynamics

The system of differential algebraic equations

$$\boldsymbol{q}'(t) = \boldsymbol{v}(t), \tag{1}$$
$$\boldsymbol{M}\boldsymbol{v}'(t) = \boldsymbol{f}(\boldsymbol{q}(t)) - \boldsymbol{G}(\boldsymbol{q}(t))^T \boldsymbol{\lambda}(t), \tag{2}$$
$$\boldsymbol{g}(\boldsymbol{q}(t)) = \boldsymbol{0}. \tag{3}$$

is solved using the SHAKE algorithm

$$\boldsymbol{v}_{n+1/2} = \boldsymbol{v}_{n-1/2} + \boldsymbol{h}\boldsymbol{M}^{-1}\left(\boldsymbol{f}(\boldsymbol{q}_n) - \boldsymbol{G}(\boldsymbol{q}_n)^T \boldsymbol{\lambda}\right), \tag{4}$$
$$\boldsymbol{q}_{n+1} = \boldsymbol{q}_n + h\boldsymbol{v}_{n+1/2}, \tag{5}$$
$$\boldsymbol{g}(\boldsymbol{q}_{n+1}) = \boldsymbol{0}. \tag{6}$$

Molecular dynamics

Key questions

Does it matter

1. if the force-field

$$\boldsymbol{q} \rightarrow \boldsymbol{f}(\boldsymbol{q})$$

   is smooth or not?

2. if the nonlinear constraint equation

$$\boldsymbol{g}(\boldsymbol{q}_{n+1}(\boldsymbol{\lambda})) = \boldsymbol{0} \tag{7}$$

   is solved accurately with respect to $\boldsymbol{\lambda}$ or not?

The primary point of this talk

If one of the following is true:

1. the central functions are not smooth enough
2. the central equations are not solved accurately enough

then we cannot:

1. estimate the modelling error
2. validate the model against the physical reality

The key terms of this talk

1. P: physical quantity that can be measured
2. T: approximation of P predicted by our model
3. A_h: approximation of T returned by our algorithm
4. $\hat{A}_h$: the computed value of A_h.

The three different error terms

1. $P - T$ is the modelling error and

$$P - T \neq 0 \tag{8}$$

because our model is simpler than the real world.

2. $T - A_h$ is the discretization error and

$$T - A_h \neq 0 \tag{9}$$

because we cannot solve most differential equations exactly.

3. $A_h - \hat{A}_h$ is the computational error and

$$A_h - \hat{A}_h \neq 0 \tag{10}$$

due to rounding errors and truncation errors.

Why should we care?

We validate our models by demonstrating that

$$P - T \approx 0 \tag{11}$$

is a good approximation, but

$$P - T \approx P - \hat{A}_h \tag{12}$$

is not necessarily a good approximation. We have

$$P - T = (P - \hat{A}_h) - (T - A_h) - (A_h - \hat{A}_h) \tag{13}$$

so we need to assert that

$$|T - A_h| \ll |P - \hat{A}_h| \tag{14}$$

$$|A_h - \hat{A}_h| \ll |P - \hat{A}_h| \tag{15}$$

Practical error estimation

It is frequently possible to simultanously

1. assert that the computational error

$$A_h - \hat{A}_h$$

   is irrelevant, and
2. estimate the discretization error

$$T_h - A_h$$

   accurately

The key is the existence of an asymptotic error expansion

$$E_h = T - A_h = \alpha h^p + \beta h^q + O(h^r), \quad h \to 0_+ \tag{16}$$

where $0 < p < q < r$.

Elementary results

Define

$$R_h := \frac{A_h - A_{2h}}{2^p - 1}, \quad F_h := \frac{A_{2h} - A_{4h}}{A_h - A_{2h}} \tag{17}$$

If

$$E_h = T - A_h = \alpha h^p + \beta h^q + O(h^r), \quad h \to 0_+ \tag{18}$$

then

$$\frac{E_h - R_h}{h^q} \to \text{constant} \tag{19}$$

and

$$\frac{2^p - F_h}{h^{q-p}} \to \text{constant} \tag{20}$$

which implies

$$\log|2^p - F_h| \approx \log|\text{constant}| + (q-p)\log h \tag{21}$$

An example from elementary numerical analysis

Our target value is

$$T = \int_0^1 f(x)dx, \quad f(x) = \exp(x) \tag{22}$$

Our approximation is the composite trapezoidal rule

$$A_h = \frac{h}{2} \sum_{j=0}^{n-1} \left(f(x_i) + f(x_{i+1}) \right), \quad x_i = ih, \quad nh = 1 \tag{23}$$

We compute A_h for

$$h = h_k = 2^{-k} \tag{24}$$

The evolution of F_h and the quality of R_h

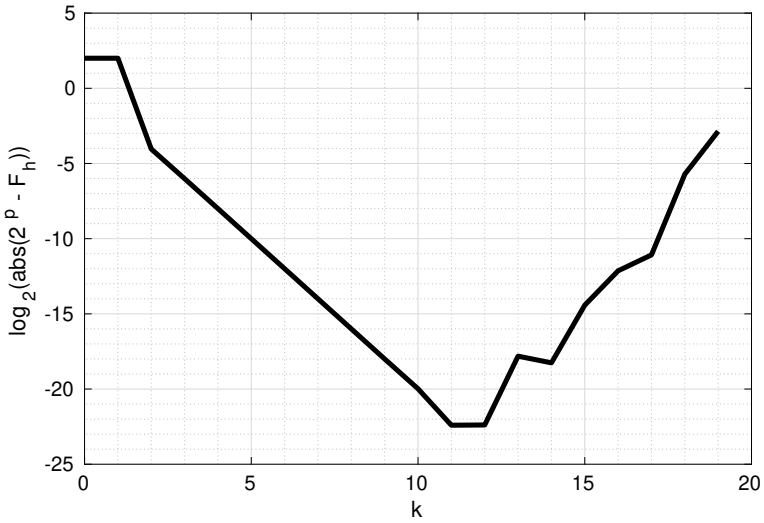


Figure: The evolution of F_h

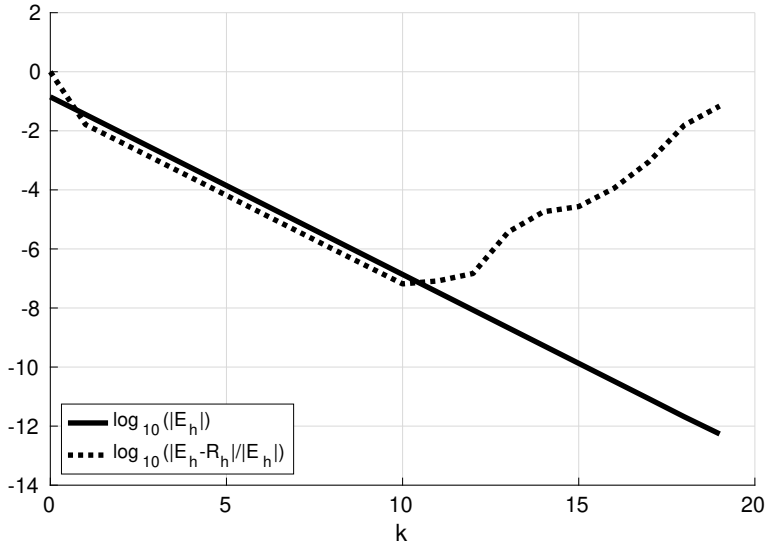


Figure: The accuracy of R_h

Strictly speaking we are not observing F_h and R_h

we are observing $\hat{F}_h$ and $\hat{R}_h$

The discrepancy is controlled by the computational error

$$A_h - \hat{A}_h$$

A spectacular failure

GROMACS simulation of hen egg white lysozyme in water:

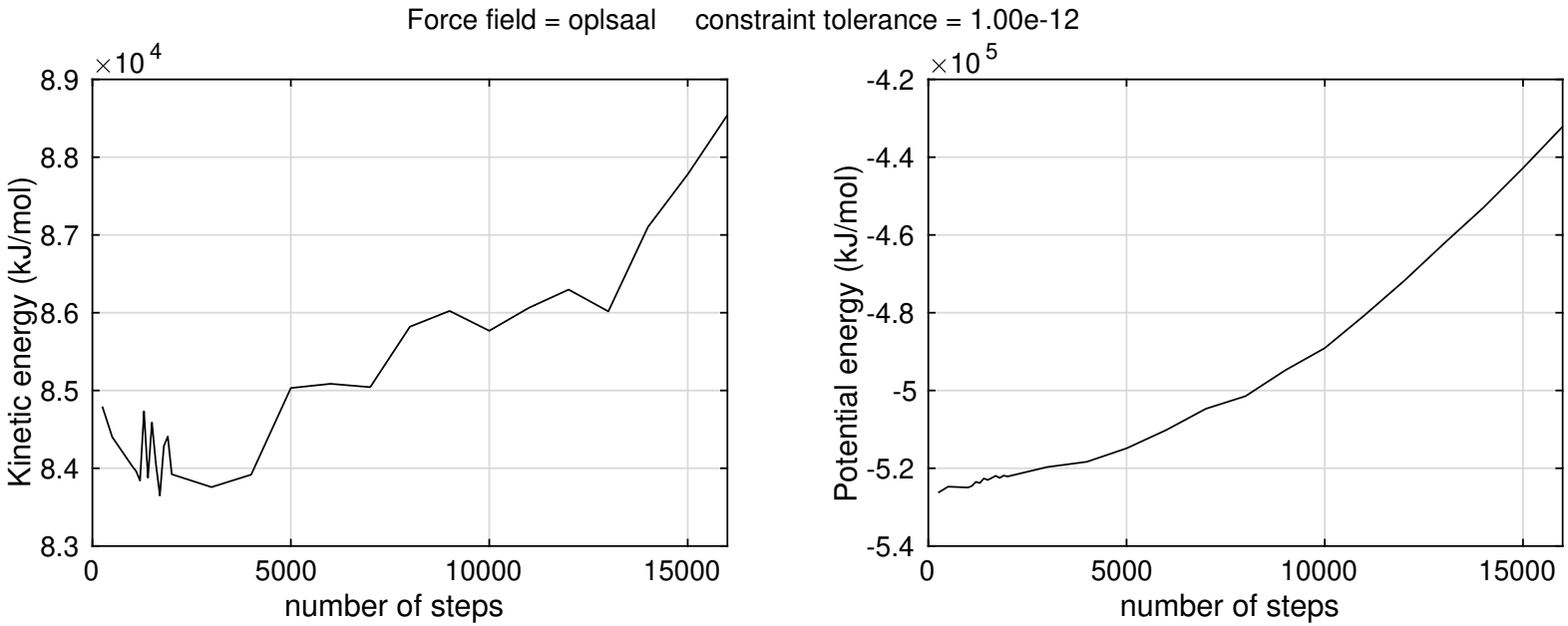
1. T: total energy of the simulation at the end
2. A_h: the approximation of T computed using SHAKE
3. $\hat{A}_h$: the value of A_h returned by the computer

Temporal matters:

1. The length of the simulations was 10^{-12} s (1 ps)
2. A common step size in MD is $10^{-15}s$ (1 fs)

So, a mere 1000 steps! What could possibly go wrong?

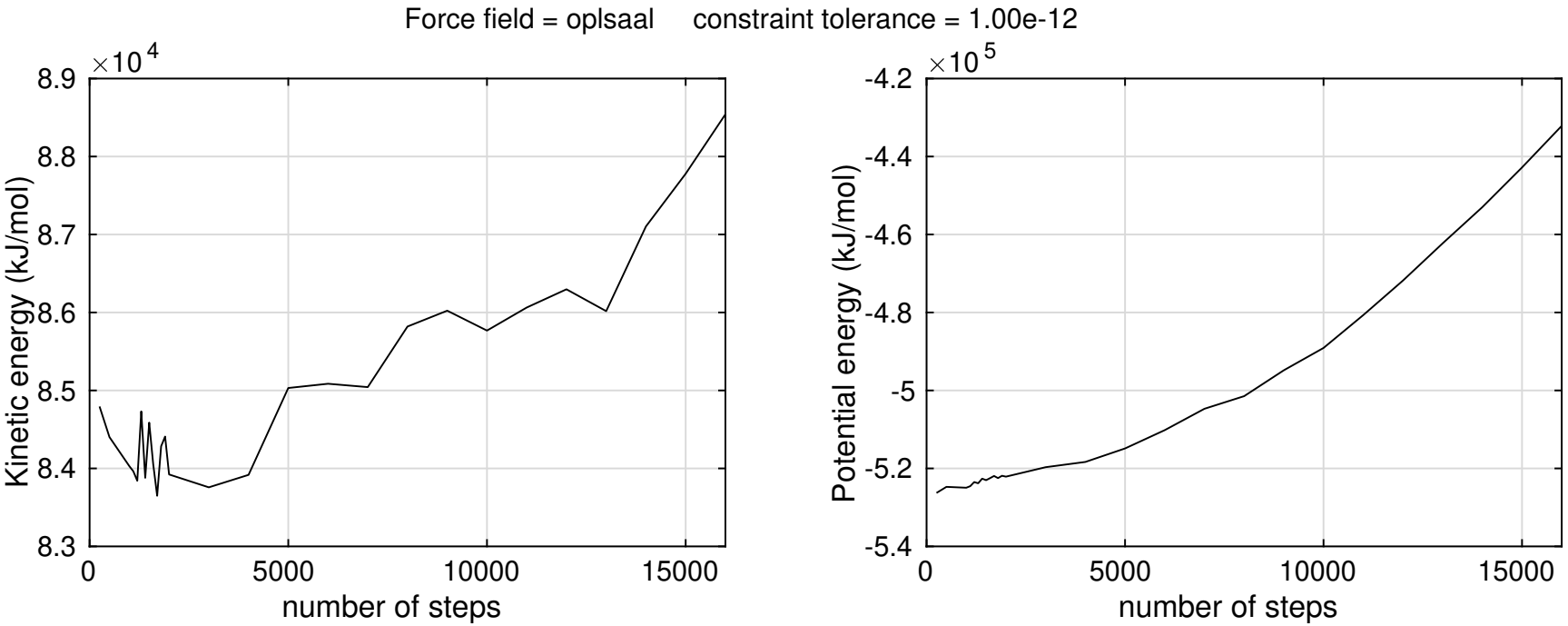
A spectacular failure



The rapid growth of the energy for large value of n

can likely be cured using compensated summation.

A spectacular failure



- The wiggles near $n = 1000$ steps are a great concern.
- If there is an AEX, then 1 fs is not inside the asymp. range.
- We cannot assert that rounding errors are irrelevant
- We cannot estimate the discretication error

When do we have an AEX?

Deriving an AEX is an exercise in Taylor expansions. If

our functions are not many times differentiable

then the foundation crumbles.

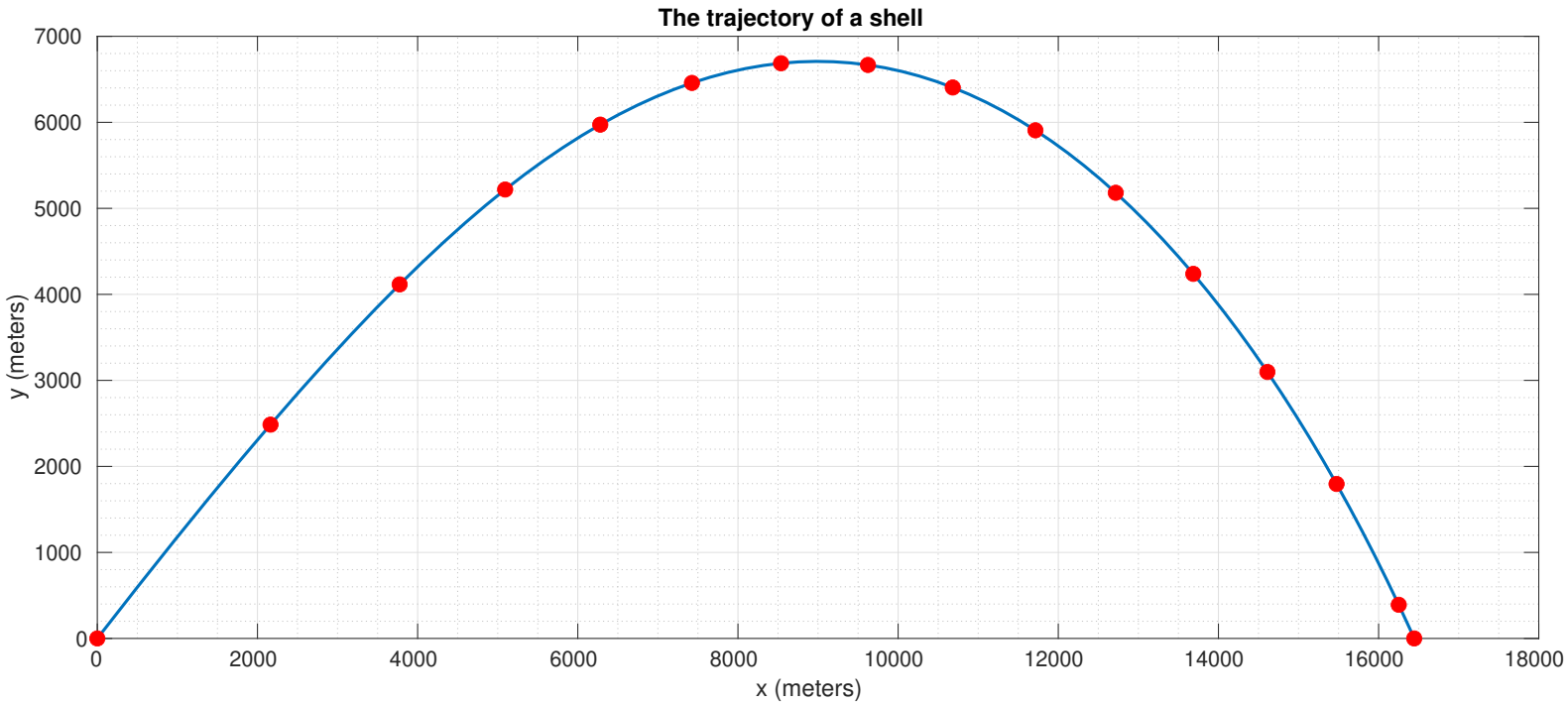
Every AEX refers to the exact value of the A_h. If

$$\hat{A}_h \approx A_h$$

is not a good approximation, then

$\hat{A}_h$ will not behave nicely

External ballistics



The total force $\boldsymbol{F}$ acting on the shell

$$\boldsymbol{F} = m\boldsymbol{g} - \frac{1}{2}\rho(y)AC_D(\nu, y)\|\boldsymbol{v} - \boldsymbol{w}\|_2(\boldsymbol{v} - \boldsymbol{w}) \qquad (25)$$

is the combination of gravity and aerodynamic drag.

Computing the optimal range of the a howitzer

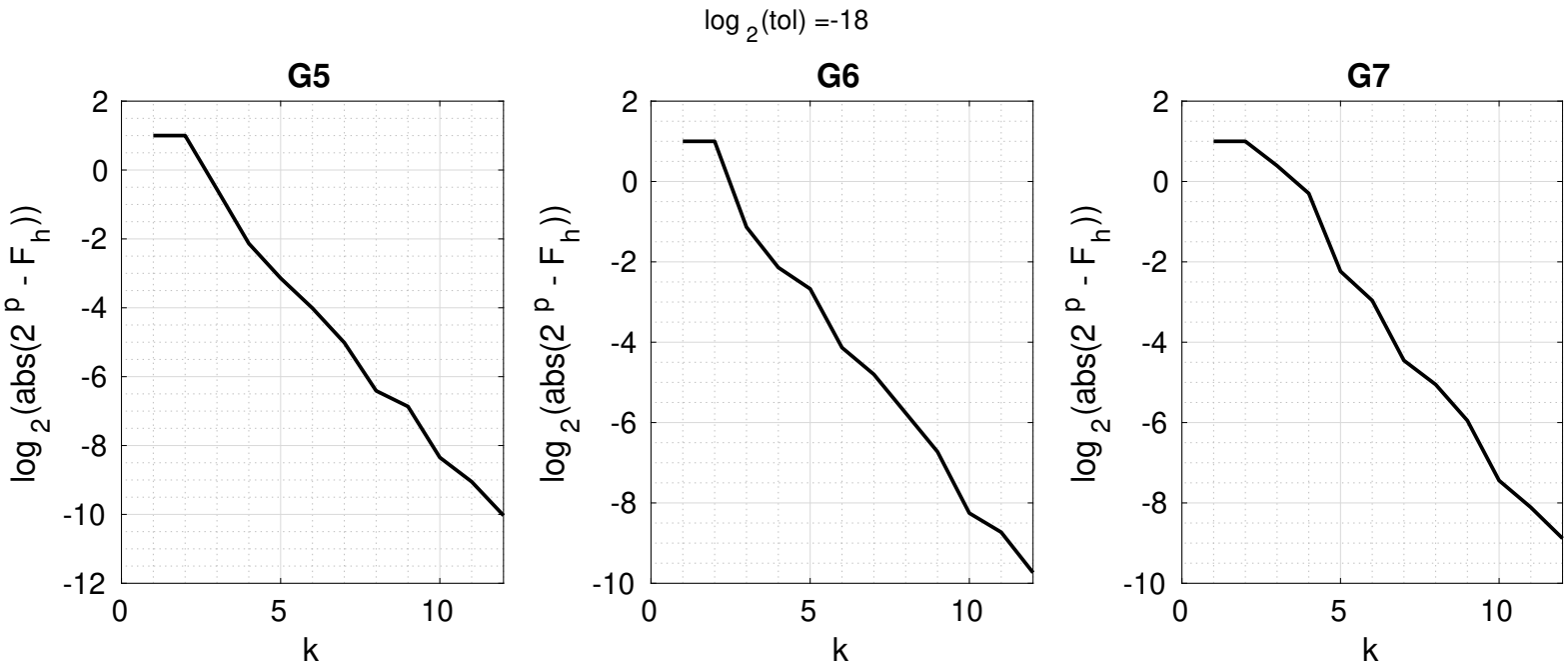


Figure: The evolution of Richardson's fraction for 3 different drag coeffients, Euler's explicit method and sufficiently accurate event location.

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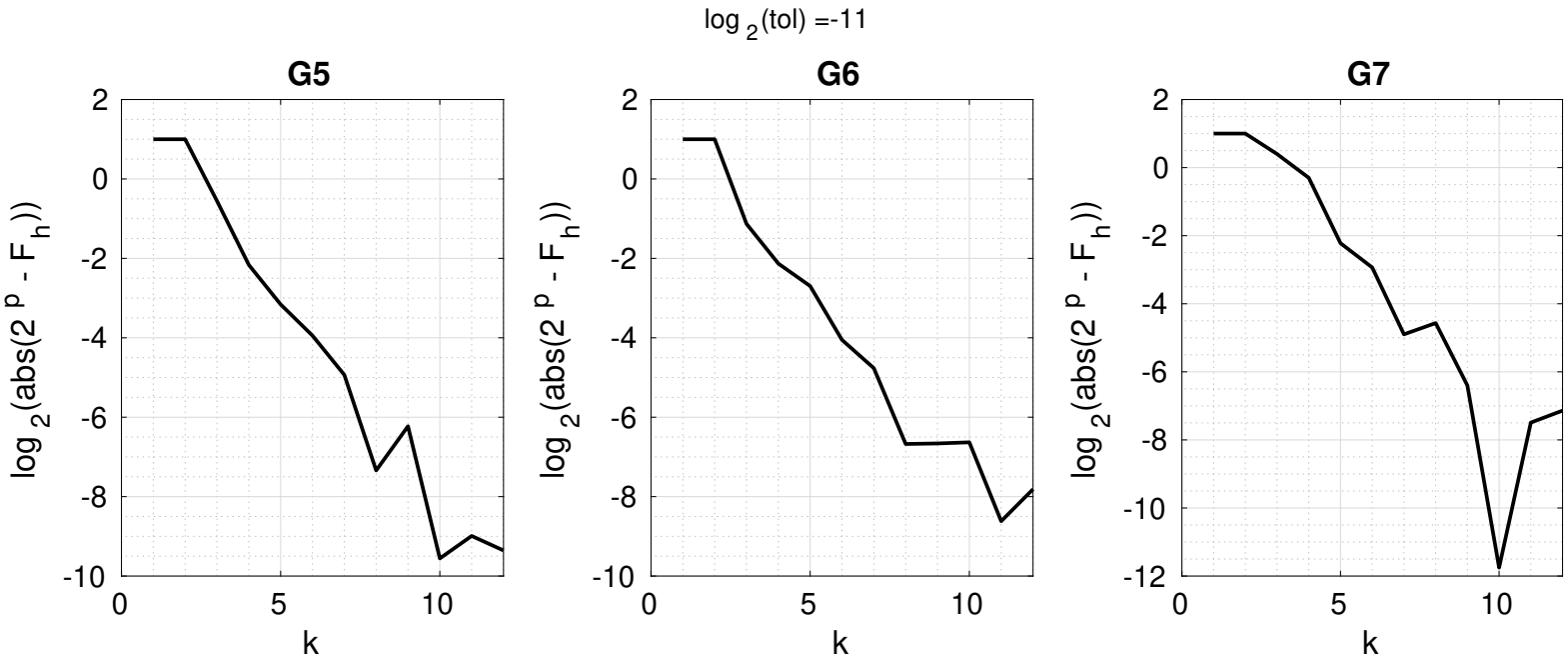

Figure: The evolution of Richardson's fraction for 3 different drag coeffients, Euler's explicit method and inaccurate event location.

Modelling ions

Molecular dynamics: Truncation of force-fields

- Simple simulation with 4 ions
- Each ion is attached to the origin with a spring
- The electrostatic forcefields are trunctated.

Why should this concern the PPAM community?

We use every trick in the book to

1. reduce time-to-solution
2. increase the parallel efficicency
3. reduce energy-to-solution

We should not forget to ask the question:

Did we just compromise our ability to validate our models against the real world?