



ML potentials and their training

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4 July 2024

You have already used the KREG models.

- The operating principle of these models is the same: for a given geometry, they predict energies.
- Such models are called **machine learning (interatomic) potentials** (MLP or MLIP), as they represent potential energy surfaces (PES) of molecules (function of energy E with respect to nuclear coordinates R in the Born–Oppenheimer approximation):

$$E = f(\mathbf{R})$$

- QM methods provide the first-principles way to calculate this energy, but they are slow.

(Supervised)

Machine learning serves for function approximation[1]

ML takes little time for making new predictions

Quantum Chemical Property(molecule) = function(nuclear coordinates)

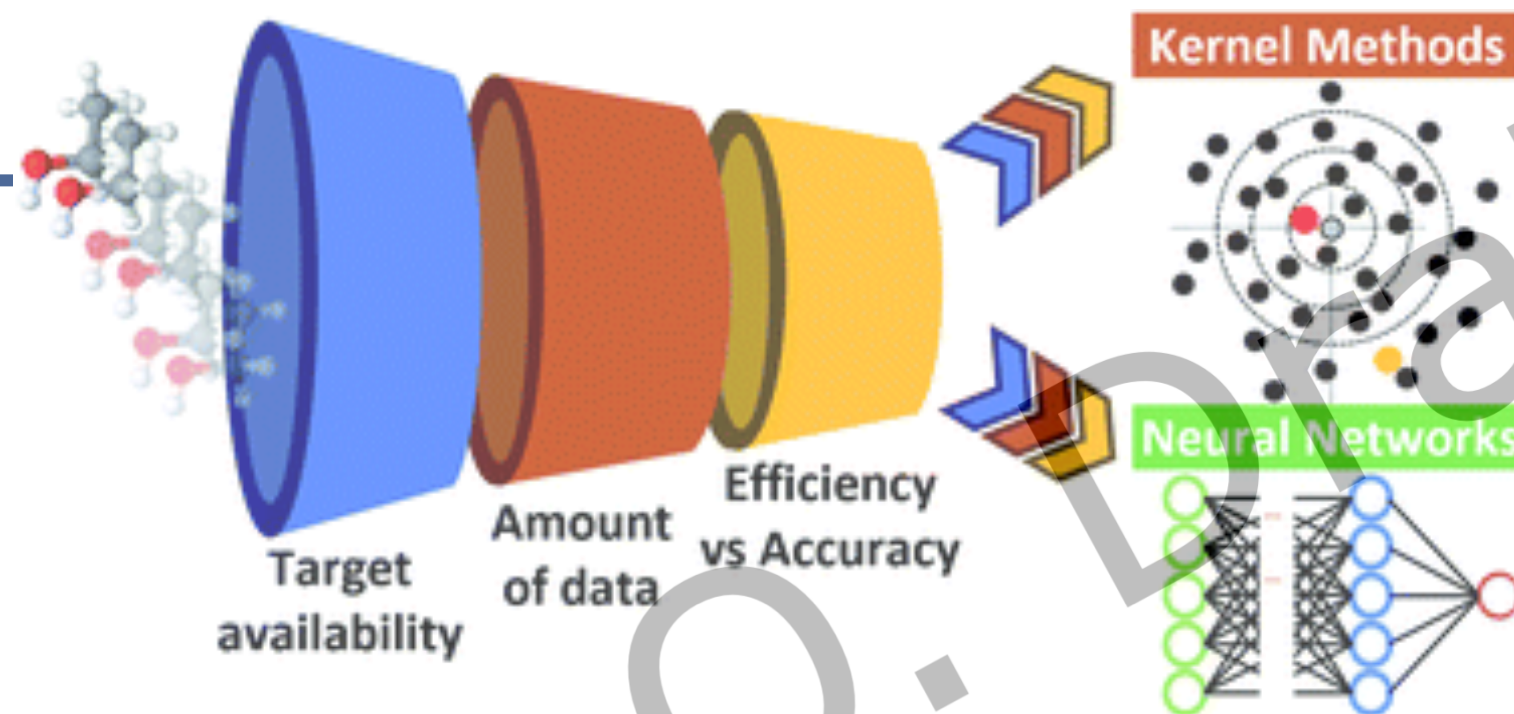




Mario
Barbatti



Max
Pinheiro
Jr



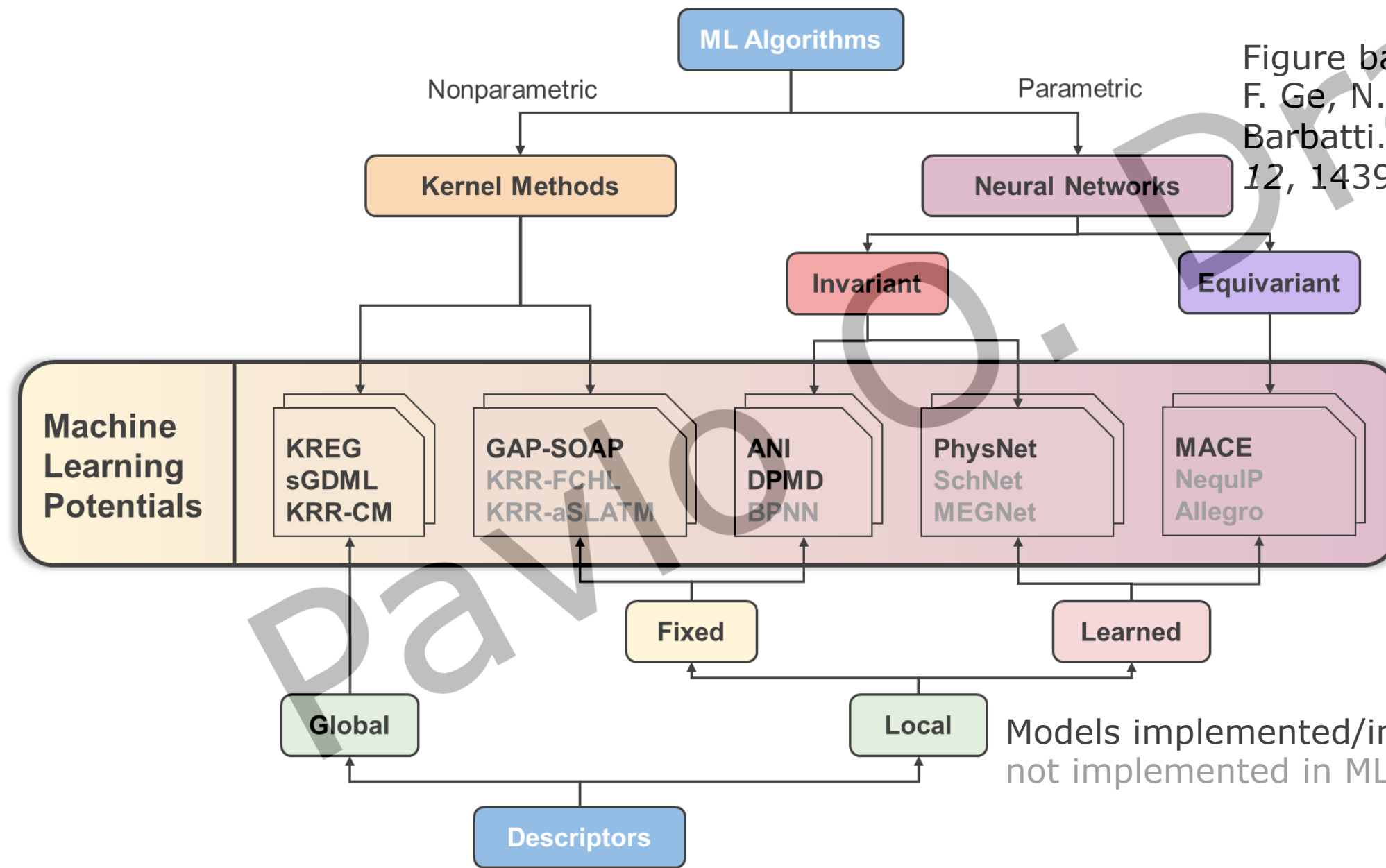
What machine learning potential to choose?



Fuchun Ge

M. Pinheiro Jr, F. Ge, N. Ferré, P. O. Dral, M. Barbatti. *Chem. Sci.* **2021**, 12, 14396–14413
P. O. Dral, F. Ge, B.-X. Xue, Y.-F. Hou, M. Pinheiro Jr, J. Huang, M. Barbatti. *Top. Curr. Chem.*
2021, 379, 27

Figure based on M. Pinheiro Jr, F. Ge, N. Ferré, P. O. Dral, M. Barbatti. *Chem. Sci.* **2021**, *12*, 14396–14413



Models implemented/interfaced in MLatom
not implemented in MLatom

Train the ANI-type MLP for the H₂ molecule (see instructions below) and obtain the bond length with this model.

Questions:

1. How much time did it take to train the model?
2. What are the training and validation errors?
3. What is the bond length of H₂ obtained with your model?
4. How do these results compare to the KREG model you used in previous task?

Training the model

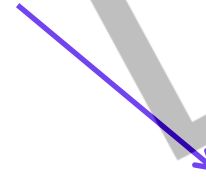
```
createMLmodel           # Specify the task for MLatom
MLmodelType=ANI         # Specify the model type
MLmodelOut=energies_ani.pt # Save model in energies_ani.pt
XYZfile=h2.xyz          # File with XYZ geometries
Yfile=E_FCI_451.dat     # The file with FCI energies but can be any other property
ani.max_epochs=1000    # Only train 1000 epochs
```

Using the model, e.g., for optimization

```
geomopt                 # Request geometry optimization
MLmodelType=ANI         # of the KREG type
MLmodelIn=energies_ani.pt # in energies_ani.pt file
XYZfile=h2_init.xyz     # The file with initial guess
optXYZ=eq_ANI.xyz       # optimized geometry output
```

Linear regression

$$f(\mathbf{x}_i; \boldsymbol{\beta}) = \beta_0 + \beta_1 x_{i1} + \beta_2 x_{i2} + \dots$$



Kernel ridge regression (KRR)

$$f(\mathbf{x}_i; \boldsymbol{\alpha}) = \sum_{j=1}^{N_{tr}} \alpha_j k(\mathbf{x}_i, \mathbf{x}_j)$$

'nonparametric model'

Examples: KREG, KRR-CM

Neural networks (NN)

Number of parameters is fixed

$$f(\mathbf{x}; \boldsymbol{\beta}) = \beta_0 + \beta_1 Z_1 + \beta_2 Z_2 + \dots$$

$$Z_m = \sigma(\alpha_{m0} + \alpha_{m1} x_1 + \alpha_{m2} x_2 + \dots)$$

'parametric model'

Examples: ANI-1ccx, AIQM1

$$f(\mathbf{x}_i) = \sum_{j=1}^{N_{\text{tr}}} \alpha_j k(\mathbf{x}_i, \mathbf{x}_j) \quad k(\mathbf{x}_i, \mathbf{x}_j) = \exp\left(-\frac{1}{2\sigma^2} \sum_s^{N_x} (x_{i,s} - x_{j,s})^2\right) \quad x = \left(\dots \frac{Req}{R} \dots\right)^T$$

the Gaussian kernel function
(σ is the kernel width)

RE descriptor

Analytical solution for the regression coefficients α given N_{tr} training points

$$\begin{pmatrix} k(\mathbf{x}_1, \mathbf{x}_1) + \lambda & \dots & k(\mathbf{x}_1, \mathbf{x}_{N_{\text{tr}}}) \\ \vdots & \ddots & \vdots \\ k(\mathbf{x}_{N_{\text{tr}}}, \mathbf{x}_1) & \dots & k(\mathbf{x}_{N_{\text{tr}}}, \mathbf{x}_{N_{\text{tr}}}) + \lambda \end{pmatrix} \begin{pmatrix} \alpha_1 \\ \vdots \\ \alpha_{N_{\text{tr}}} \end{pmatrix} = \begin{pmatrix} y_1 \\ \vdots \\ y_{N_{\text{tr}}} \end{pmatrix}$$

λ is the regularization parameter ensuring transferability

$$(\mathbf{K} + \lambda \mathbf{I})\alpha = \mathbf{y}$$

Back-propagation:

$$L(\boldsymbol{\theta}) = \sum_{i=1}^N (f(\mathbf{x}_i; \boldsymbol{\theta}) - y_i)^2$$

gradient descent update with learning rate γ

$$\theta_k^{(r+1)} = \theta_k^{(r)} - \gamma \frac{\partial L(\boldsymbol{\theta})}{\partial \theta_k}$$

Well parallelized:

$$L(\boldsymbol{\theta}) = \sum_{i=1}^N L_i = \sum_{i=1}^N (f(\mathbf{x}_i; \boldsymbol{\theta}) - y_i)^2$$

The training set is often split into the minibatches (**batches**)

Update of parameters after the sweep over the entire training set is called an **epoch**.

No analytical solution, hence, one can get **different NNs fitted on the same data!**

One can exploit this:

- Take average of multiple NNs to get more stable prediction
- Use deviation between NN predictions to estimate prediction uncertainty (e.g. useful in our previous examples for heats of formation and in active learning)

Pavlo O. Dral

Behler–Parrinello

ANI

PhysNet

SchNet

GAP-SOAP

FCHL

aSLATM

...

Overview & benchmark in:

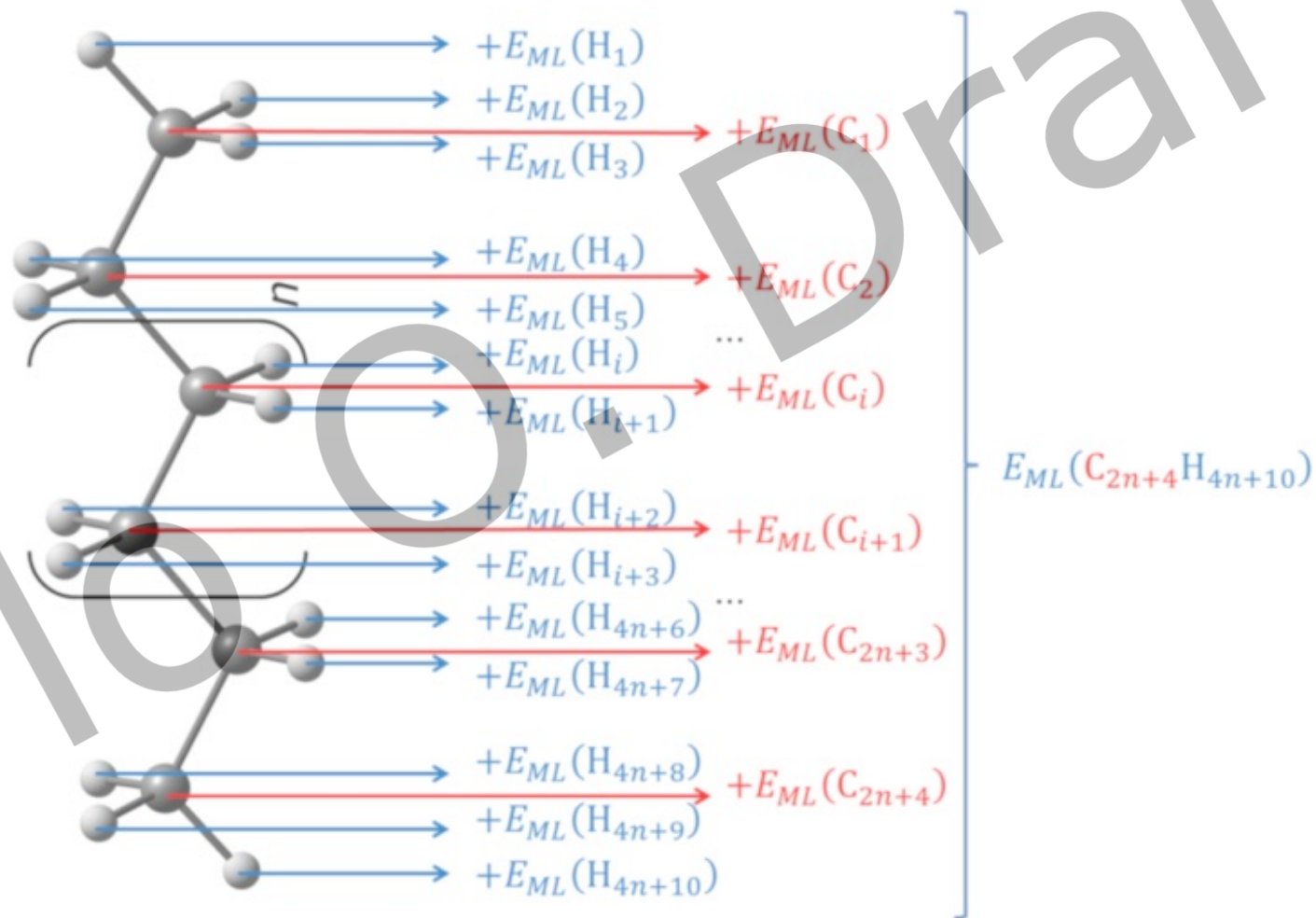
M. Pinheiro Jr, F. Ge,

N. Ferré, P. O. Dral,

M. Barbatti.

Chem. Sci. **2021**, *12*,

14396–14413



Approach: Behler, Parrinello, *Phys. Rev. Lett.* **2007**, *98*, 146401

ANI environment vectors (AEVs) consist of radial and angular atomic terms. Each element has its own subAEV:

$$G_k^R = \sum_{j \neq i} e^{-\eta(R_{ij} - R_s^{(k)})^2} f_c(R_{ij})$$

$$G_{p,q}^A = 2^{1-\zeta} \sum_{j,k \neq i} \left(1 + \cos(\theta_{ijk} - \theta_s^{(q)})\right)^\zeta e^{-\eta\left(\frac{R_{ij} + R_{ik}}{2} - R_s^{(p)}\right)^2} f_c(R_{ij}) f_c(R_{ik}).$$

the cutoff function

$$f_{\text{cut}}(r) = \begin{cases} 1, & r \leq r_{\text{cut}} - r_{\Delta}, \\ \frac{1}{2} \left(\cos\left(\pi \frac{r - r_{\text{cut}} + r_{\Delta}}{r_{\Delta}}\right) + 1 \right), & r_{\text{cut}} - r_{\Delta} < r \leq r_{\text{cut}}, \\ 0, & r > r_{\text{cut}}, \end{cases}$$

Gaussian approximation potential (GAP)[1] with Smooth Overlap of Atomic Positions (SOAP)[2] descriptor

the atomic neighborhood density

$$\rho_i(\mathbf{r}) = \sum_j \exp\left(-\frac{|\mathbf{r} - \mathbf{r}_{ij}|^2}{2\sigma_{atom}^2}\right) f_{cut}(|\mathbf{r}_{ij}|),$$

the cutoff function

$$f_{cut}(r) = \begin{cases} 1, & r \leq r_{cut} - r_{\Delta}, \\ \frac{1}{2} \left(\cos\left(\pi \frac{r - r_{cut} + r_{\Delta}}{r_{\Delta}}\right) + 1 \right), & r_{cut} - r_{\Delta} < r \leq r_{cut}, \\ 0, & r > r_{cut}, \end{cases}$$

[1] A. P. Bartók, M. C. Payne, R. Kondor, G. Csányi, Phys. Rev. Lett. **2010**, 104, 136403

[2] A. P. Bartók, R. Kondor, G. Csányi, Phys. Rev. B **2013**, 87, 187115

PhysNet is using message-passing NN and so called 'learned' local descriptors

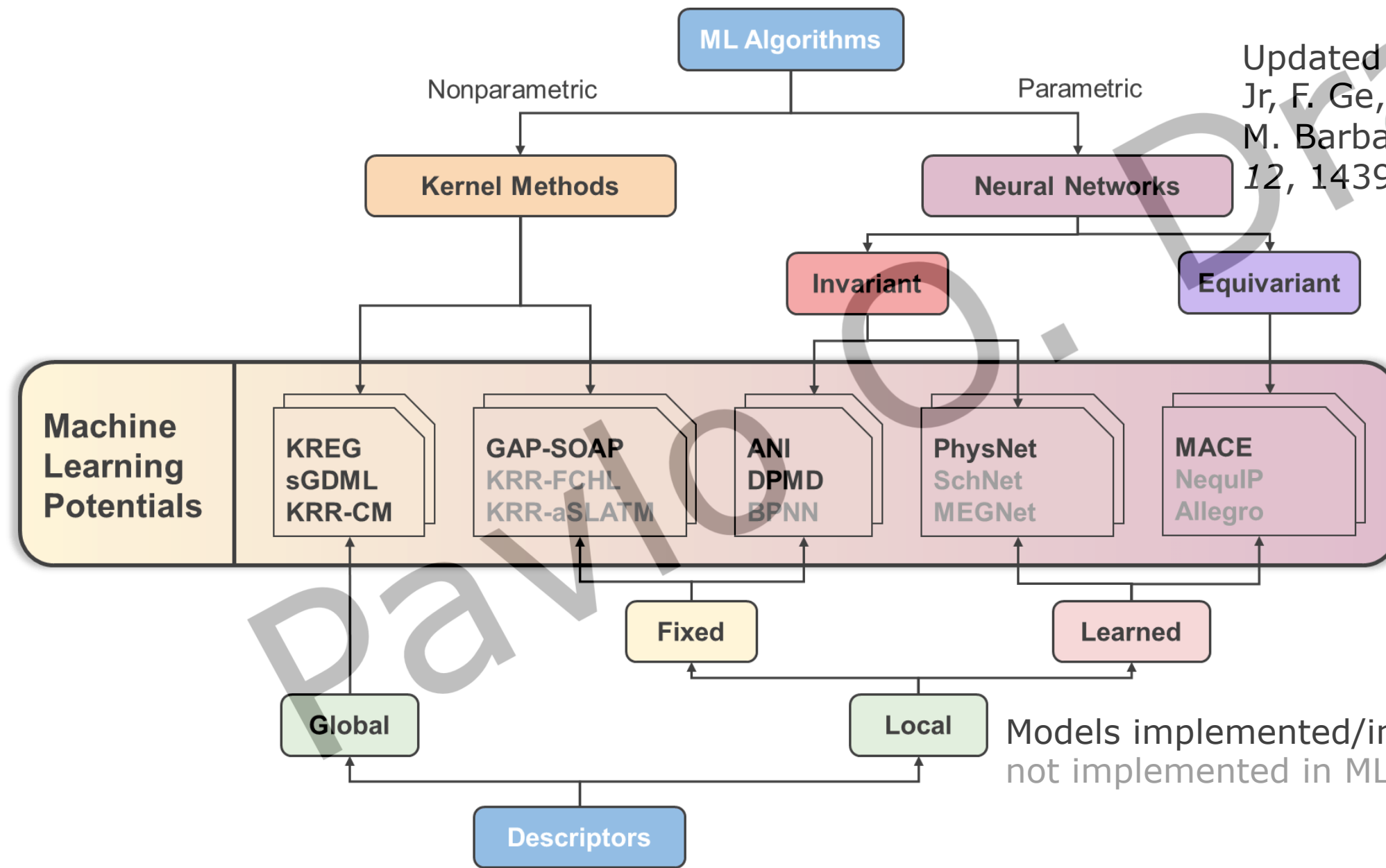
the embedding vector

$$\mathbf{x}_i^0 = \mathbf{e}_{z_i}$$

the coordinates are transformed to

$$g_k(r_{ij}) = f_c(r_{ij}) \cdot e^{-\beta_k(e^{-r_{ij}} - \mu_k)^2}$$

Updated based on M. Pinheiro Jr, F. Ge, N. Ferré, P. O. Dral, M. Barbatti. *Chem. Sci.* **2021**, *12*, 14396–14413



Models implemented/interfaced in **MLatom**
not implemented in MLatom



Certificate of appreciation Highly cited article

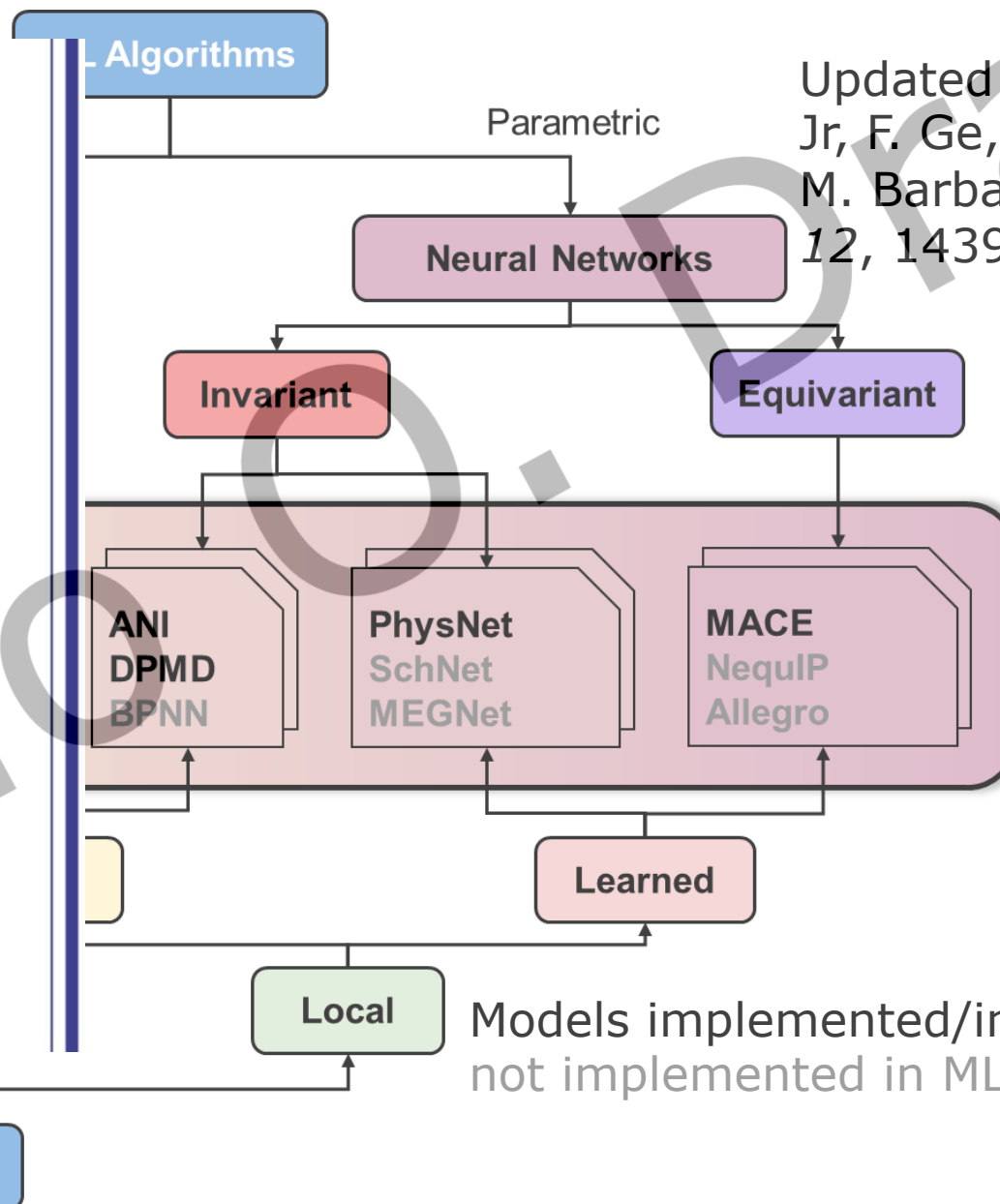
This certificate is awarded to

Choosing the right molecular machine learning potential

Max Pinheiro, Fuchun Ge, Nicolas Ferré, Pavlo O. Dral and Mario Barbatti

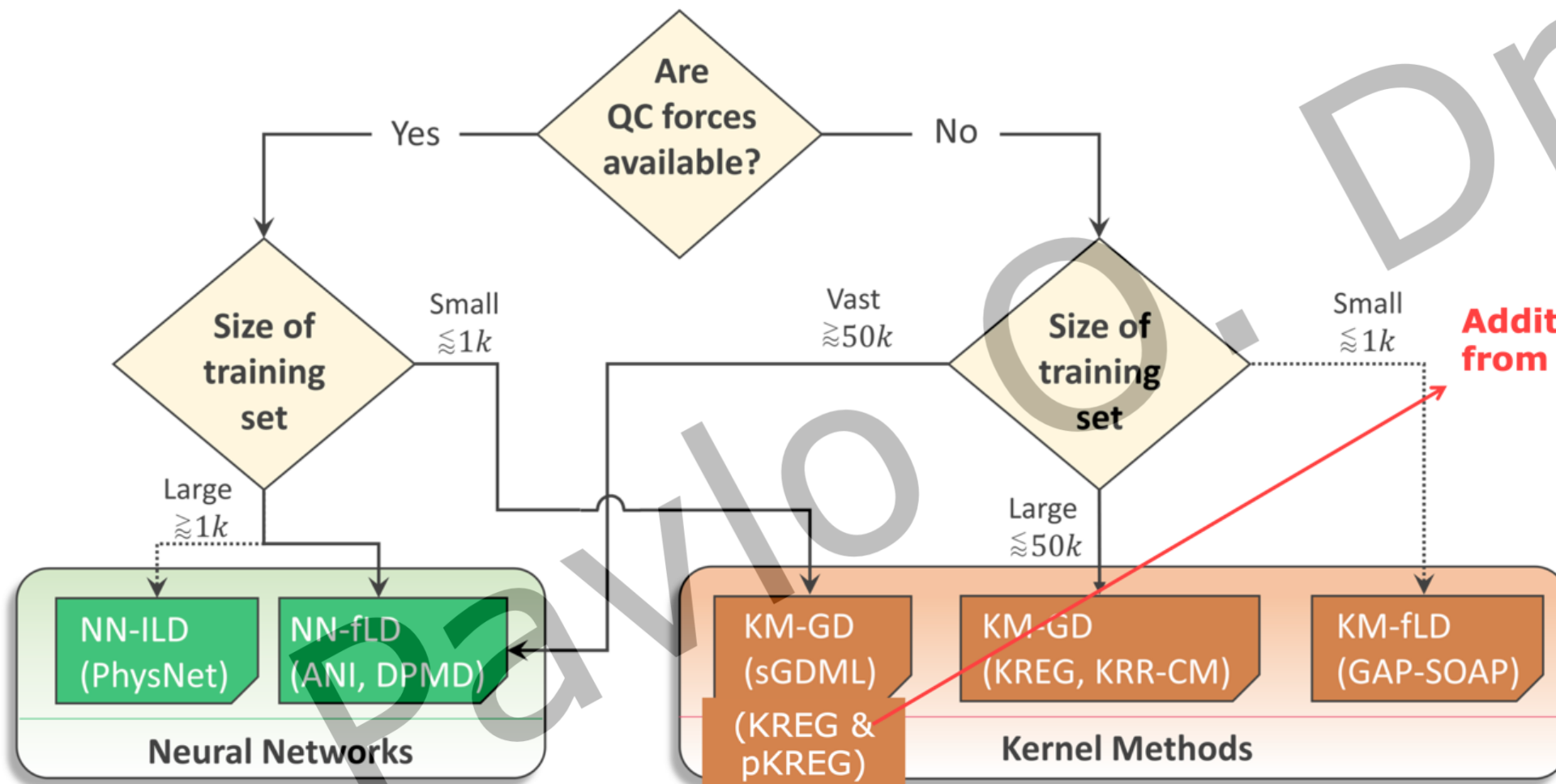
Chemical Science, 2021, 12, 43, 14396

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Updated based on M. Pinheiro Jr, F. Ge, N. Ferré, P. O. Dral, M. Barbatti. *Chem. Sci.* **2021**, 12, 14396–14413

Recommendations from 2021



Addition from 2023

KREG & pKREG:
Y.-F. Hou, F. Ge,
P. O. Dral. *J. Chem. Theory Comput.* **2023**, *19*, 2369–2379

After 2021, open questions such as: where is the place for equivariant NNs?

Train the KREG model for the H₂ molecule with the settings provided below. With this model, calculate energies for the potential energy curve of H₂ (see instructions below).

Questions:

1. What is the training error (RMSE) of the model?
2. Does the potential energy curve (energy as a function of the bond length) look reasonable?

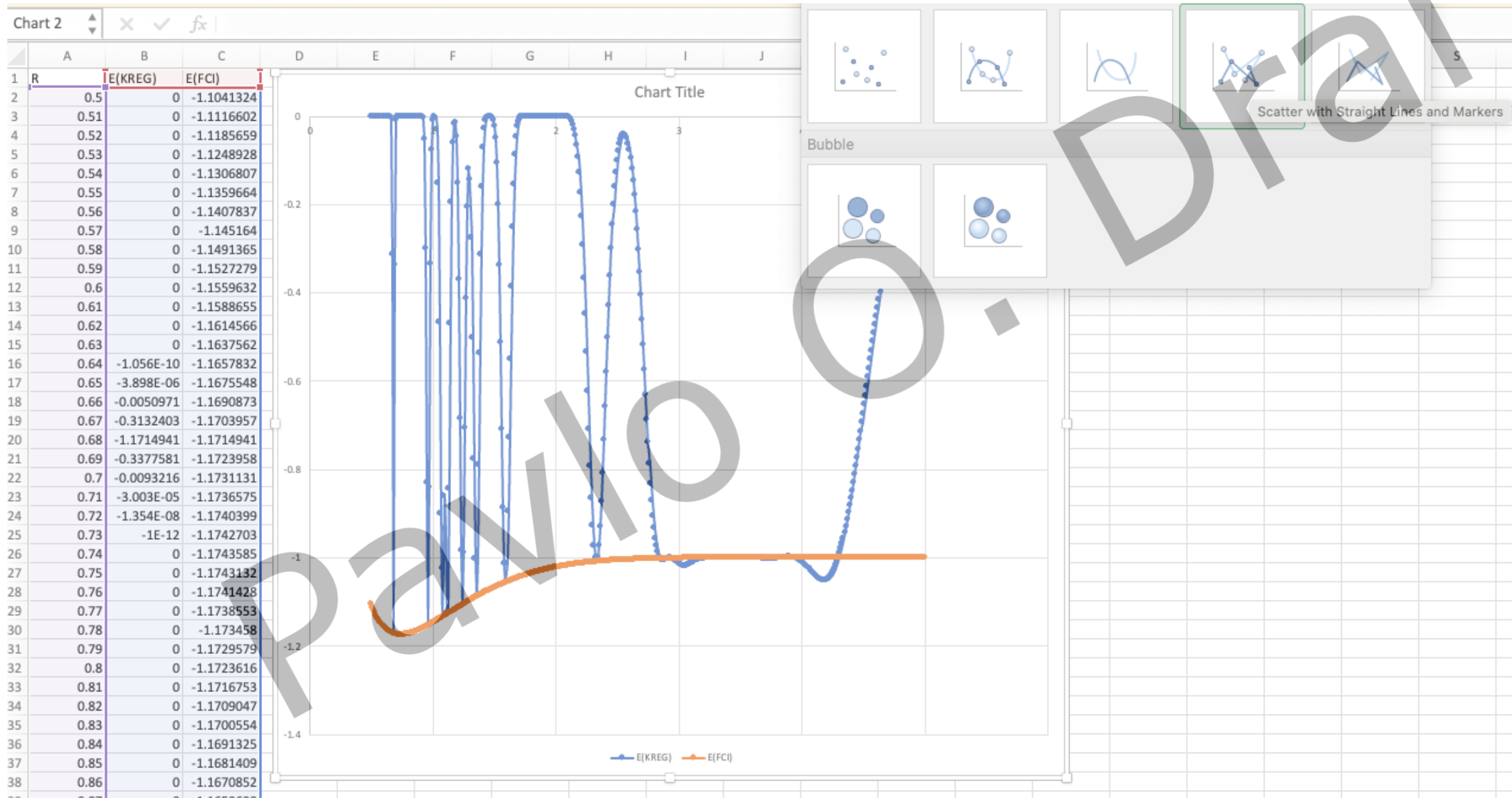
Input file for training KREG model:

```
createMLmodel      # Specify the task for MLatom
MLmodelType=KREG   # Specify the model type
MLmodelOut=kreg.unf # Save model in kreg.unf
XYZfile=h2.xyz     # File with XYZ geometries
Yfile=E_FCI_451.dat # The file with FCI energies
Ntrain=50
sigma=0.01
lambda=0.0
```

Input file for predicting energies with the ML model:

```
useMLmodel      # Specify the task for MLatom
MLmodelType=KREG # Specify the model type
MLmodelIn=kreg.unf # Save model in kreg.unf
XYZfile=h2.xyz   # File with XYZ geometries
YestFile=E_FCI_451_kreg_est.dat # The file with FCI energies
```

The predicted energies will be saved in `E_FCI_451_kreg_est.dat`. You can plot them in Excel as a function of the interatomic distance provided in the file [R_451.dat](#) and compare to the reference energies with full CI in the file [E_FCI_451.dat](#).



Everyone will get different results due to random sampling!

- Need to repeat many times to collect enough statistics
- For small data – use cross validation
- (You can fix splitting in special cases like debugging)

Pavlo

Dr. Dral

- Often ML error for its own training set is close to zero
- We should estimate errors on a **completely independent test set**



Example PES3.

Estimate the accuracy of the KREG model for the H₂ molecule for the test set.

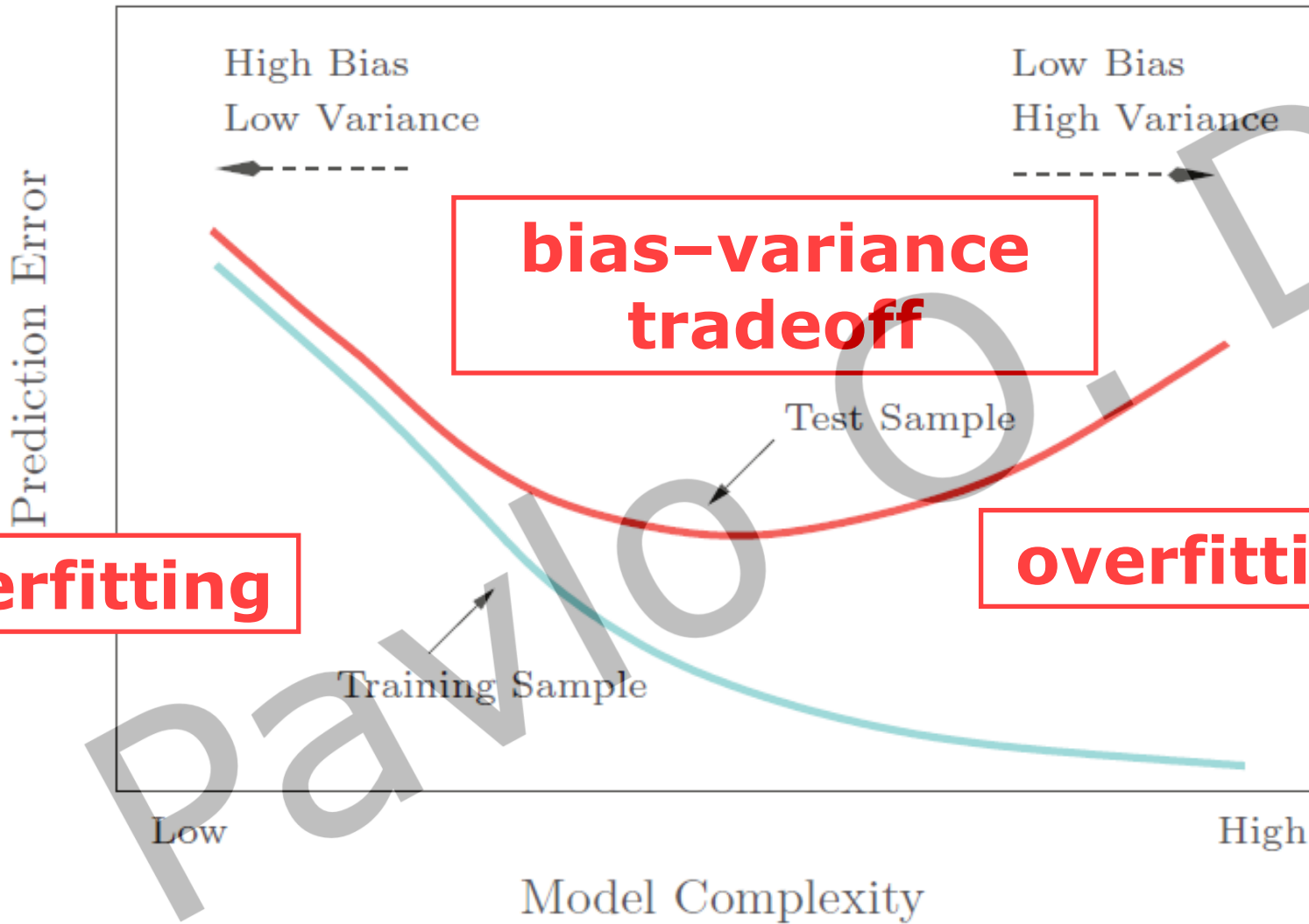
Questions:

1. What is the test error (RMSE) of the model?
2. How does it compare to the training error?
3. Does the model test error reflect its performance for the potential energy curve in [previous task](#)?

Input file:

```
estAccMLmodel           # Specify the task for MLatom
MLmodelType=KREG        # Specify the model type
XYZfile=h2.xyz          # File with XYZ geometries
Yfile=E_FCI_451.dat     # The file with FCI energies
Ntrain=50
sigma=0.01
lambda=0.0
```

Use the auxiliary files from the [previous tasks](#).



Choosing ML model settings to make it work

Pavlo O. Dral

$$f(\mathbf{x}_i) = \sum_{j=1}^{N_{tr}} \alpha_j k(\mathbf{x}_i, \mathbf{x}_j)$$

$$k(\mathbf{x}_i, \mathbf{x}_j) = \exp\left(-\frac{1}{2\sigma^2} \sum_s^{N_x} (x_{i,s} - x_{j,s})^2\right)$$

the Gaussian kernel function
(σ is the kernel width)

$$\mathbf{x} = \left(\dots \frac{R^{eq}}{R} \dots\right)^T$$

RE descriptor

Pavlo O. Dral

$$f(\mathbf{x}_i) = \sum_{j=1}^{N_{tr}} \alpha_j k(\mathbf{x}_i, \mathbf{x}_j)$$

$$k(\mathbf{x}_i, \mathbf{x}_j) = \exp\left(-\frac{1}{2\sigma^2} \sum_s^{N_x} (x_{i,s} - x_{j,s})^2\right)$$

the Gaussian kernel function
(σ is the kernel width)

$$\mathbf{x} = \left(\dots \frac{Req}{R} \dots\right)^T$$

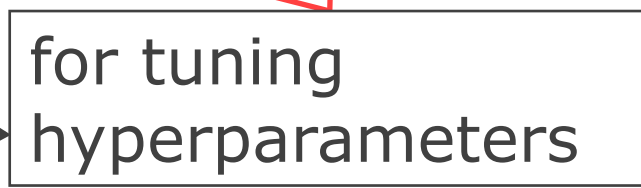
RE descriptor

Analytical solution for the regression coefficients α given N_{tr} training points

$$\begin{pmatrix} k(\mathbf{x}_1, \mathbf{x}_1) + \lambda & \dots & k(\mathbf{x}_1, \mathbf{x}_{N_{tr}}) \\ \vdots & \ddots & \vdots \\ k(\mathbf{x}_{N_{tr}}, \mathbf{x}_1) & \dots & k(\mathbf{x}_{N_{tr}}, \mathbf{x}_{N_{tr}}) + \lambda \end{pmatrix} \begin{pmatrix} \alpha_1 \\ \vdots \\ \alpha_{N_{tr}} \end{pmatrix} = \begin{pmatrix} y_1 \\ \vdots \\ y_{N_{tr}} \end{pmatrix}$$

λ is the regularization parameter ensuring transferability

$$(\mathbf{K} + \lambda \mathbf{I})\alpha = \mathbf{y}$$



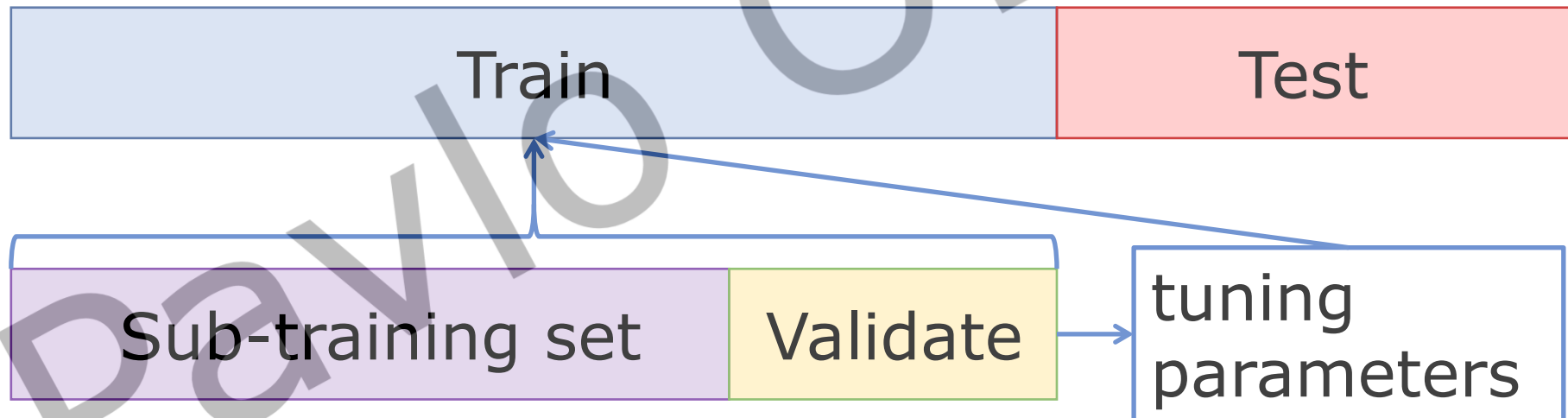
The **KREG** model (**K**ernel ridge regression [KRR] with **RE** descriptor and the **G**aussian kernel function; RE descriptor stands for Internuclear distances **Relative to Equilibrium**) to complete all the ML tasks.

Choosing ML model settings to make it work

How to choose hyperparameters?

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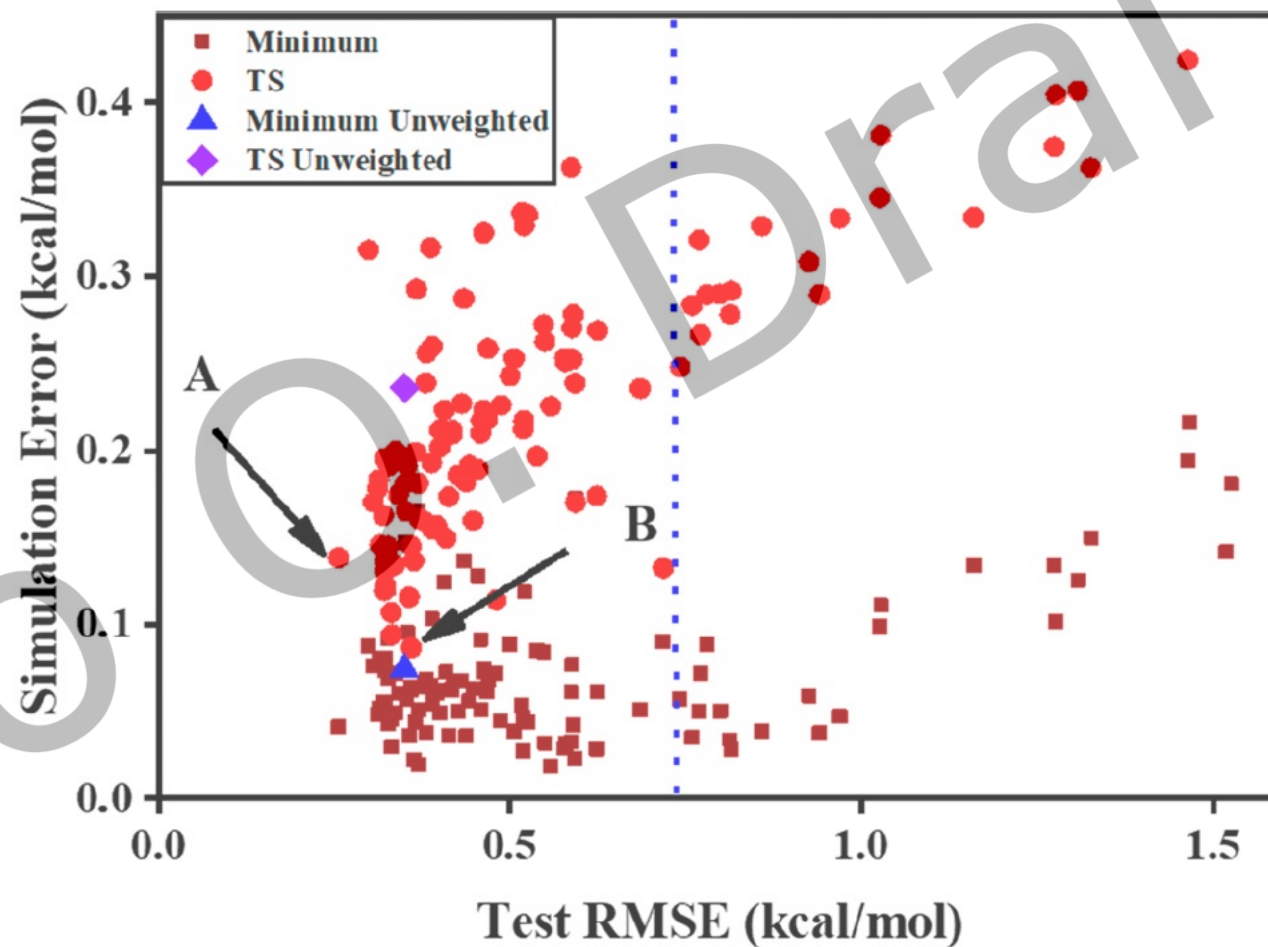
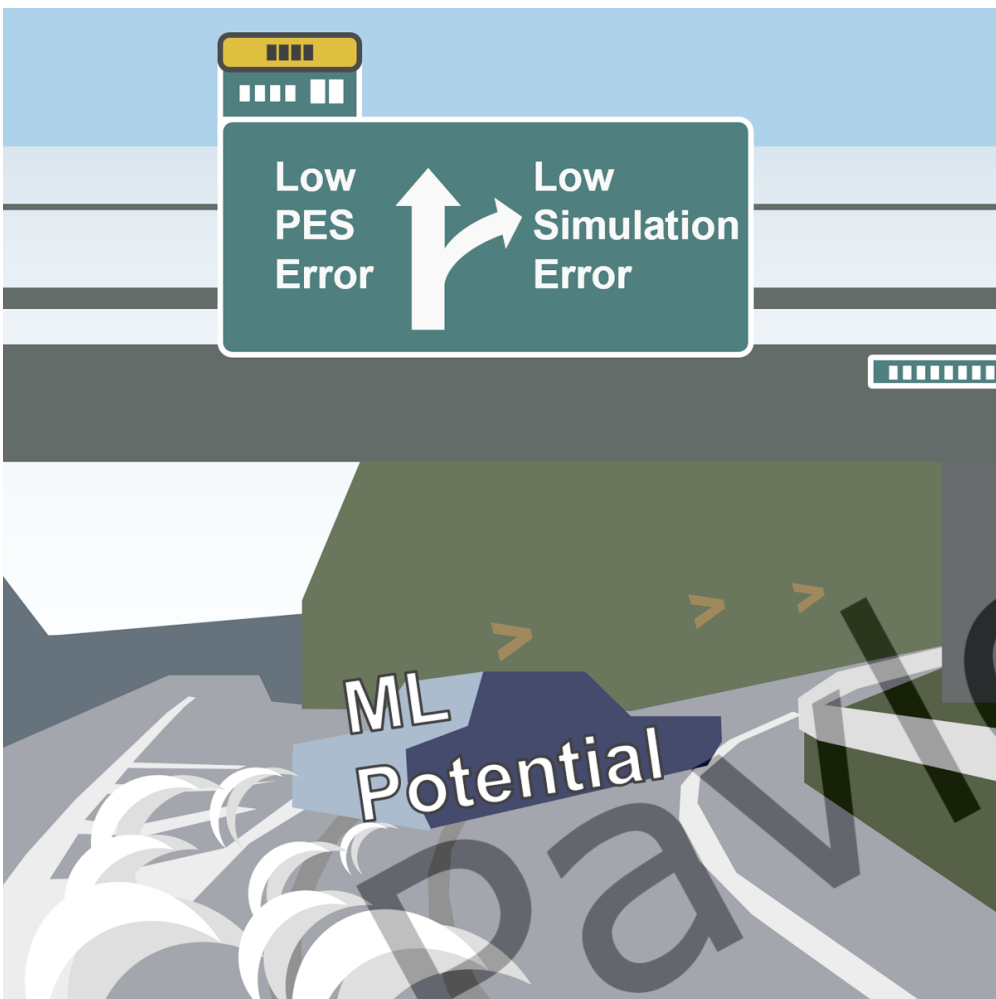
- Often ML error for its own training set is close to zero
- Using errors in the validation set would be also incorrect, because their minimization is a part of the training process
- We should estimate errors on a **completely independent test set**

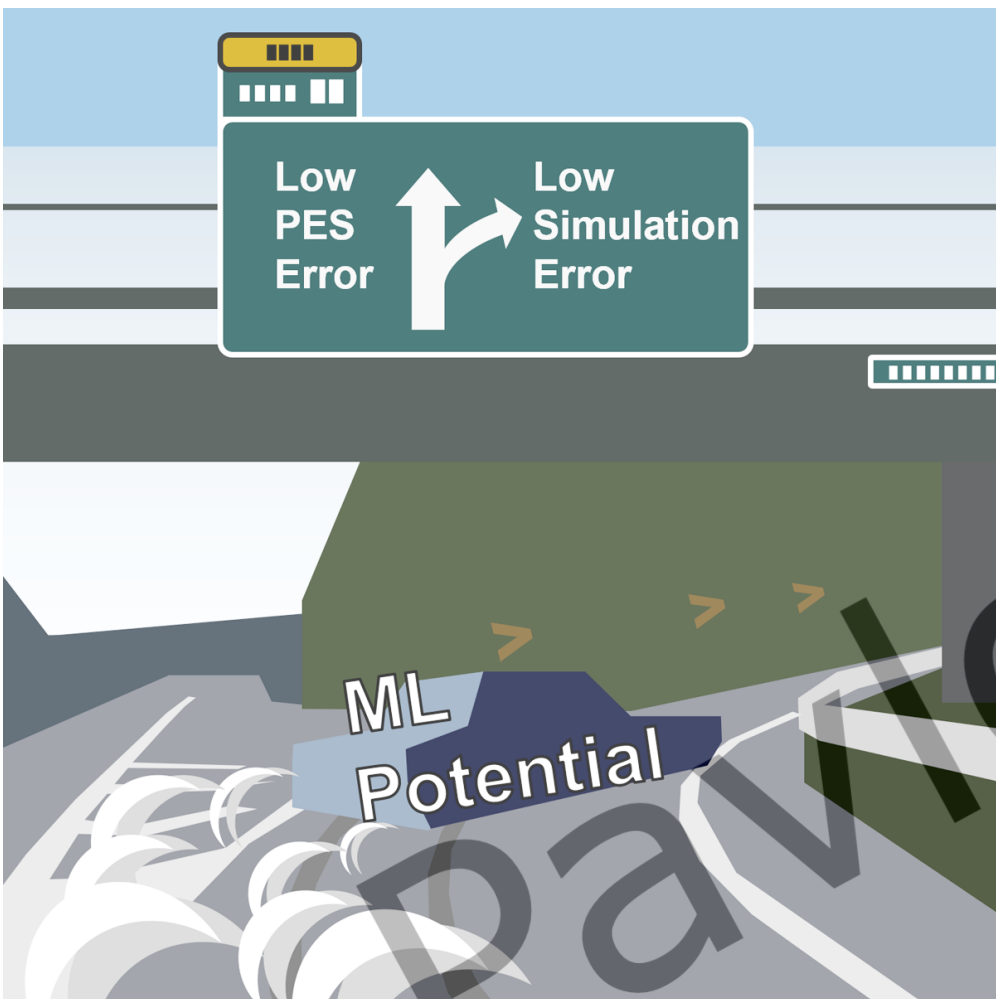


The ultimate test is the performance in the required application!

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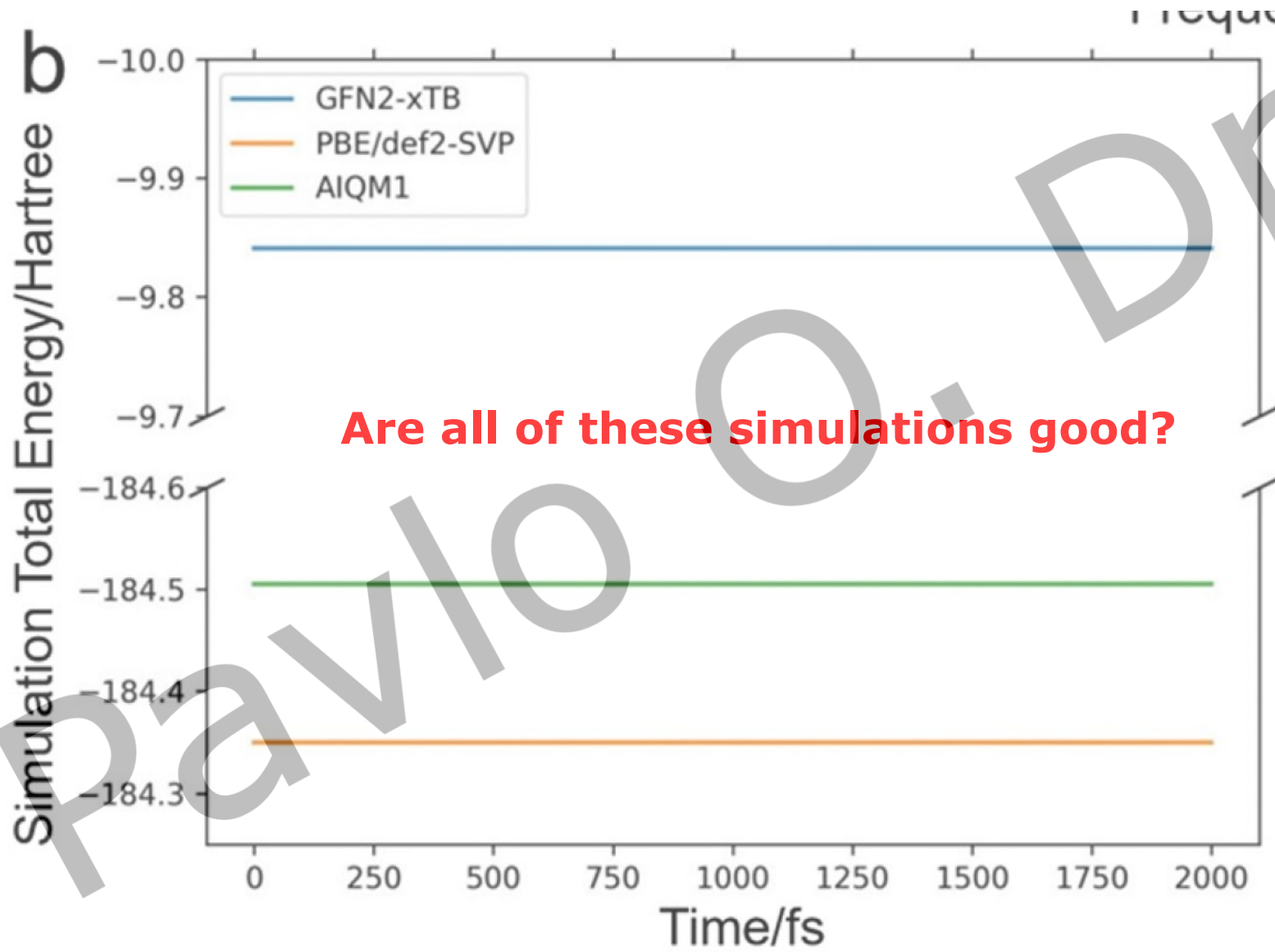
Quality of simulation \neq quality of fit

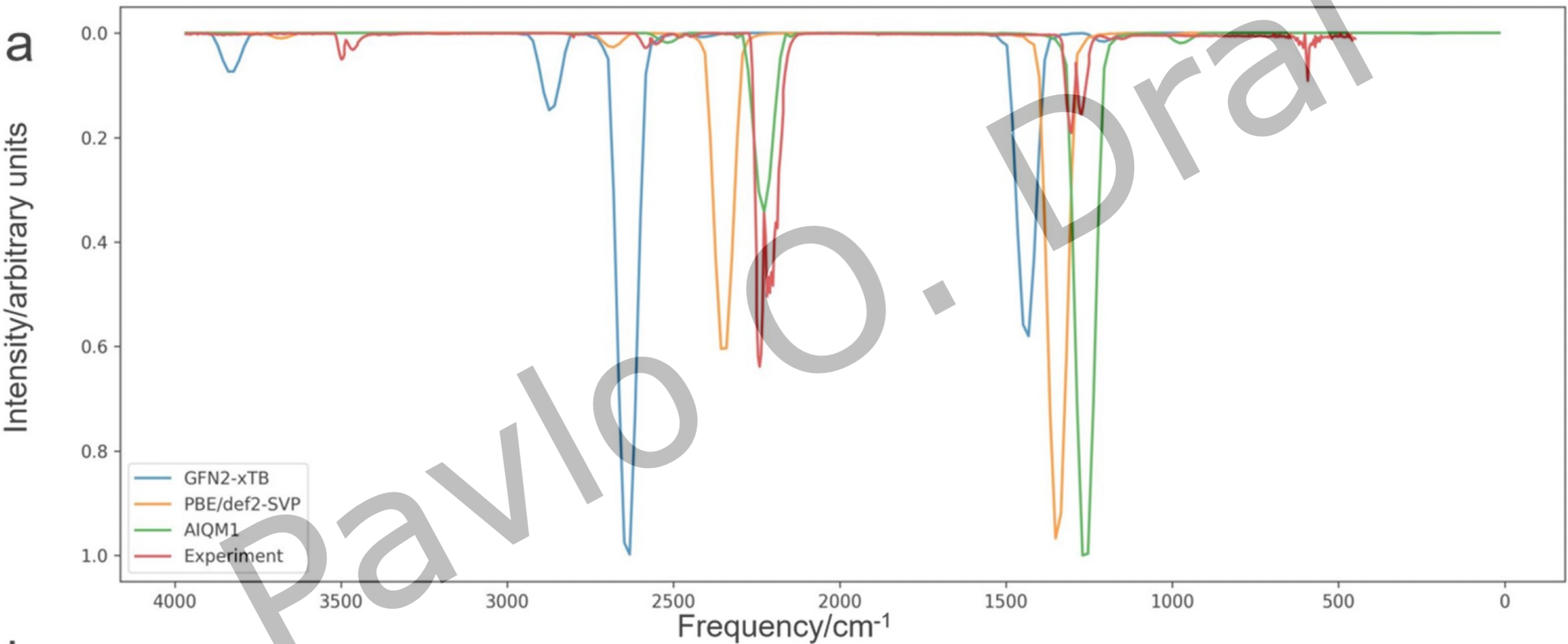




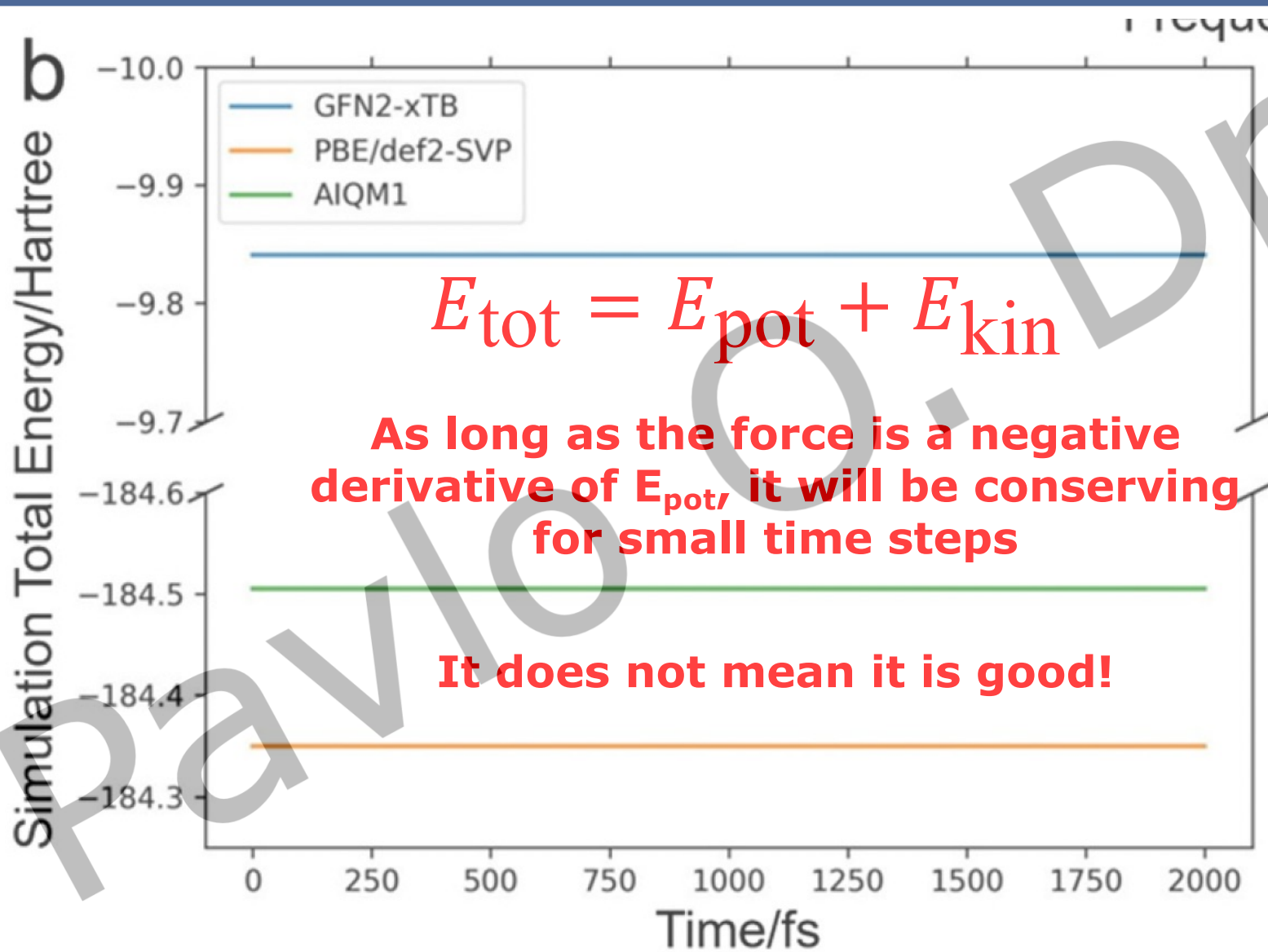
"One [diffusion Monte Carlo] simulation for a single conformer requires 30000 walkers and 55000 steps comprising roughly **$1.6 \cdot 10^9$** potential evaluations with B3LYP."

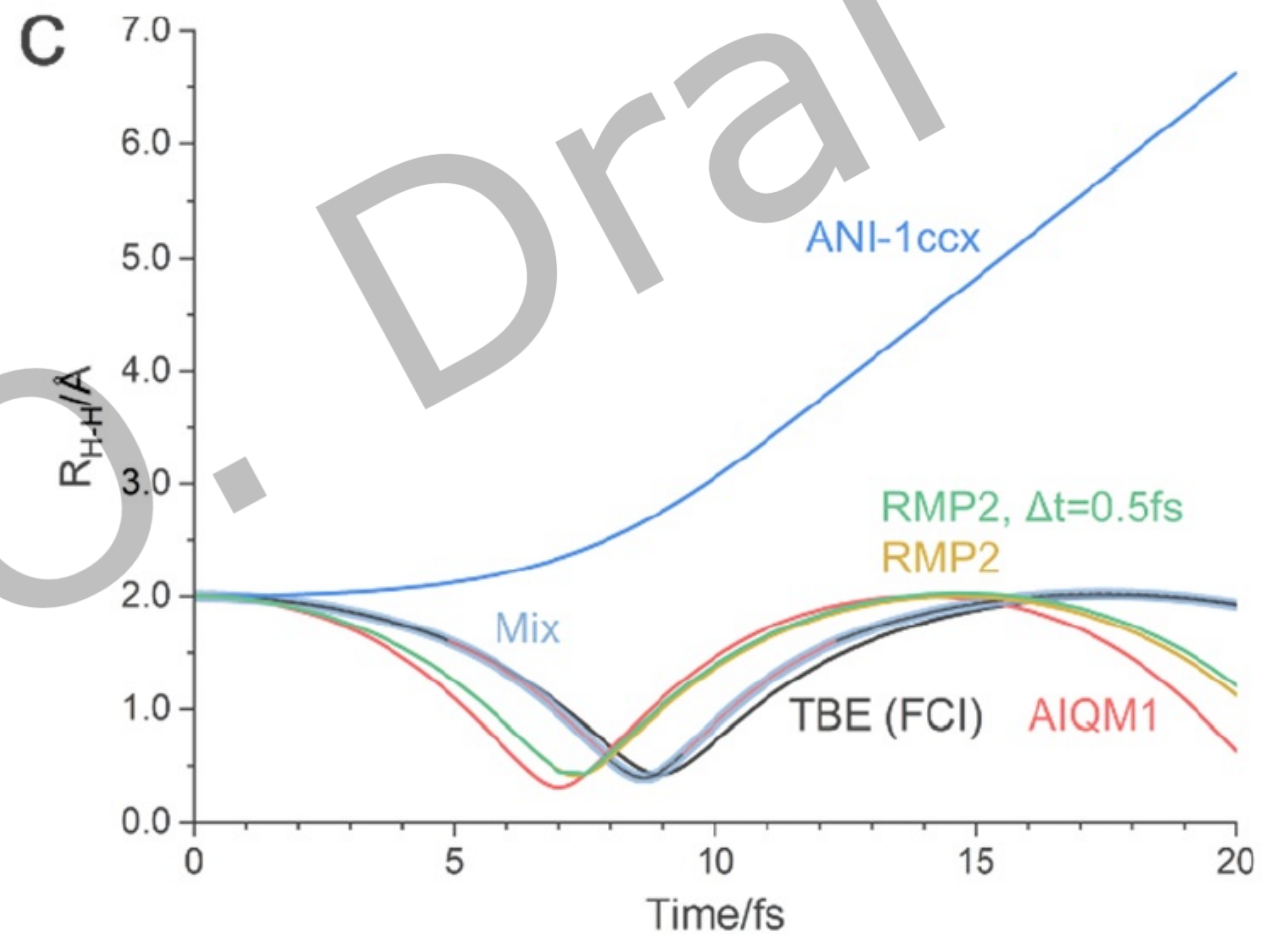
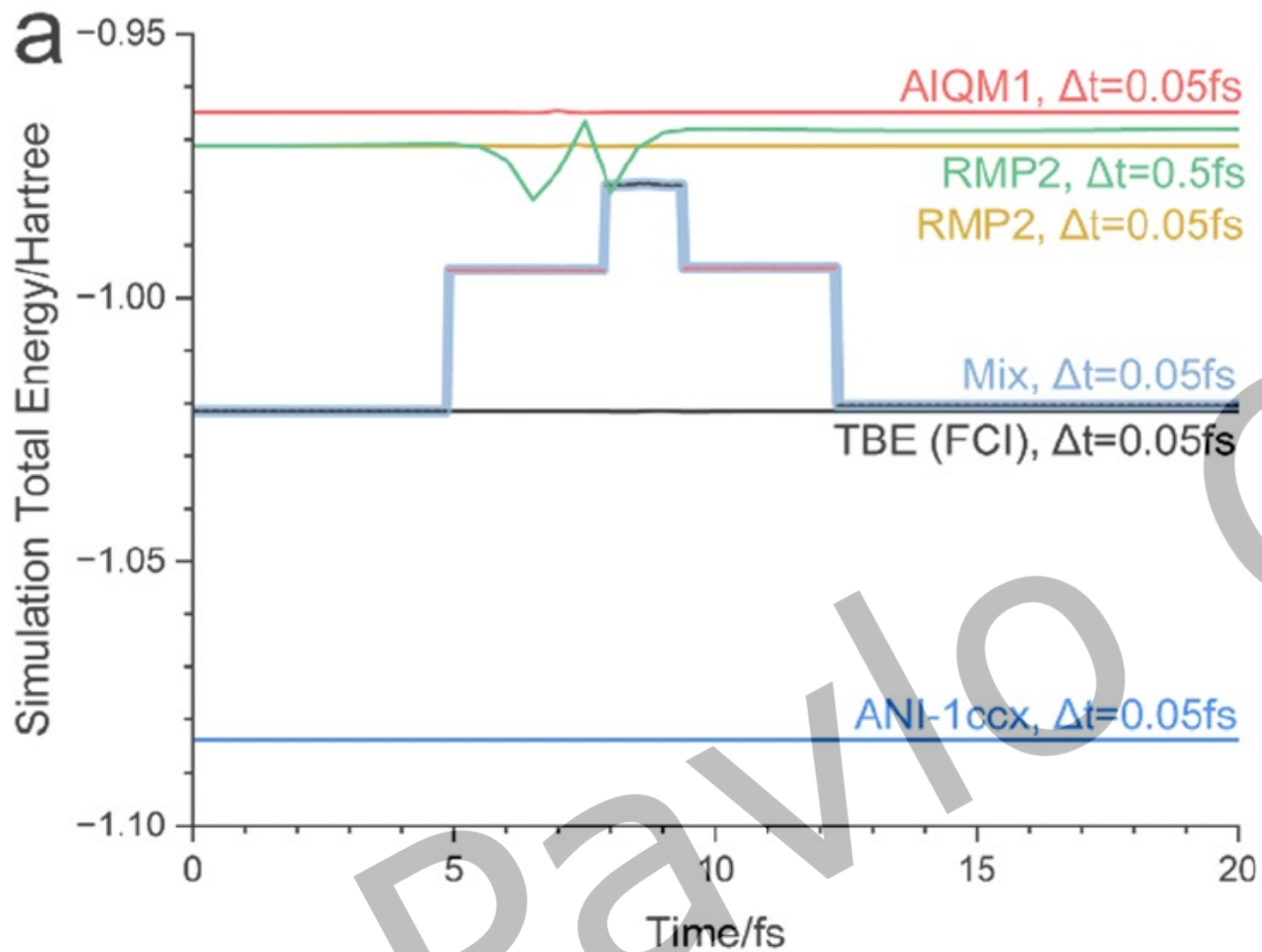
→ 60 hours on a single GPU with ANI...

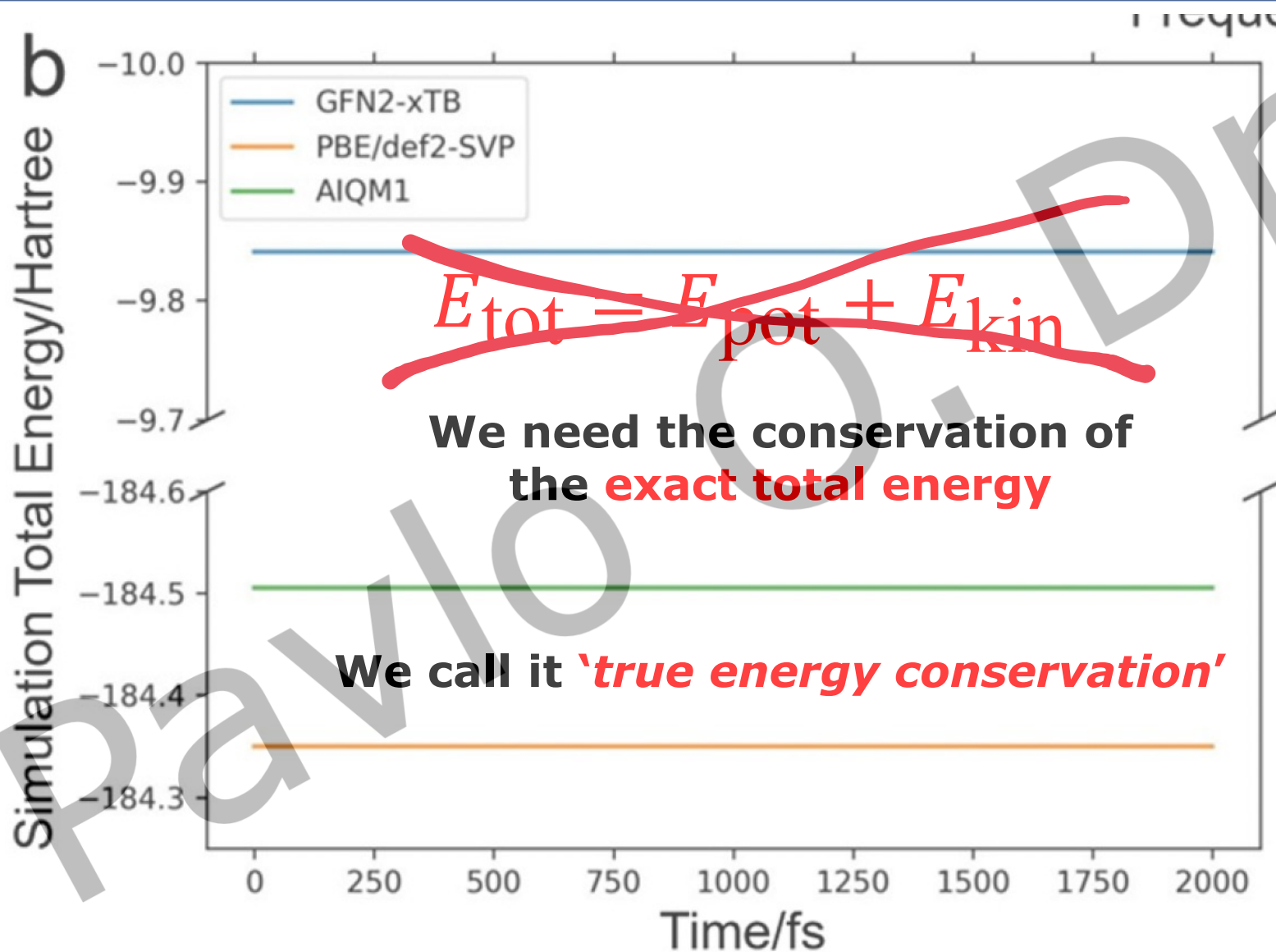


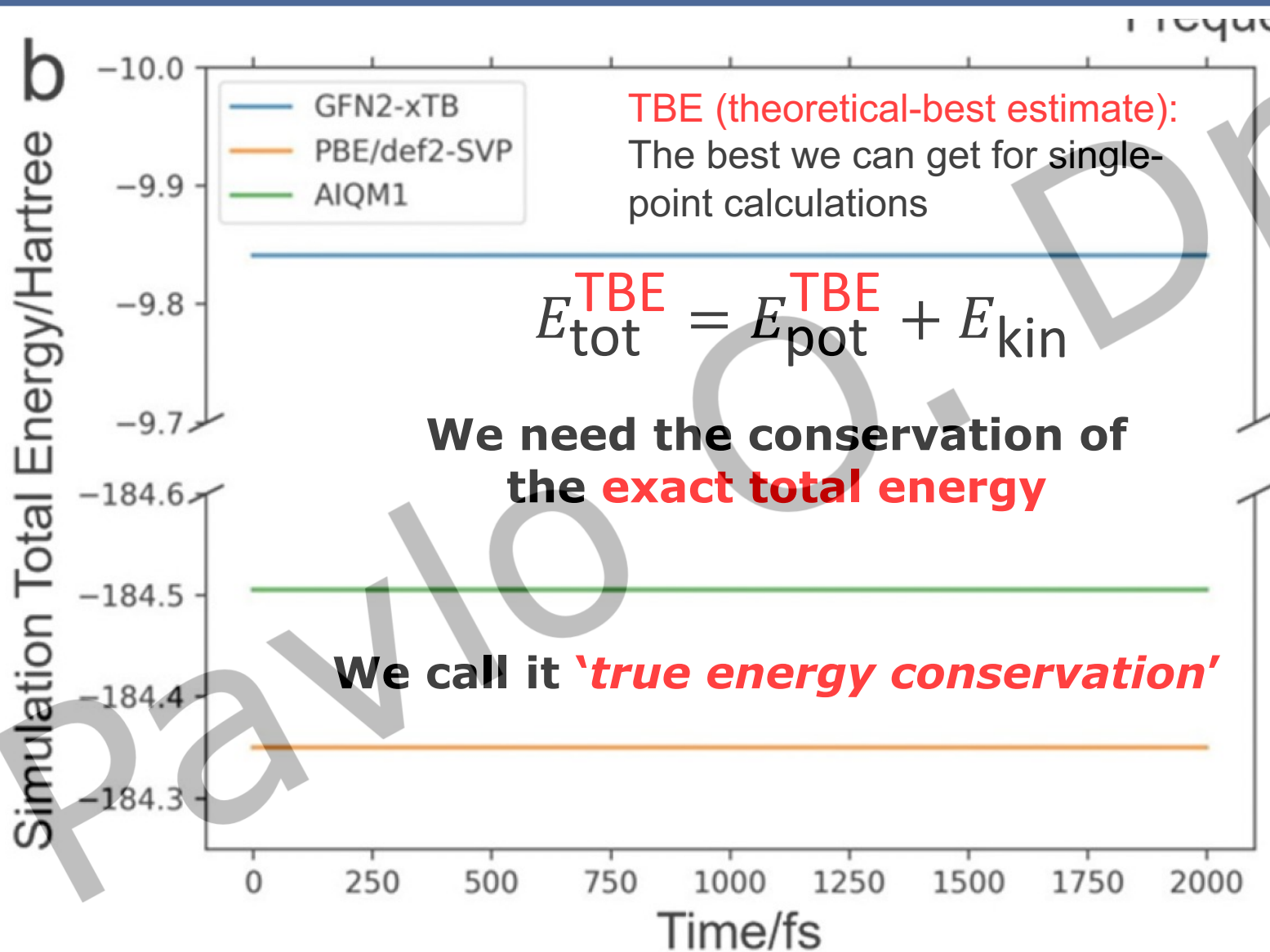


Why are they so different in accuracy?





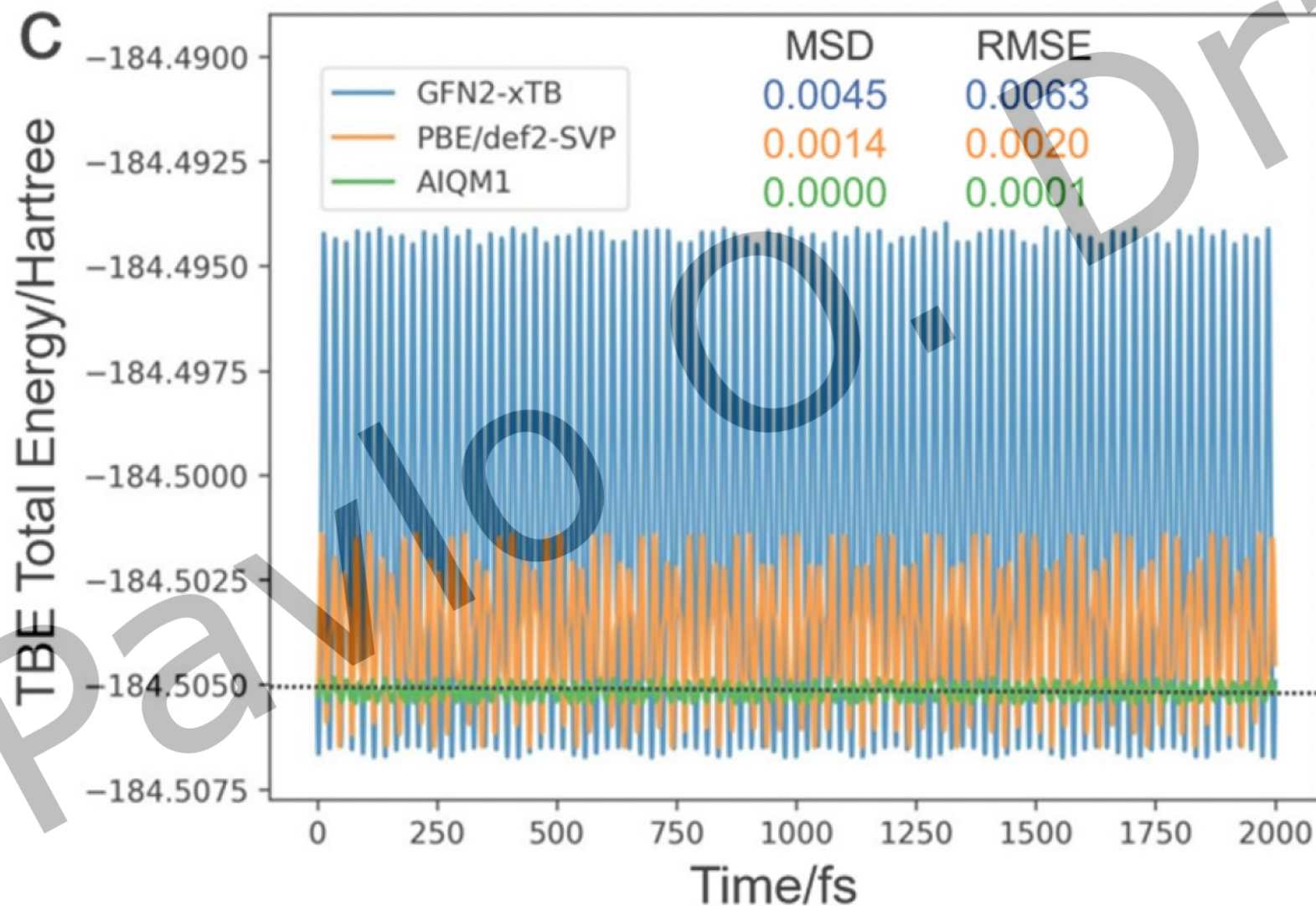


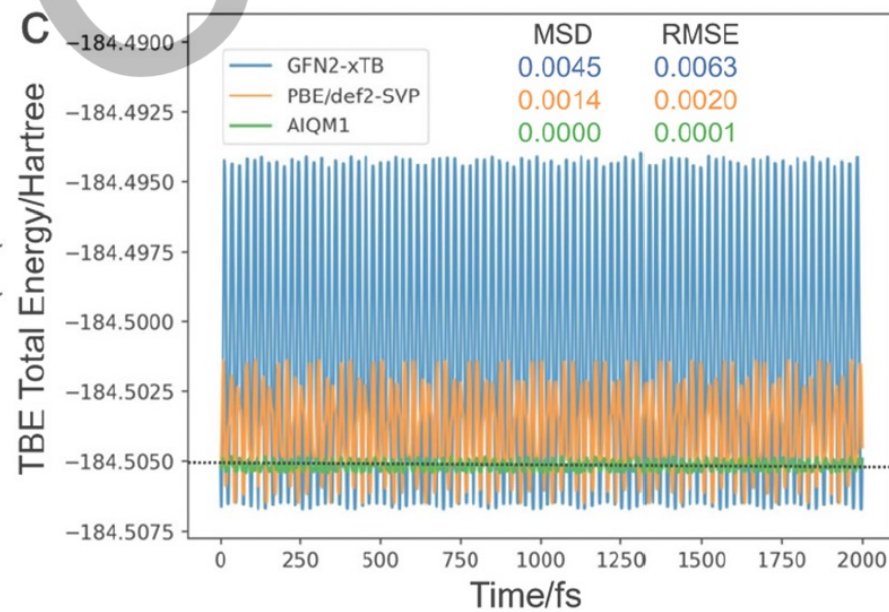
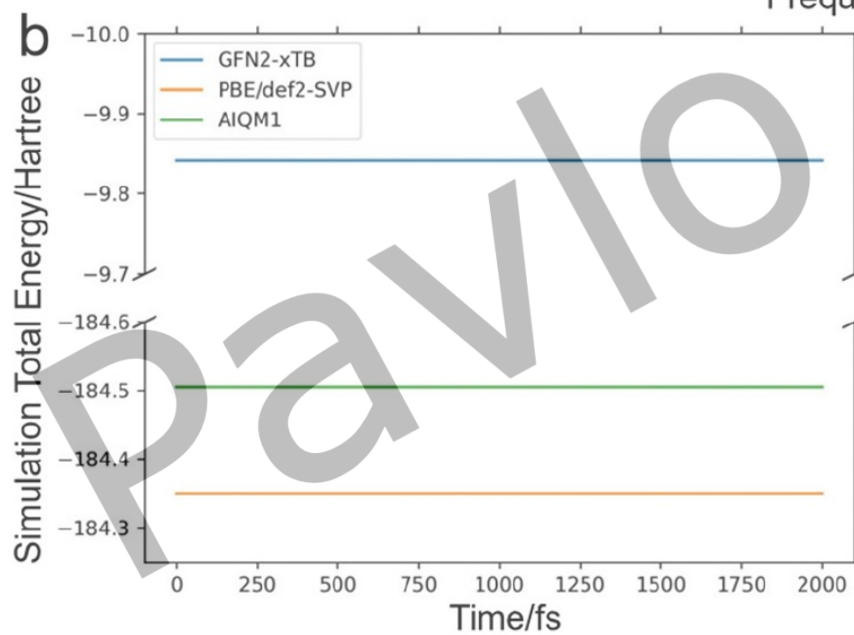
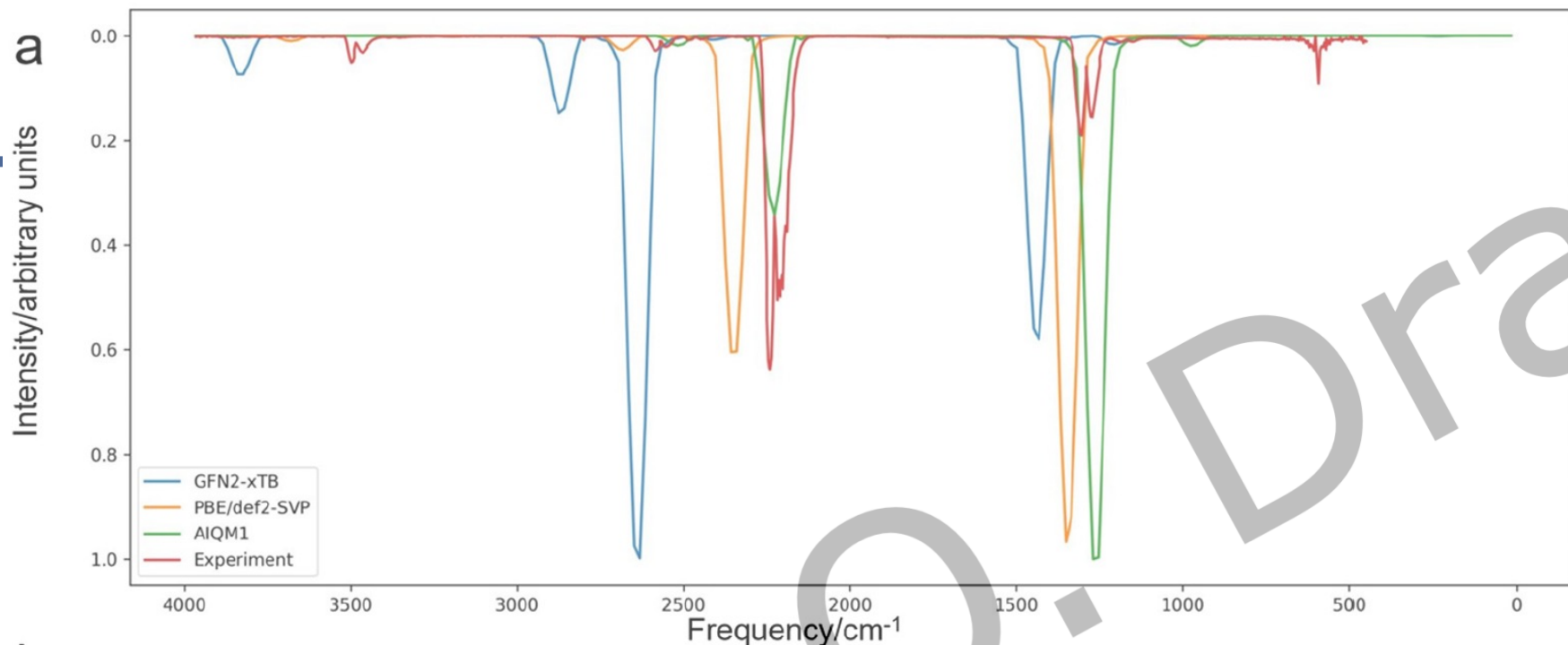


$$\text{RMSE} = \sqrt{1/\text{number of time steps} \sum \left(E_{\text{tot}}^{\text{TBE}}(\text{time step}) - E_{\text{tot}}^{\text{TBE}}(\text{time zero}) \right)^2}$$

$$\text{MSD} = 1/\text{number of time steps} \sum \left(E_{\text{tot}}^{\text{TBE}}(\text{time step}) - E_{\text{tot}}^{\text{TBE}}(\text{time zero}) \right)$$

TBE: CCSD(T)*/CBS





Example PES4.

Estimate the accuracy of the KREG model for the H₂ molecule for the test set.

Questions:

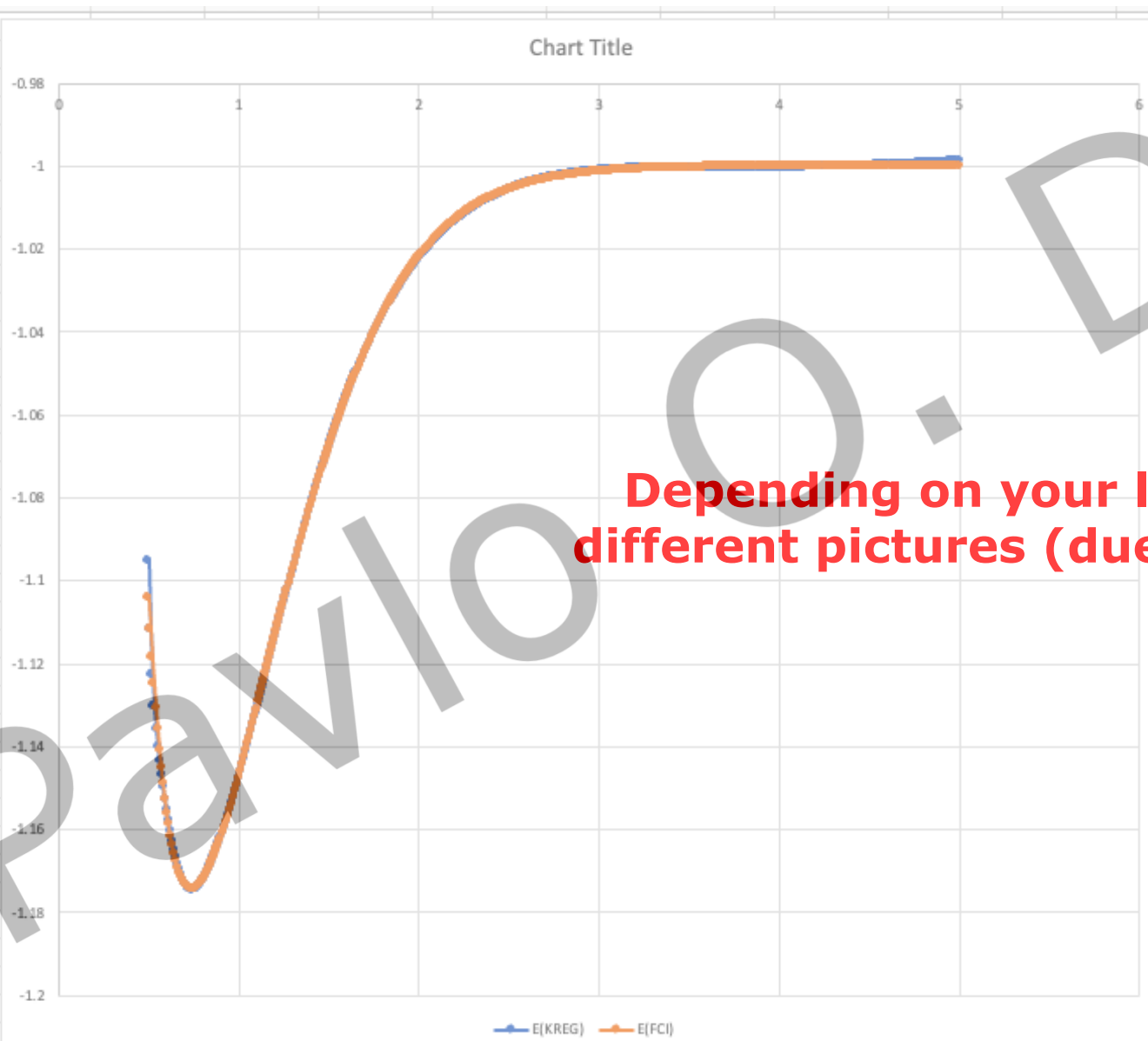
1. What are the training, validation, and test errors (RMSE) of the model?
2. How does the potential energy curve now looks like? (Adapt input file from the [previous task](#))

Input file:

```
estAccMLmodel           # Specify the task for MLatom
MLmodelType=KREG        # Specify the model type
MLmodelOut=kreg_opt.unf # Save model in kreg_opt.unf
XYZfile=h2.xyz          # File with XYZ geometries
Yfile=E_FCI_451.dat     # The file with FCI energies
Ntrain=50
sigma=opt
lgSigmaL=-4            # Lower bound of log2(sigma)
lambda=opt
```

Use the auxiliary files from the [previous tasks](#).

R	E(KREG)	E(FCI)
0.5	-1.0952055	-1.1041324
0.51	-1.1116607	-1.1116602
0.52	-1.1226388	-1.1185659
0.53	-1.1302139	-1.1248928
0.54	-1.1357334	-1.1306807
0.55	-1.1400459	-1.1359664
0.56	-1.1436606	-1.1407837
0.57	-1.1468859	-1.145164
0.58	-1.1498826	-1.1491365
0.59	-1.1527206	-1.1527279
0.6	-1.1554383	-1.1559632
0.61	-1.1580248	-1.1588655
0.62	-1.1604676	-1.1614566
0.63	-1.1627427	-1.1637562
0.64	-1.1648372	-1.1657832
0.65	-1.1667376	-1.1675548
0.66	-1.1684246	-1.1690873
0.67	-1.1698978	-1.1703957
0.68	-1.1711619	-1.1714941
0.69	-1.1722143	-1.1723958
0.7	-1.1730593	-1.1731131
0.71	-1.1737061	-1.1736575
0.72	-1.1741656	-1.1740399
0.73	-1.1744488	-1.1742703
0.74	-1.1745676	-1.1743585
0.75	-1.1745317	-1.1743132
0.76	-1.1743587	-1.1741428
0.77	-1.1740494	-1.1738553
0.78	-1.1736193	-1.173458
0.79	-1.1730809	-1.1729579
0.8	-1.1724471	-1.1723616
0.81	-1.1717182	-1.1716753
0.82	-1.1708958	-1.1709047
0.83	-1.1700126	-1.1700554
0.84	-1.1690501	-1.1691325
0.85	-1.1680262	-1.1681409



Depending on your luck, you may obtain different pictures (due to random sampling)

Example PES5.

Check how the test error changes when you include energy gradients during the training of an MLP. Note also, how much time you need to train with and without energy gradients.

You might need to repeat calculations couple of times and might want to change the number of training points.

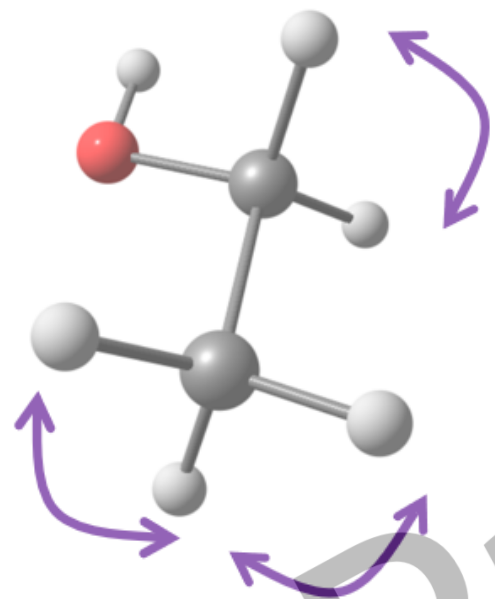
Input file:

```
estAccMLmodel           # Specify the task for MLatom
MLmodelType=KREG        # Specify the model type
MLmodelOut=kreg_grad.unf # Save model in kreg_opt.unf
XYZfile=H2.xyz          # file with geometries
Yfile=H2_HF.en          # file with energies
YgradXYZfile=H2_HF.grad # file with energy gradients
Ntrain=20
Nsubtrain=0.9           # request 90% of the training points to be used for validation
sigma=opt
lgSigmaL=-4             # Lower bound of log2(sigma)
lambda=opt
lgLambdaL=-8           # Lower bound of log2(lambda)
```

The [provided data](#) is generated at HF/STO-3G and you can download it as a zipped folder. It contains:

- [H2.xyz](#) - xyz coordinates
- [H2_HF.en](#) - energies at HF/STO-3G
- [H2_HF.grad](#) - energy gradients at HF/STO-3G

(p)KREG



Permutations

$$\begin{pmatrix} \mathbf{K} + \lambda_{\mathbf{v}} & \frac{\partial \mathbf{K}}{\partial \mathbf{M}} \\ \frac{\partial \mathbf{K}}{\partial \mathbf{M}} & \frac{\partial^2 \mathbf{K}}{\partial \mathbf{M}^2} + \lambda_{\text{gxyz}} \end{pmatrix} \boldsymbol{\alpha} = \begin{pmatrix} \mathbf{y} - \mathbf{y}_{\text{prior}} \\ \frac{\partial \mathbf{y}}{\partial \mathbf{M}} \end{pmatrix}$$

RE descriptor

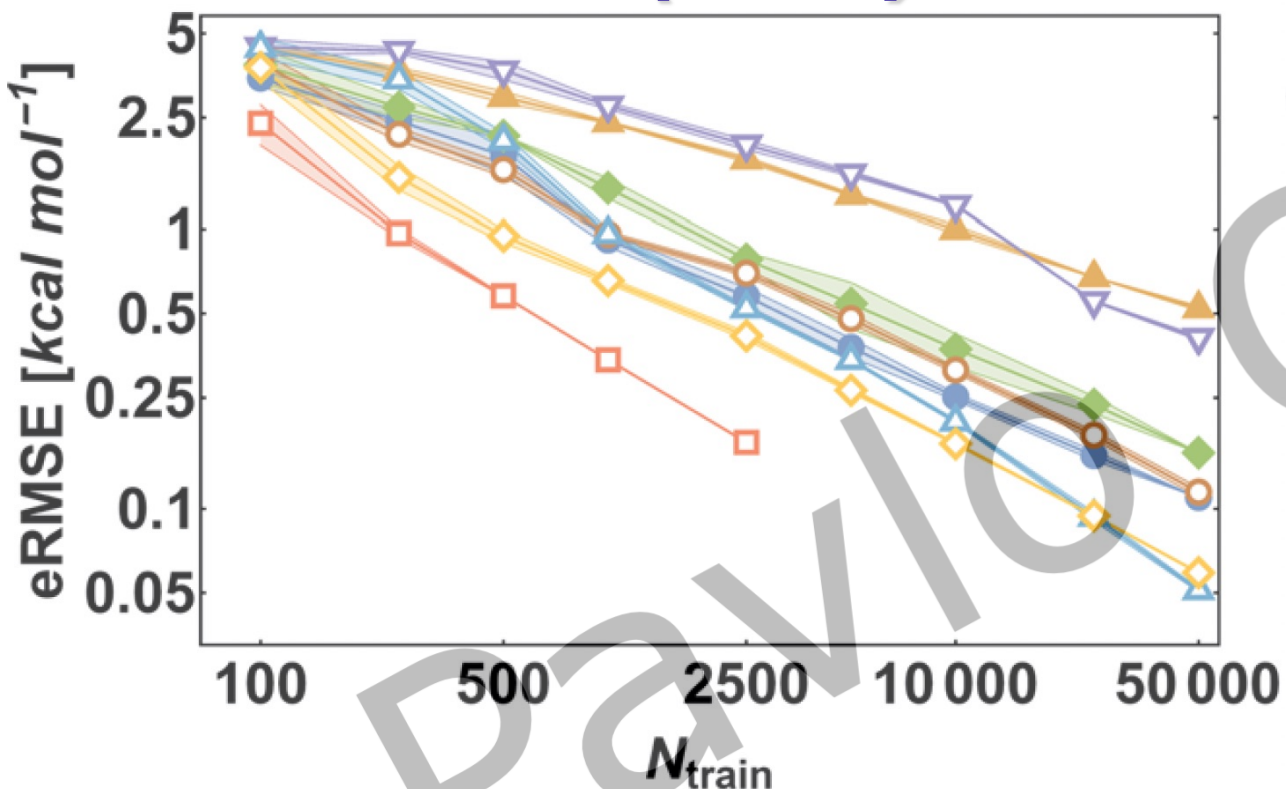
$$\mathbf{x}^T = [\dots r_{a,b \neq a}^{\text{ref}} / r_{a,b \neq a} \dots]$$

Gaussian kernel

$$k(\mathbf{x}_i, \mathbf{x}_j) = \exp\left(-\|\mathbf{x}_i - \mathbf{x}_j\|^2 / 2\sigma^2\right)$$

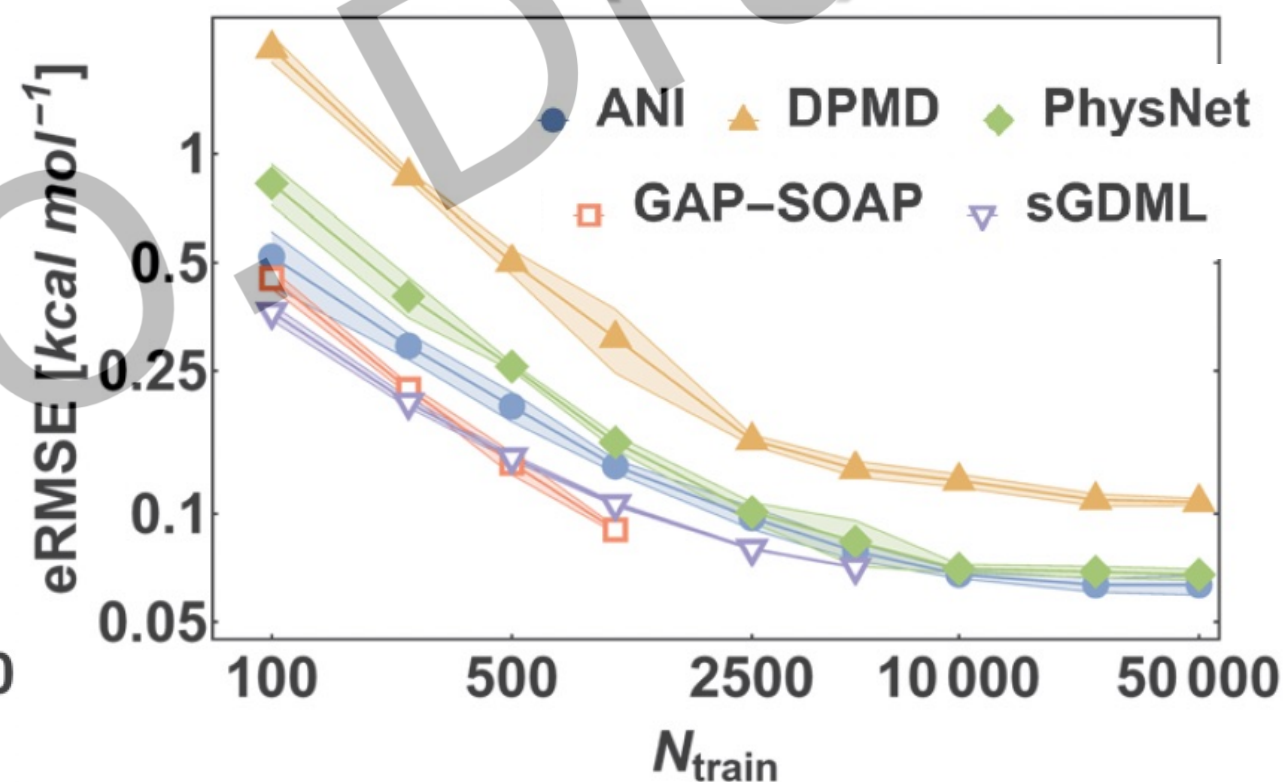
Energies-only

Ethanol (MD17)



Energies+gradients

Ethanol (MD17)



Example PES6.

Estimate the accuracy of the KREG model for the H₂ molecule for the test set by using the 9:1 splitting of the training set for hyperparameter optimization, i.e., using 10 of the training data for the validation set. To see how stability of the results change compared to 8:2 splitting, you can run this experiment several times and compare the test error and the potential energy curves.

Input file:

```
estAccMLmodel           # Specify the task for MLatom
MLmodelType=KREG        # Specify the model type
MLmodelOut=kreg_opt.unf # Save model in kreg_opt.unf
XYZfile=h2.xyz          # File with XYZ geometries
Yfile=E_FCI_451.dat     # The file with FCI energies
Ntrain=50
Nsubtrain=0.9           # request 90% of the training points to be used for validation
sigma=opt
lgSigmaL=-4            # Lower bound of log2(sigma)
lambda=opt
```

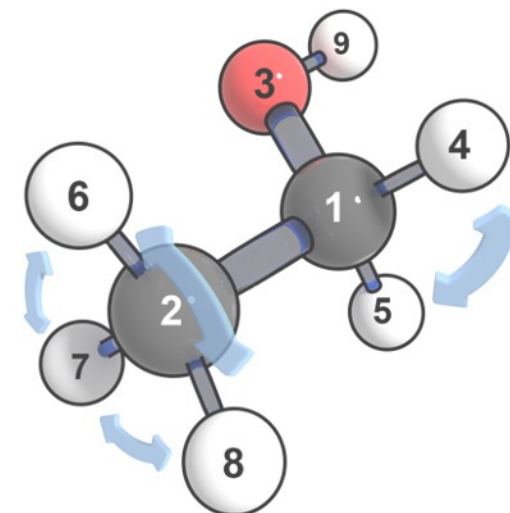
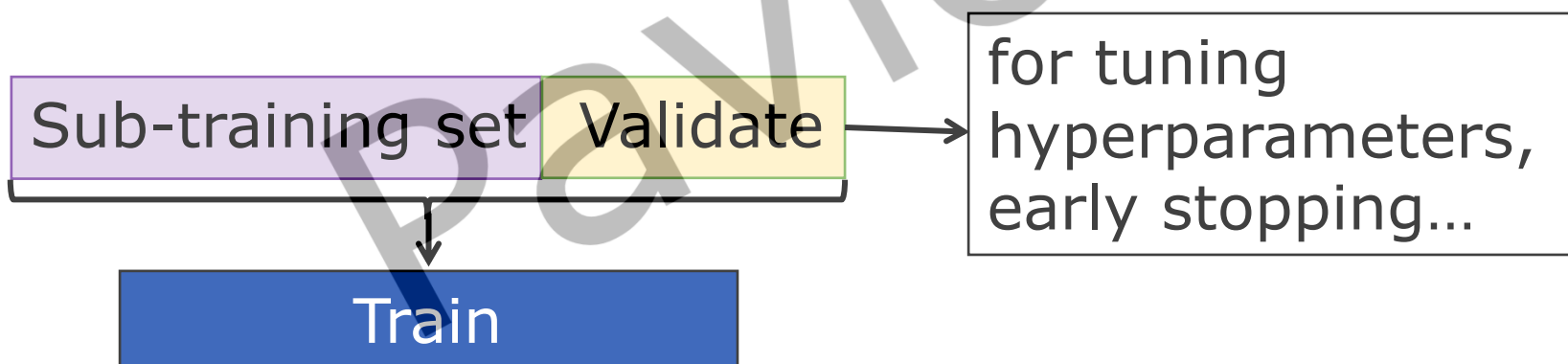
Use the auxiliary files from the [previous tasks](#).

KRR-CM – kernel ridge regression with Gaussian kernel and Coulomb matrix descriptor

Test set RMSEs in kcal/mol

Number of training points	KRR-CM	KREG
100	3.90±0.41	4.45±0.36
2500	0.70±0.02	0.52±0.01

What do we mean by '100 training points?' Is the validation set included?
Let's use the term '**sub-training set**'!



Investigate how the performance of the KREG model changes for different number of the training points. Modify the `Ntrain` parameter in the input file below. Particularly for smaller number of training points, there is a wide spread of results, so they should be repeated more times.

Input file:

```
estAccMLmodel      # Specify the task for MLatom
MLmodelType=KREG   # Specify the model type
MLmodelOut=kreg_opt.unf # Save model in kreg_opt.unf
XYZfile=h2.xyz     # File with XYZ geometries
Yfile=E_FCI_451.dat # The file with FCI energies
Ntrain=50
Nsubtrain=0.9      # request 90% of the training points to be used for validation
sigma=opt
lgSigmaL=-4        # Lower bound of log2(sigma)
lambda=opt
```

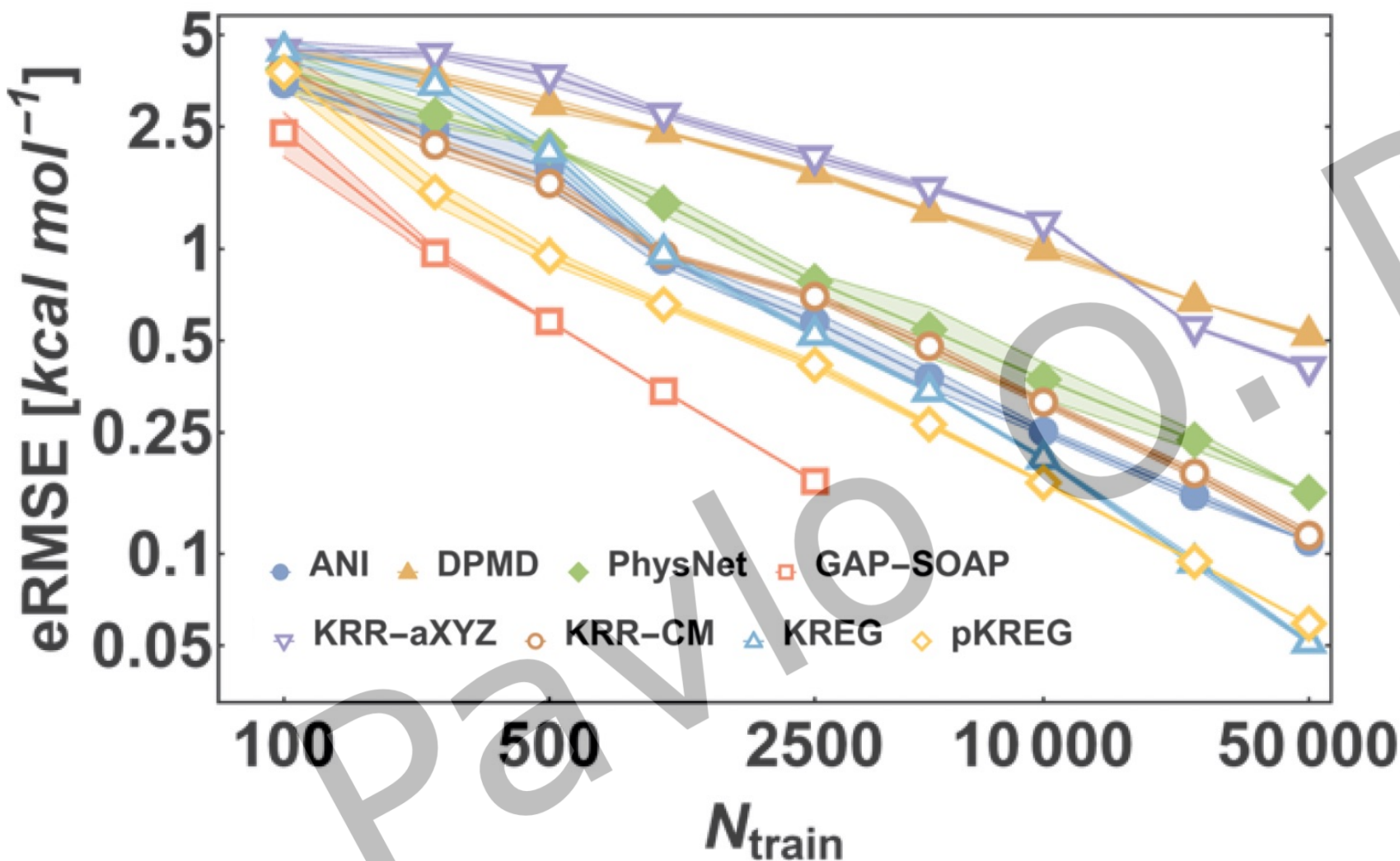
MLatom has an automatic way of generating the dependence of the test error on the size of the training set. The input file can look like:

```
learningCurve
lcNtrains=10,20,50,100,200,300
lcNrepeats=5,4,3,2,1,1
Ntest=100
MLmodelType=KREG      # Specify the model type
MLmodelOut=kreg_opt.unf # Save model in kreg_opt.unf
XYZfile=h2.xyz        # File with XYZ geometries
Yfile=E_FCI_451.dat   # The file with FCI energies
Nsubtrain=0.9
sigma=opt
lgSigmaL=-4          # Lower bound of log2(sigma)
lambda=opt
```

The results of these calculations will be saved in `learningCurve/mlatomf_KREG_en` folder, where the file `lcy.csv` collates the information which you can, e.g., plot in Excel.

Use the auxiliary files from the [previous tasks](#).

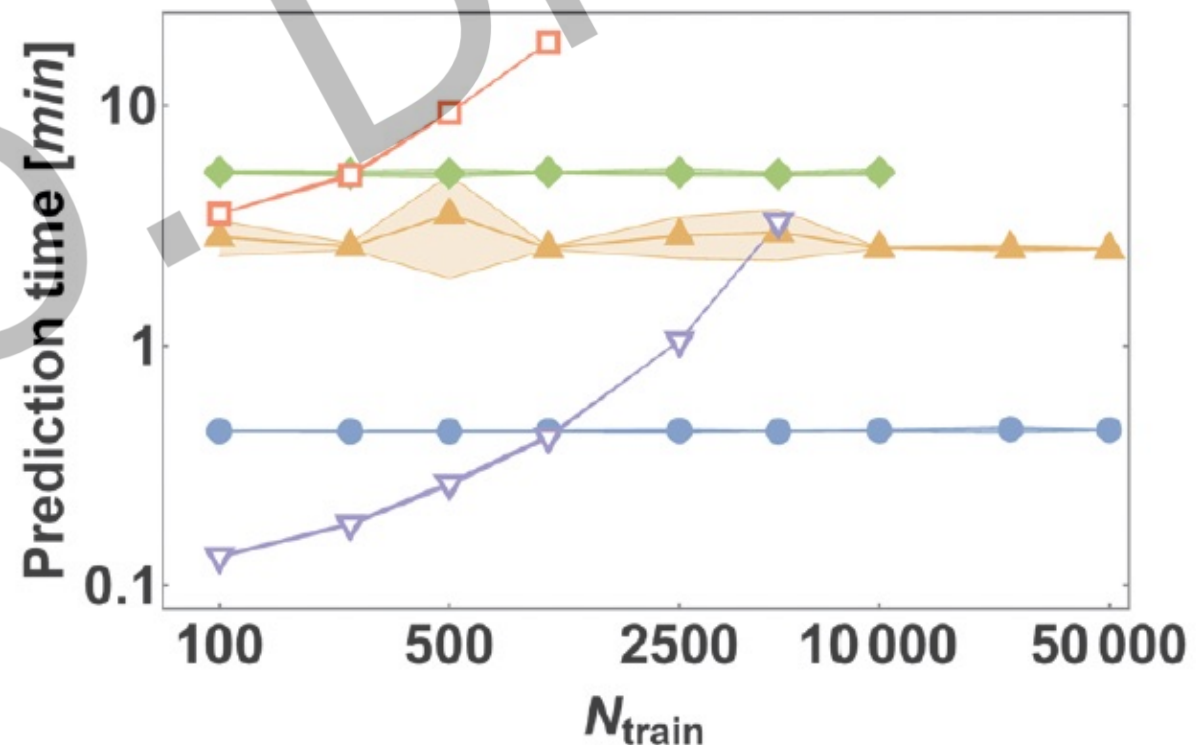
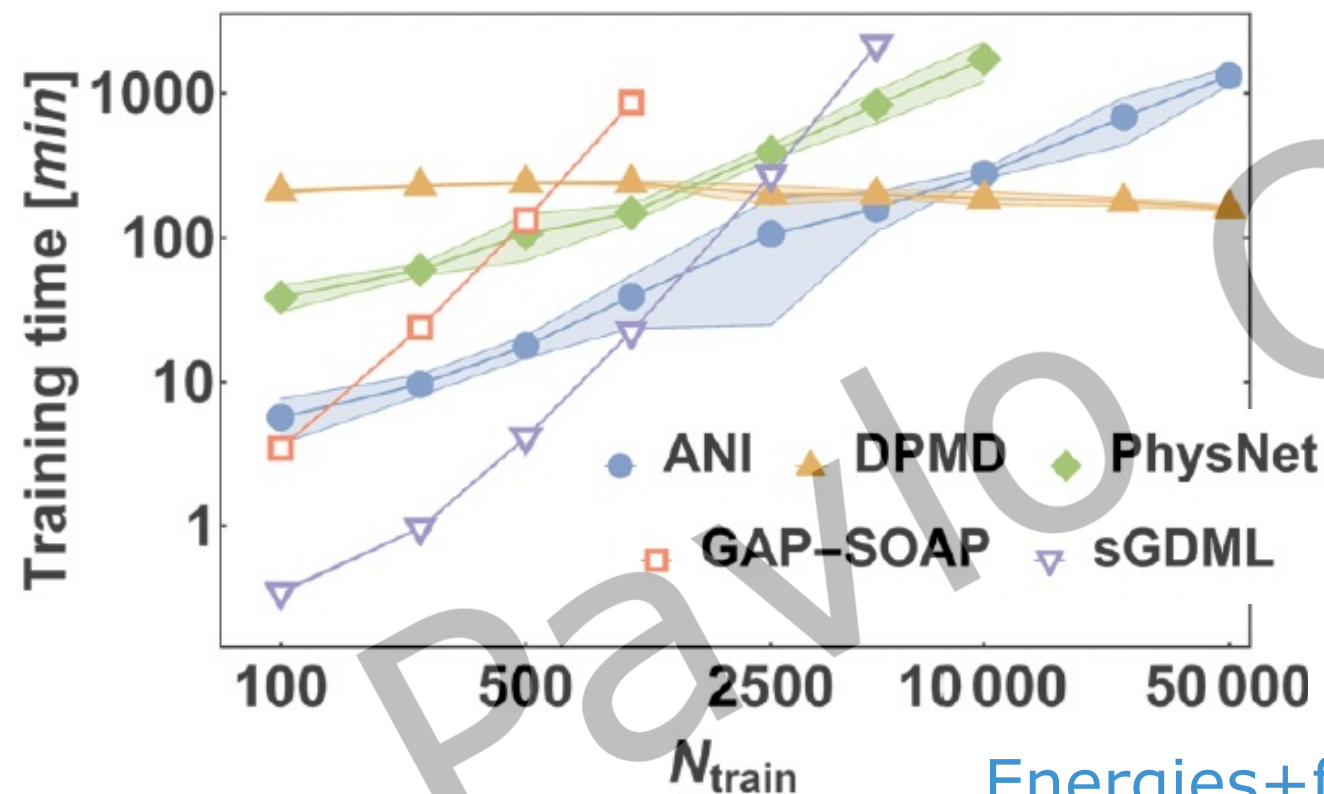
Learning curves (energies-only)



$$\varepsilon = \varepsilon_a + \frac{a}{N_{\text{tr}}^b}$$

$$\log(\varepsilon) \approx \log(a) - b \log N_{\text{tr}}$$

For small training sets kernel methods (open markers) are often both more accurate and faster for training and prediction than neural networks (filled markers)



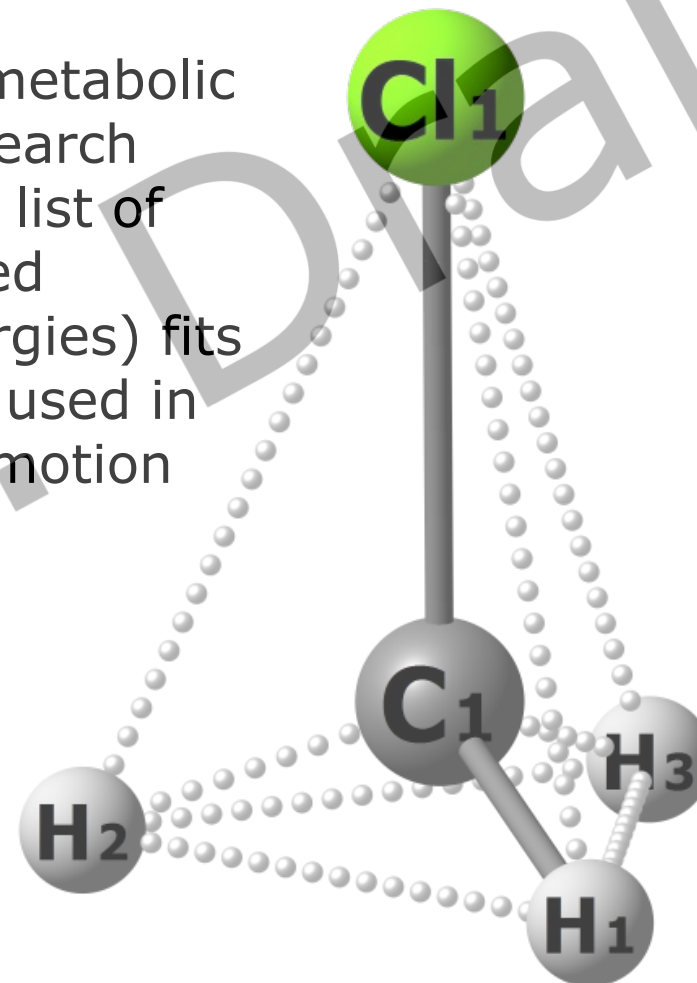
Energies+forces

The same hardware!

- Biomarker produced from a secondary metabolic process: useful for extraterrestrial life search
- Highly accurate and comprehensive line list of the rotation-vibration spectrum is needed
- **TROVE** (Theoretical ROVibrational Energies) fits analytic representation of PES, which is used in variational approach to solving nuclear motion problem

$$\left(\sum_{i=1}^N \frac{-\hbar^2}{2M_i} \nabla_i^2 + V \right) \Psi = E\Psi$$

Fundamental term values are reproduced by TROVE with RMSE of **0.75** cm⁻¹



A. Owens, S. N. Yurchenko, A. Yachmenev, J. Tennyson, W. Thiel, *J. Chem. Phys.* **2015**, *142*, 244306

TROVE: S. N. Yurchenko, W. Thiel, P. Jensen, *J. Mol. Spectrosc.* **2007**, *245*, 126

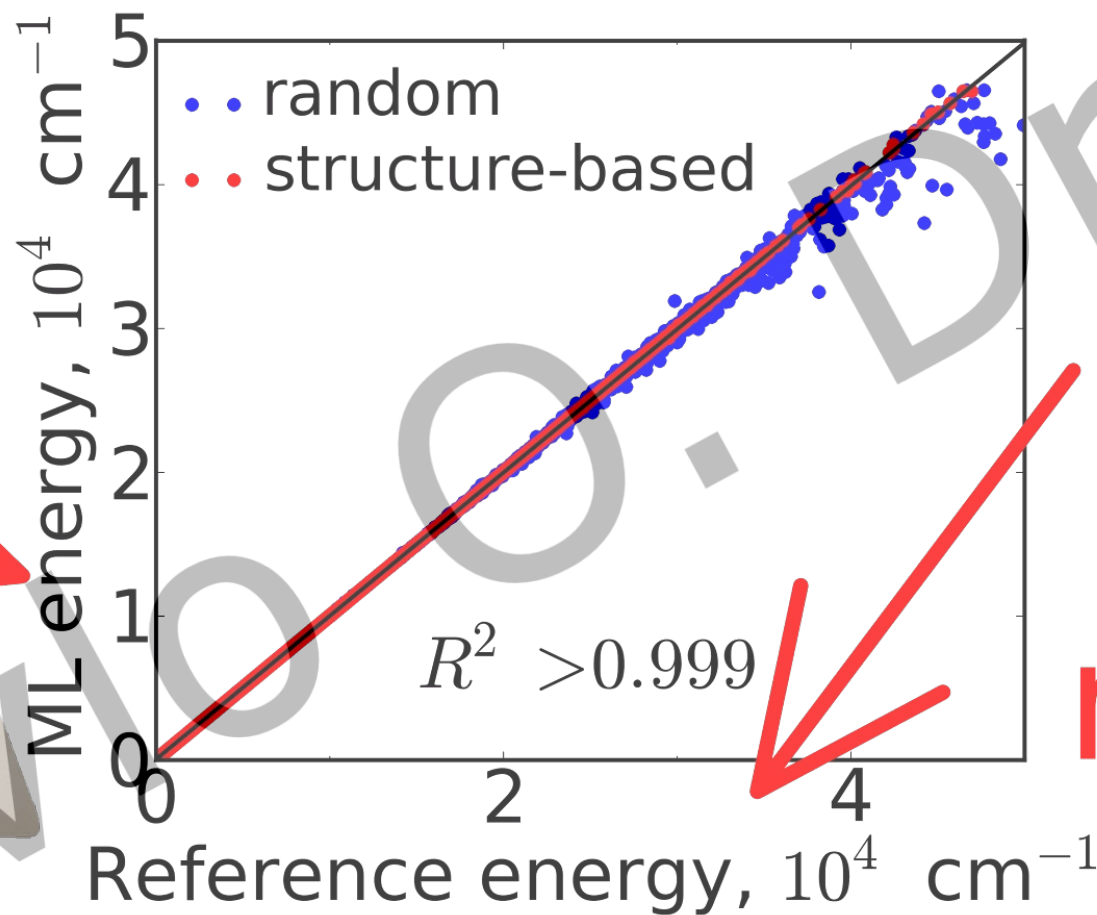
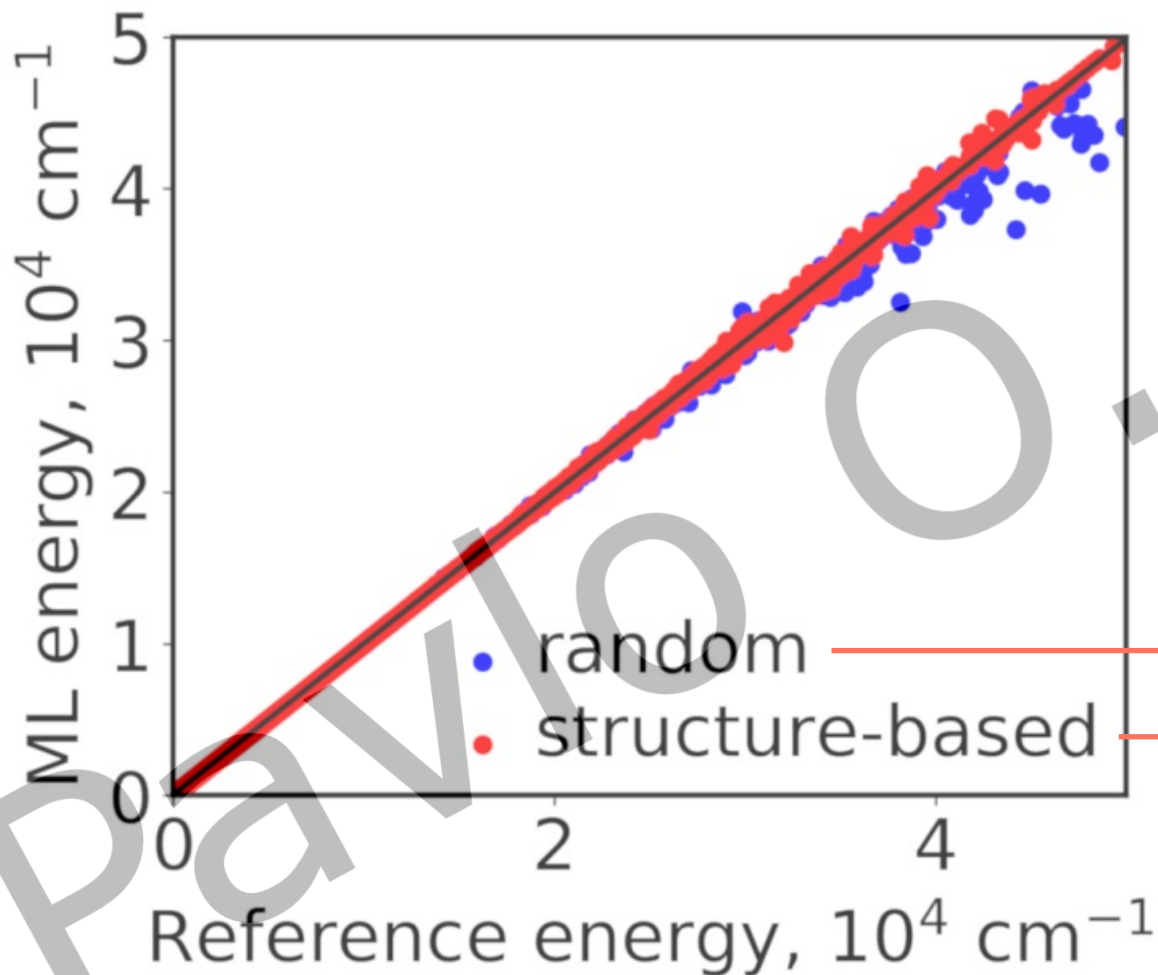


Figure from: P. O. Dral, *J. Phys. Chem. Lett.* **2020**, *11*, 2336



Online tutorial:
MLatom.com/AQCtutorial/

Training set

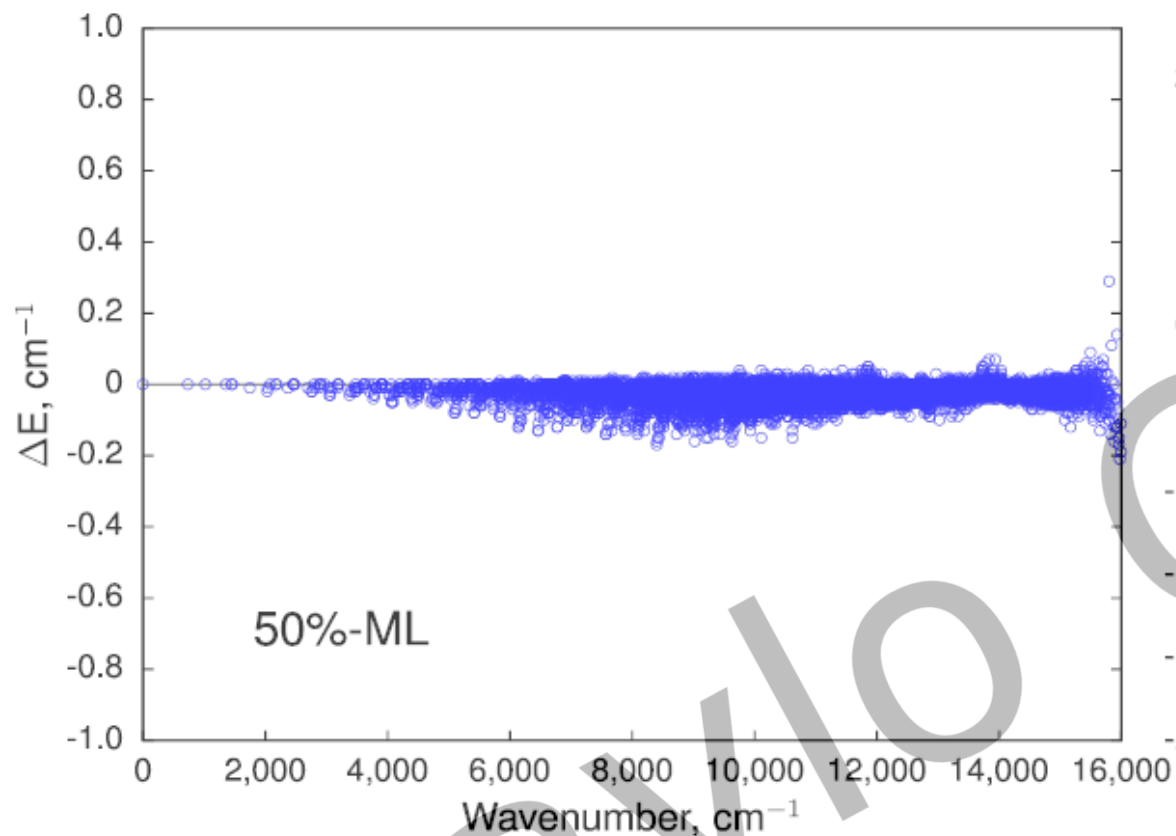
→ 50% of QC data

→ 10% of QC data:

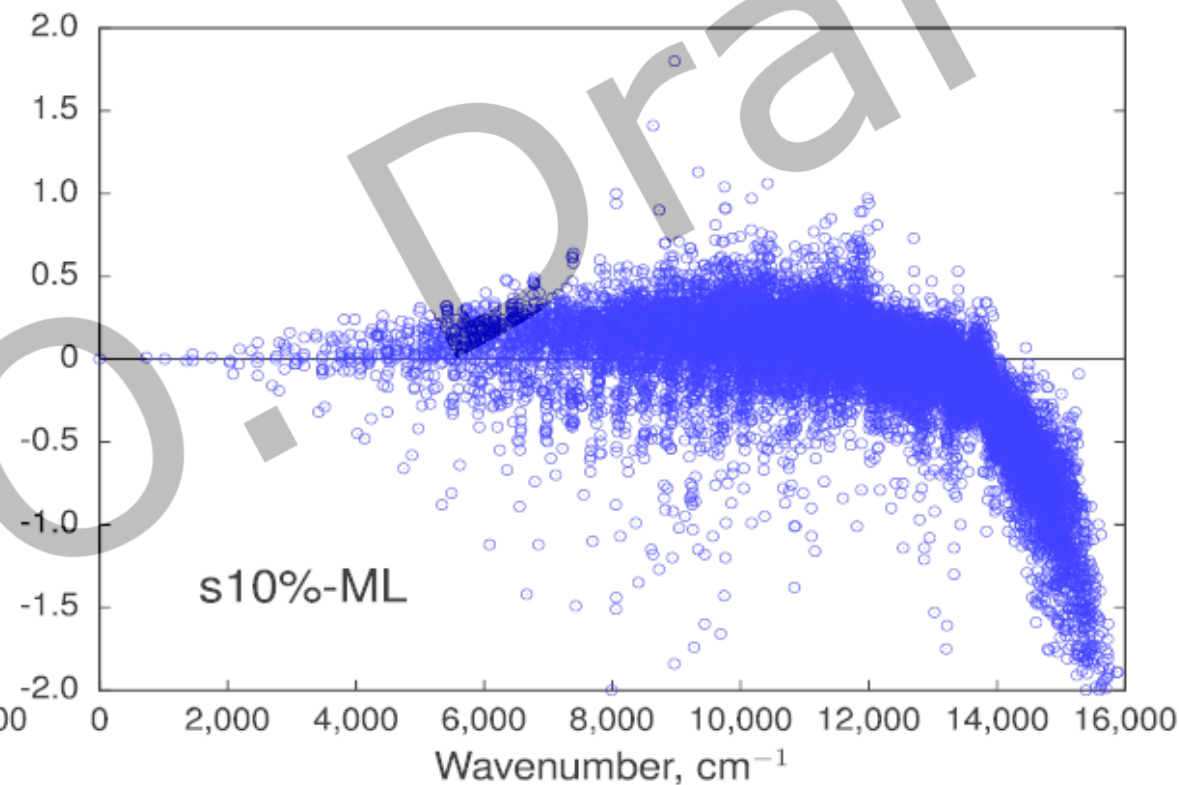
saved 90% of CPU-time!

Weighted RMSE:

3.49 cm⁻¹ = 0.01 kcal/mol



No of levels	Energy, cm ⁻¹	RMSE, cm ⁻¹
166	5,000	0.02
3,606	10,000	0.04



No of levels	Energy, cm ⁻¹	RMSE, cm ⁻¹
166	5,000	0.14
3,606	10,000	0.28

Hierarchical ML for CH_3Cl PES

Pure ML-model trained on **saved 90% of CPU-time**

Weighted RMSE:
 $3.49 \text{ cm}^{-1} = 0.01 \text{ kcal/mol}$

Hierarchical ML models:
saved 99% of CPU-time

Weighted RMSE:
 $1.12 \text{ cm}^{-1} = 0.003 \text{ kcal/mol}$

