The need for accuracy and smoothness in numerical simulations

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Introduction

This is not a talk about, say,

- computational speed
- parallelism
- energy efficency

This is a talk about

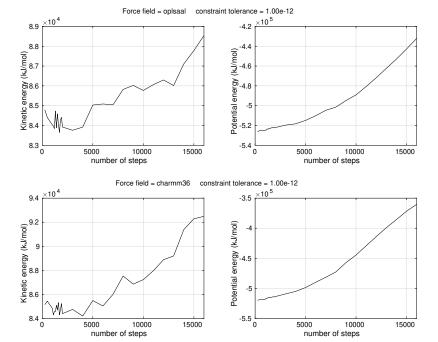
the relevance of the numbers returned by our simulations

A simple experiment

We did two sets of simulations of a molecule in water

- fixed real time
- wo different force-fields: charmm36, oopsaal
- identical initial conditions
- 4 ran the constraint solver to stagnation

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



Molecular dynamics with constraints

The system of differential algebraic equations

$$\mathbf{q}'(t) = \mathbf{v}(t),\tag{1}$$

$$\mathbf{M}\mathbf{v}'(t) = \mathbf{f}(\mathbf{q}(t)) - \mathbf{G}(\mathbf{q}(t))^{\mathsf{T}}\lambda(t),$$
 (2)

$$\mathbf{g}(\mathbf{q}(t)) = \mathbf{0}. \tag{3}$$

is solved using the SHAKE algorithm

$$\mathbf{v}_{n+1/2} = \mathbf{v}_{n-1/2} + \mathbf{h} \mathbf{M}^{-1} \left(\mathbf{f}(\mathbf{q}_n) - \mathbf{G}(\mathbf{q}_n)^T \lambda \right),$$
 (4)

$$\mathbf{q}_{n+1} = \mathbf{q}_n + h\mathbf{v}_{n+1/2},\tag{5}$$

$$\mathbf{g}(\mathbf{q}_{n+1}) = \mathbf{0}. \tag{6}$$

Molecular dynamics

Key questions

Does it matter

if the force-field

$$m{q}
ightarrow m{f}(m{q})$$

is smooth or not?

if the nonlinear constraint equation

$$oldsymbol{g}(oldsymbol{q}_{n+1}(oldsymbol{\lambda})) = oldsymbol{0}$$

is solved accurately with respect to λ or not?

The primary point of this talk

If one of the following is true:

- the central functions are not smooth enough
- the central equations are not solved accurately enough

then we may lose the ability to

- assert that rounding errors are irrelevant
- estimate the discretization error
- compare the model against the physical reality

The key terms of this talk

- P: physical quantity that can be measured
- \bullet A_h : approximation of T returned by our algorithm
- \hat{A}_h : the computed value of A_h .

The three different error terms

 \bullet P-T is the modelling error and

$$P - T \neq 0 \tag{7}$$

because our model is simpler than the real world.

 $2 T - A_h$ is the discretization error and

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

because we cannot solve most differential equations exactly.

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

$$A_h - \hat{A}_h \neq 0 \tag{9}$$

due to rounding errors and truncation errors.

Why should we care?

We validate our models by demonstrating that

$$P - T \approx 0 \tag{10}$$

is a good approximation, but

$$P - T \approx P - \hat{A}_h \tag{11}$$

is not necessarily a good approximation. We have

$$P - T = (P - \hat{A}_h) - (T - A_h) - (A_h - \hat{A}_h)$$
 (12)

so we need to assert that

$$|T - A_h| \ll |P - \hat{A}_h| \tag{13}$$

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

Practical error estimation

It is frequently possible to simultanously

1 assert that the computational error

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

is irrelevant, and

estimate the discretization error

$$T_h - A_h$$

accurately

Practical error estimation

The key is to have an asymptotic error expansion (AEX)

$$E_h = T - A_h = \alpha h^p + \beta h^q + O(h^r), \quad h \to 0_+$$
 (15)

where

$$0$$

are not necessarily integers.

Elementary results

Define

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

Then

$$\frac{E_h - R_h}{h^q} \to \text{constant} \tag{18}$$

and

$$\frac{2^p - F_h}{h^{q-p}} \to \text{constant} \tag{19}$$

which implies

$$\log|2^p - F_h| \approx \log|\text{constant}| + (q - p)\log h \tag{20}$$

An example from elementary numerical analysis

Our target value is

$$T = \int_0^1 f(x)dx, \quad f(x) = \exp(x)$$
 (21)

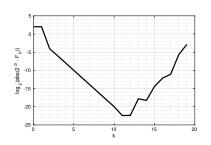
Our approximation is the composite trapezoidal rule

$$A_h = \frac{h}{2} \sum_{i=0}^{n-1} (f(x_i) + f(x_{i+1})), \quad x_i = ih, \quad nh = 1$$
 (22)

We compute A_h for

$$h = h_k = 2^{-k} (23)$$

The evolution of F_h and the quality of R_h



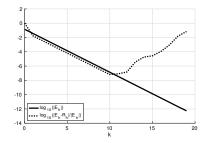


Figure: The evolution of F_h

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 difference is controlled by the computational error

$$A_h - \hat{A}_h \tag{24}$$

A spectacular failure

GROMACS simulation of hen egg white lysozyme in water:

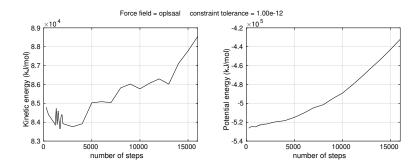
- T: total energy of the simulation at the end
- \bigcirc A_h : the approximation of T computed using SHAKE
- **3** \hat{A}_h : the value of A_h returned by the computer

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) or n = 1000 steps

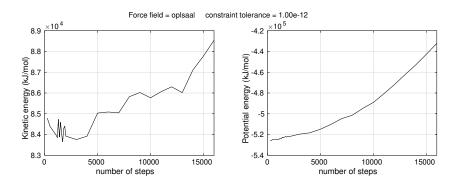
What could possibly go wrong?

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.
- \bullet If there is an AEX, then 1 fs is \underline{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?

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

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

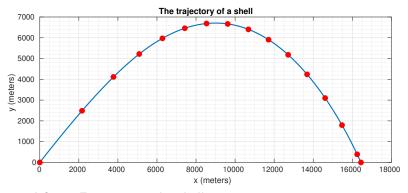
is not a good approximation, then

 \hat{A}_h will not behave nicely

and we cannot identify the asymptotic range.

② Deriving an AEX is an exercise in Taylor expansions. If our functions are not many times differentiable then the foundation crumbles.

External ballistics



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

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

is the combination of gravity and aerodynamic drag.

Computing the optimal range of the a howitzer: Success

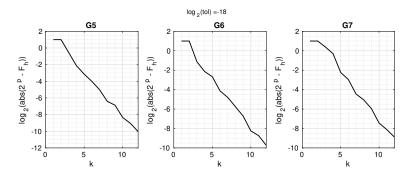


Figure: The evolution of F_h for 3 different drag coefficients, 1st order Runge-Kutta and sufficiently accurate event location.

Computing the optimal range of the a howitzer: Failure

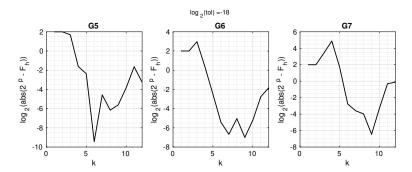


Figure: The evolution of F_h for 3 different drag coefficients, 2nd order Runge-Kutta and inaccurate event location.

Modelling ions: Setup

The total force on an ion is

$$F(\mathbf{r_i}) = -\alpha \sum_{j \neq i} \frac{1}{\|\mathbf{r_i} - \mathbf{r_j}\|^3} (\mathbf{r_i} - \mathbf{r_j}) - \beta \mathbf{r_i} - \gamma \mathbf{v_i}$$
 (26)

We measure the total kinetic energy A_h at a fixed time as function of the stepsize $h_k = 2^{-k} h_0$.

Modelling ions: Success

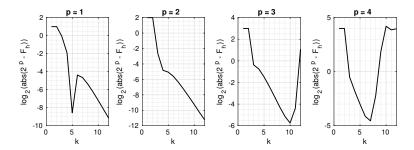


Figure: The evolution of F_h for Runge-Kutta methods of order $p \in \{1, 2, 3, 4\}$ and smooth force-fields with infinite range.

Modelling ions: Failure

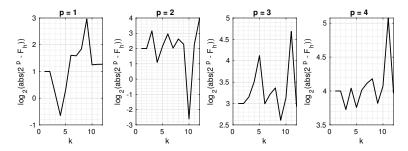


Figure: The evolution of F_h for Runge-Kutta methods of order $p \in \{1, 2, 3, 4\}$ and truncated force-fields with jump discontinuities.

Modelling ions: Success

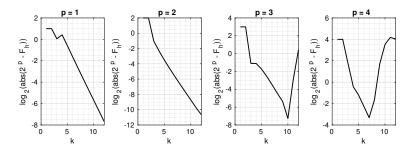


Figure: The evolution of F_h for Runge-Kutta methods of order $p \in \{1, 2, 3, 4\}$ and smoothly truncated force-fields.

Why should this concern the PPAM community?

We use every trick in the book to

- reduce time-to-solution
- increase the parallel efficiency
- reduce energy-to-solution

We should not forget to ask the question:

Can we still validate our models against the real world?