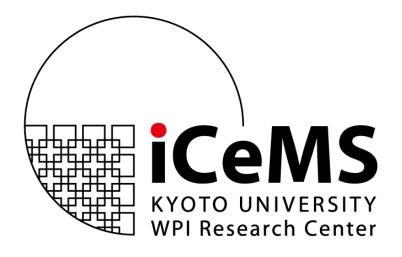
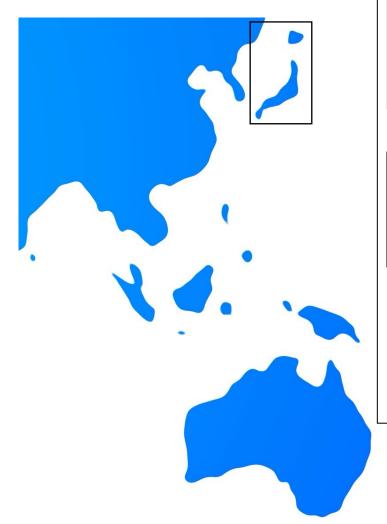
Applications of data science and machine learning to organic materials

Daniel Packwood





Self-introduction



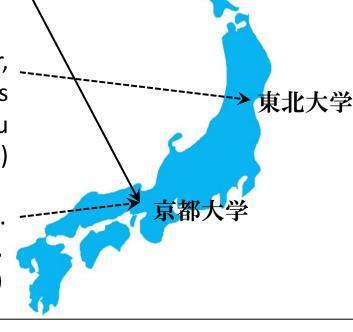


Senior lecturer and PI at iCeMS, Kyoto University (2016 - 2023) Associate Professor (2023 -)



Assistant Professor,
Mathematical Sciences
Unit, AIMR, Tohoku
University (2012 – 2016)

JSPS Postdoc, Quantum Chemistry Lab, Dept. of Chemistry, Graduate School of Science, Kyoto University (2010-2012)





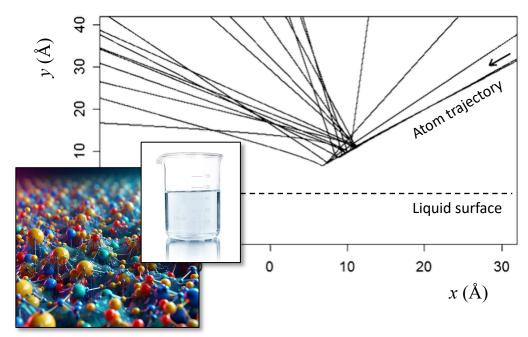
University of Canterbury (PhD 2010) Major: Chemistry, Minor: Statistics



Why did I come to Japan?

Graduate school research (late 2000s)

Studied atom scattering from liquid surfaces using non-equilibrium statistical mechanics and stochastic differential equations.



Two names frequently appeared during my study:



Kiyoshi Ito

- Kyoto University mathematician
- Stochastic differential equations pioneer



Ryogo Kubo

- Tokyo University physicist
- Non-equilibrium statistical mechanics pioneer

Realization: my field was pioneered in Japan!

Why did I come to Japan?



■ 第2回HOPEミーティング開催概要

日時: 2009年9月27日(日)~10月1日(木)

会場: ザ・プリンス箱根 テーマ: Art in Science

対象分野: 化学及び関連分野(物理学、生物学等)

主催: (独) 日本学術振興会

https://www.jsps.go.jp/hope/gaiyou2.html



- Gathering of around 50 students from the Asia-Pacific region. Activities with Japanese graduate students and lectures from Japanese Nobel laureates.
- High level of research from the students impressed me, left me with a strong impression.

→ Go to Japan for postdoctoral research!

Career in Japan

Tanimura laboratory, Department of Chemistry, Grad. School of Science, **Kyoto University**





2010 Postdoc 2012

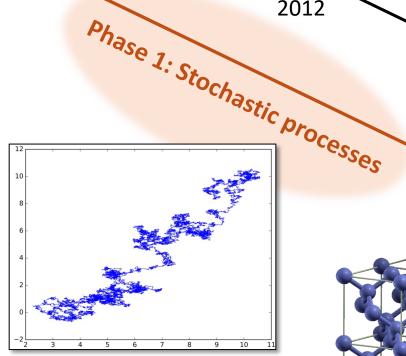
Mathematical Sciences Unit, **Advanced Institute for Materials** Research, Tohoku University





Assistant Professor

Institute for Integrated Cell-Material Sciences (iCeMS), Kyoto University





Phase 2: Computational chemistry

2016

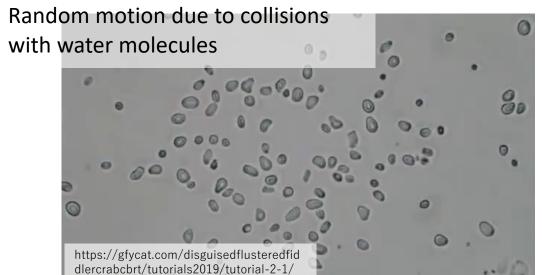
Associate Professor

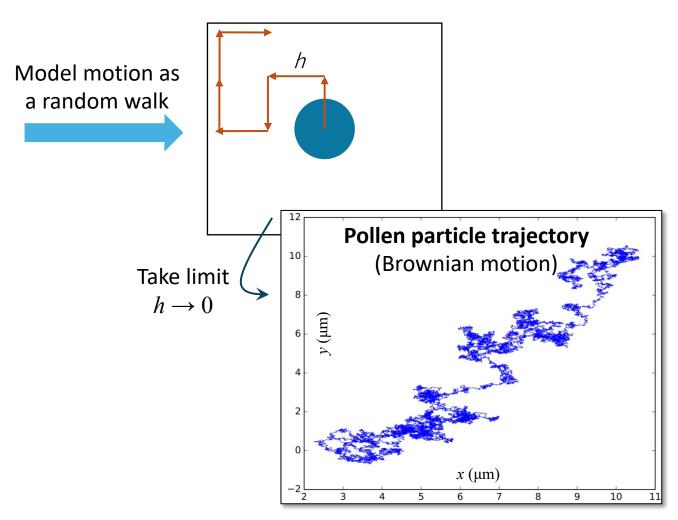
My previously research...

I studied stochastic processes (random walks) in physics and chemistry.

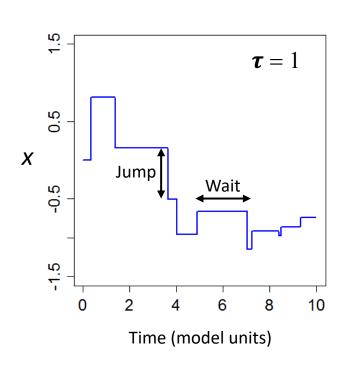
The most famous type of random walk in these fields is **Brownian motion**:

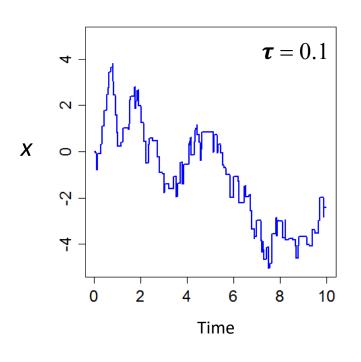
Pollen particles on water

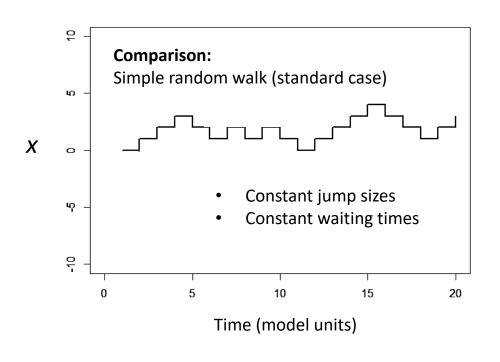




Postdoc research (2010 – 2012) Continuous-time random walk



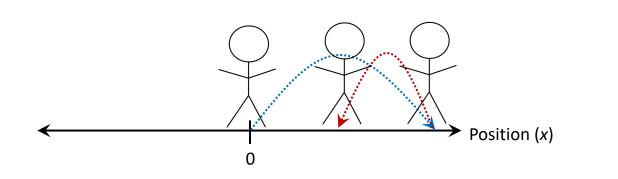




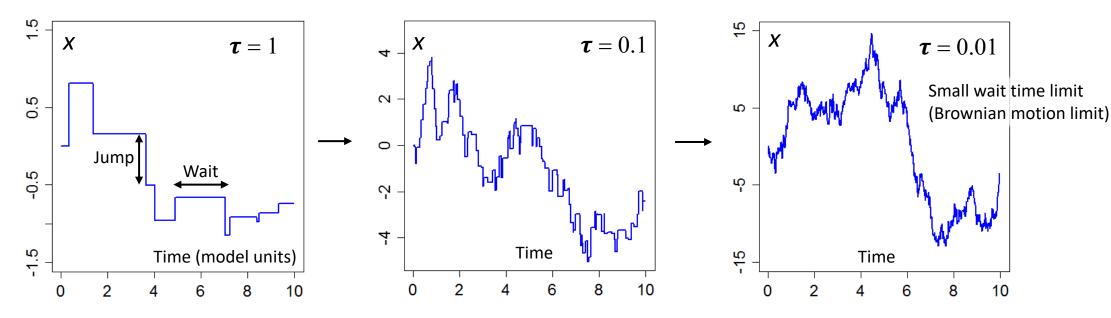
Consider a person hopping in one dimension. Let x denote their position.

In the continuous-time random walk,

- the waiting times between jumps are random (average waiting time = τ), and
- the jump size is random



Typical results



1. Derivation of conditions for convergence to Brownian motion as wait times go to zero.

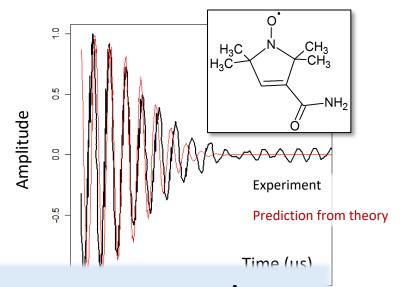
(the maximum jump size M must become $(3\tau)^{1/2}$)

J. Phys. A.: Math. Theor. **43**, 2010, 464001 arXiv: 1105,6283 (2011) Phys. Rev. E. **84**, 2011, 61111

2. Derivation of the linear response function (important in spectroscopy)

$$F(t) = e^{-t/\tau} e^{i\omega_0 t} \exp\left(\frac{1}{\tau M} \int_0^t \frac{\sin r/\tau}{r} dr\right)$$

Phys. Rev. E. 86, 2012, 11130



Fun, but a very narrow topic...

Career in Japan

Tanimura laboratory, Department of Chemistry, Grad. School of Science, **Kyoto University**





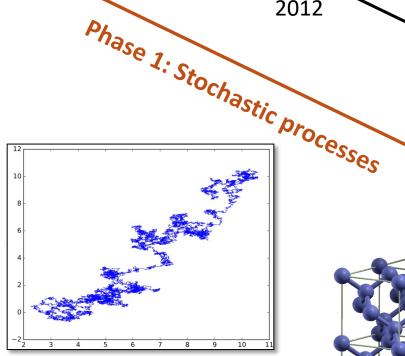
2010 Postdoc Mathematical Sciences Unit, **Advanced Institute for Materials** Research, Tohoku University 2012





Assistant Professor

Institute for Integrated Cell-Material Sciences (iCeMS), Kyoto University





Phase 2: Computational chemistry

2016

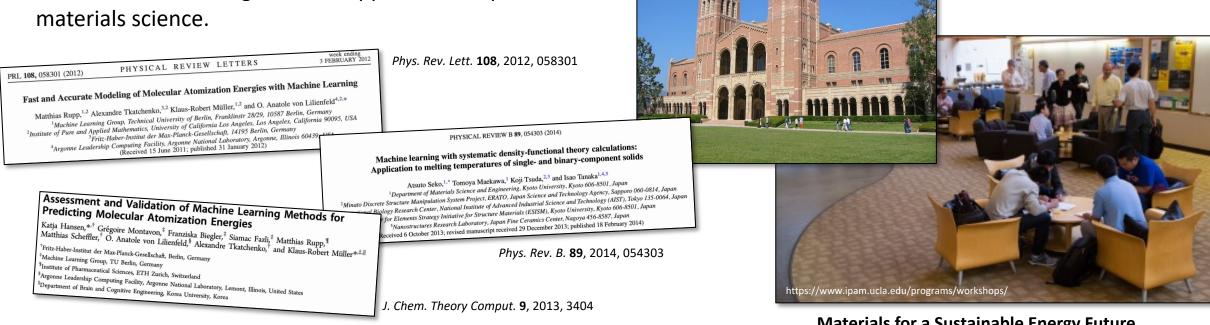
Associate Professor

Chance to shift to computational research:

Emergence of data science in computational materials science

https://www.inspiritai.com/blogs/ai-blog/what-is-ucla-known-for

Around 2012 – 2014, several papers appeared showing how machine learning could be applied in computational materials science.



Moreover, in 2013 I got to spend time with some of the authors during a stay at University of California, Los Angeles (UCLA)

Materials for a Sustainable Energy Future
Long program at the Institute for Pure and Applied
Mathematics, UCLA, Sep – Dec 2013

Machine learning and data science gave mathematicians a way to enter the computational materials science field!

... we just had to learn how to do density functional theory calculations.

Research in the Packwood group

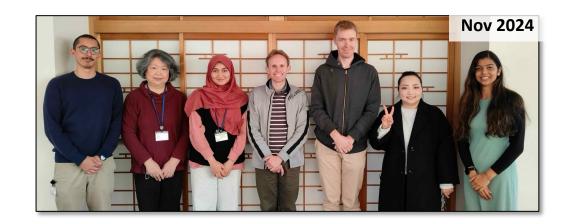
organic materials x simulation x data science

Visualization of organic semiconductor database (Adv. Theory Simul. 2023)

Visualization of organic semiconductor database (Adv. Theory Simul. 2023)

Average gap (eV)

Disease detection potential in a MOF-



Small molecule aggregation (2021 – now)

Bioactive molecule discovery (2021 – now)

Coordination polymers / metal-organic frameworks (2018 – now)

Game theory analysis of peptide dimer dynamics (in process)

semiconductor sensor (Adv. Theory Simul. 2025)

Organic semiconductor (2021 – now)

On-surface molecular self-assembly (2015 – 2022)

2015

Simulation of metal-

complex self-assembly

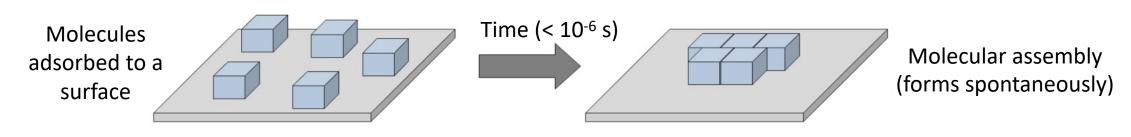
(Adv. Physics Res. 2022)

Lecture topics

Simulation of on-surface molecular self-assembly

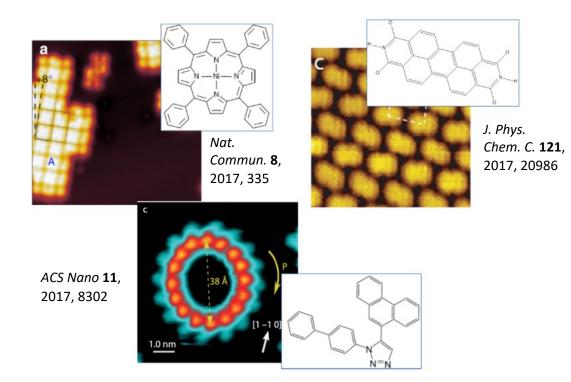
Machine learning for organic photovoltaic materials

On-Surface Molecular Self-Assembly

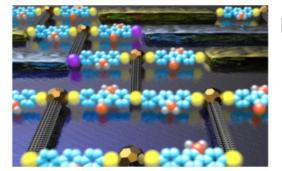


Many experimental reports...

(Scanning tunneling microscopy images)



... and many potential applications

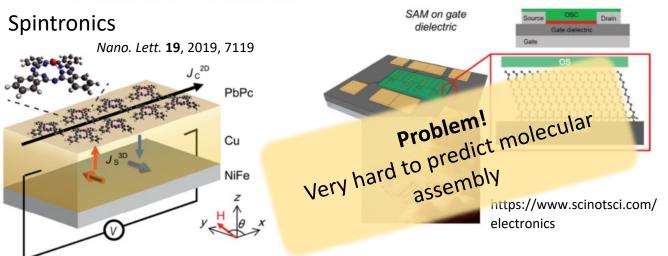


Molecular electronics

http://asdn.net/asdn/electronics/ molecular_electronics.php

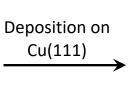
Organic electronics

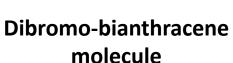
Chem. Soc. Rev. 46, 2017, 40

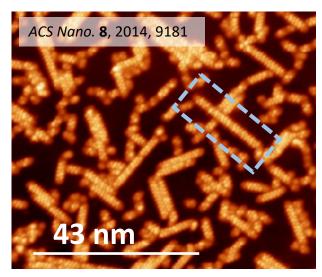


Br Br

How I came to this topic?







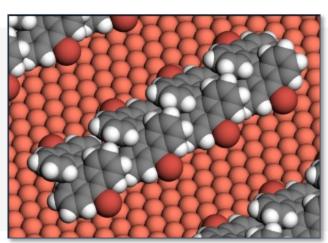
Self-assembly of molecular chains

About 10 years ago, colleagues at Tohoku University were studying molecular self-assembly using scanning tunneling microscopy (STM).

They wanted to know whether the chains could be predicted computationally.

Collaborating together, we created a computational method to predict chain formation.

Nat. Commun. 8, 2017, 14463

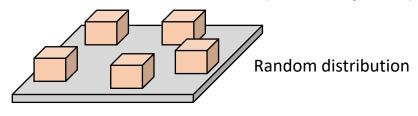


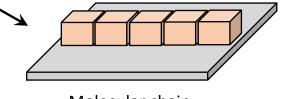






Prof. Taro Hitosugi (now at Tokyo Univ)

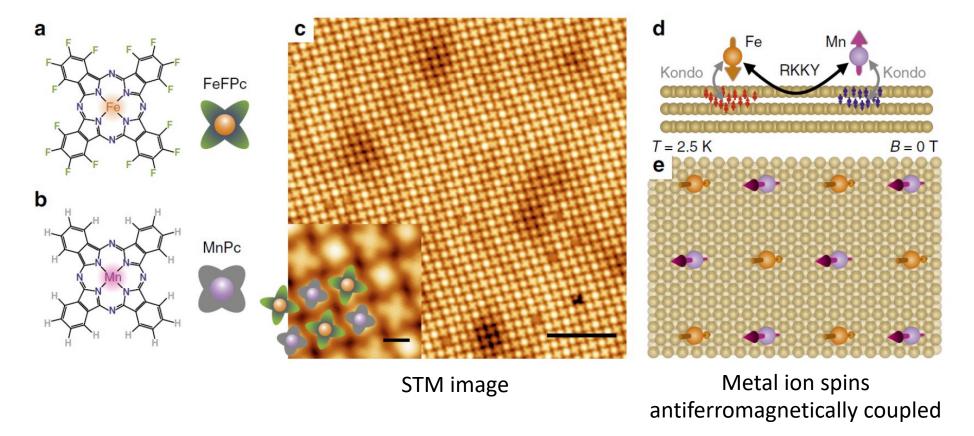




Molecular chain

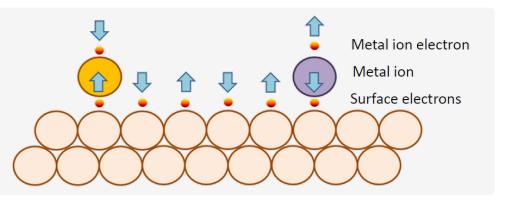
Today, I will discuss an updated version of this method applied to a different type of system...

Self-assembly of FeFPc and MnPc on Au(111)

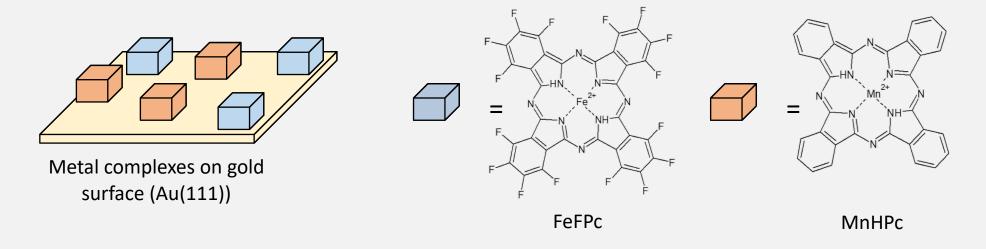


The antiferromagnetic coupling is due to the Ruderman-Kittel-Kasuya-Yoshida (RKKY) interaction

Can we reproduce this result with computation?



Q1. How to build a simplified model for the system?

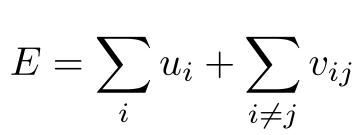


Q2. How to obtain predictions about self-assembly from the model?



Model assumptions

- Perfectly crystalline surface
- Two types of molecules on the surface; n_1 of the first type, n_2 of the second type.
- Finite number of adsorption sites (places where the molecules can sit)
- Finite number of molecule orientations.
- Rigid molecules. All molecules of the same type have the same conformation.
- Two-body energy function



Surface unit cell

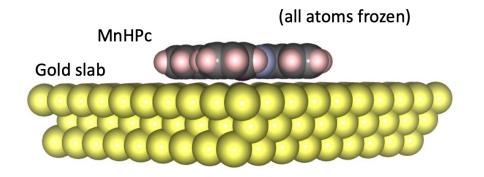
Molecule

 u_i = molecule *i*-surface interaction energy v_{ij} = molecule *i*-molecule *j* interaction energy

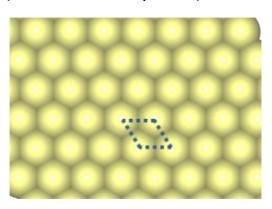
Surface atom

Molecule-surface interaction energies – assign using DFT*

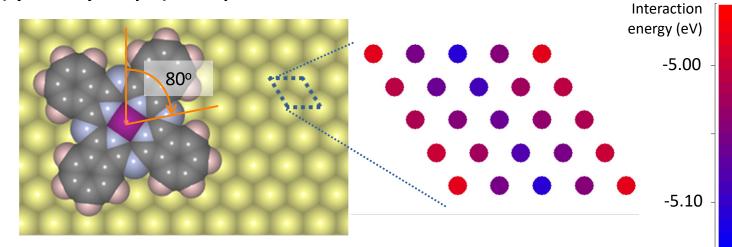
i. Obtain the optimal molecule-surface adsorption height



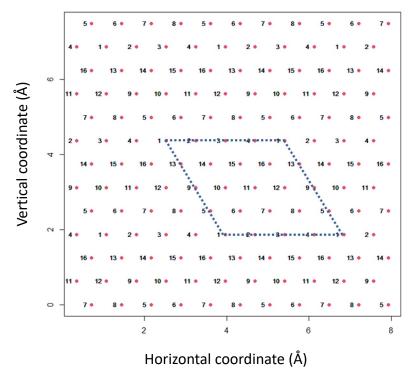
ii. Discretize surface (around 40,000 points)



iii. Compute interaction energy at each (symmetry unique) adsorption site



Step iii is performed for various molecule orientations (0°, 40°, 80°, ..., 320°)



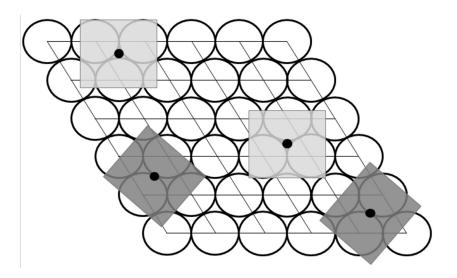
→ Surface-molecule interaction parameters assigned!

$$E = \sum_{i} u_i + \sum_{i \neq j} v_{ij}$$

^{*} DFT as implemented in FHI-aims, with the PBE exchange-correlation functional, TS vdW corrections, and "light" basis set defaults.

Molecule-molecule interaction energies

$$E = \sum u_i + \sum v_{ij}$$



Problem!

For a model with 40,000 adsorption sites, around 10¹¹ unique molecule-molecule interactions are possible.

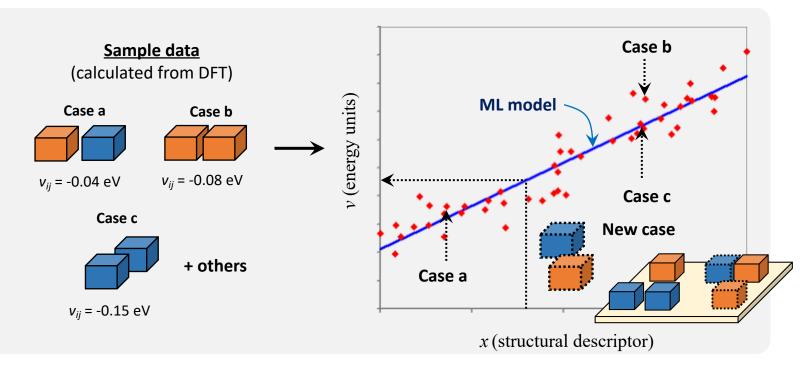
We cannot calculate the energy of each one individually using DFT.

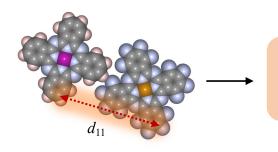
Our solution

Take a small sample of around 5000 intermolecular interactions, calculate their energies with DFT.

Use the sample data to build a machine-learning (ML) model.

Use the model to assign the energies of the remaining cases.



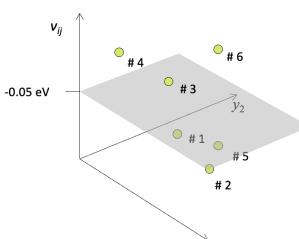


Coulomb-type descriptors

$$x_1 = 1/d_{11}, x_2 = 1/d_{12}, \dots$$

Input case (interaction energy = v_{ij})

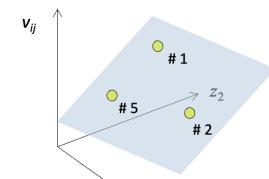
 y_1



Support vector machine

Transform data so that it can be separated by a linear plane $(x_1, x_2, ...) \Rightarrow (y_1, y_2, ...)$

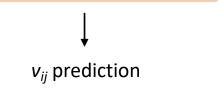
$$v_{ij} < -0.05 \text{ eV}$$
 $-0.05 \text{ eV} \le v_{ij} \le 0$



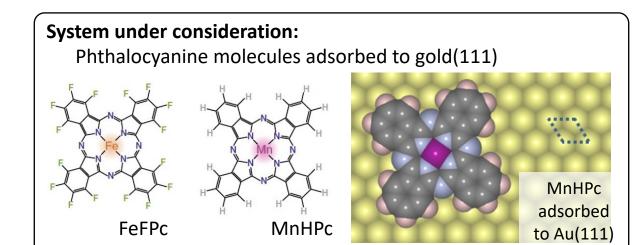
Kernel ridge regression

Transform data so that it lies on a linear plane

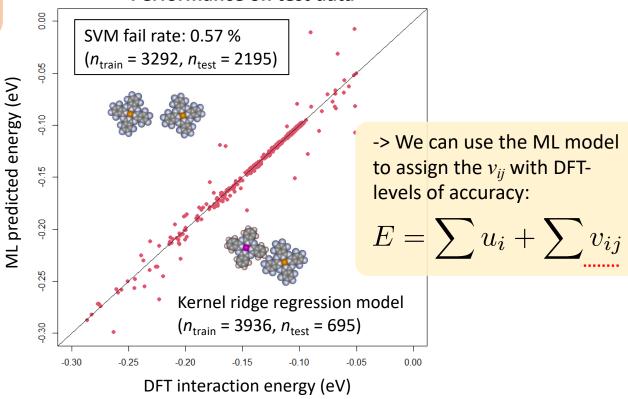
$$(y_1, y_2, ...) \Rightarrow (z_1, z_2, ...)$$



 $v_{ii} = 0$

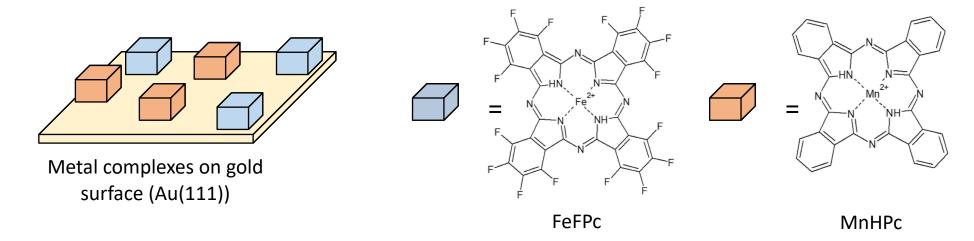


Performance on test data



DFT details: FHI-aims code, PBE xc functional, TS vdW corrections, 'light' basis set defaults.

Q1. How to build a simplified model for the system?



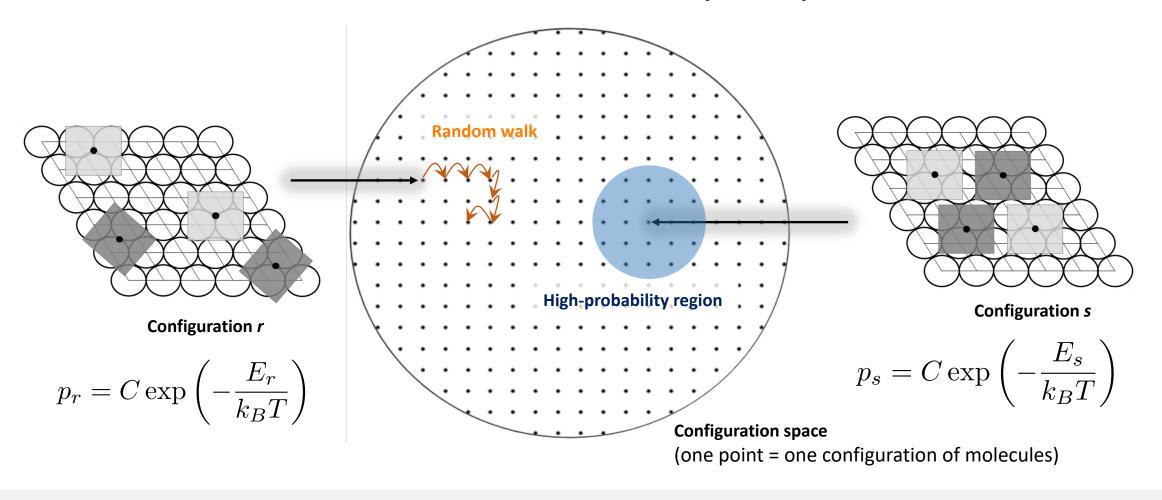
Q2. How to obtain predictions from the model?



We need to identify molecule configurations with high formation probability *p*:

$$p = C \exp\left(-\frac{E}{k_B T}\right)$$

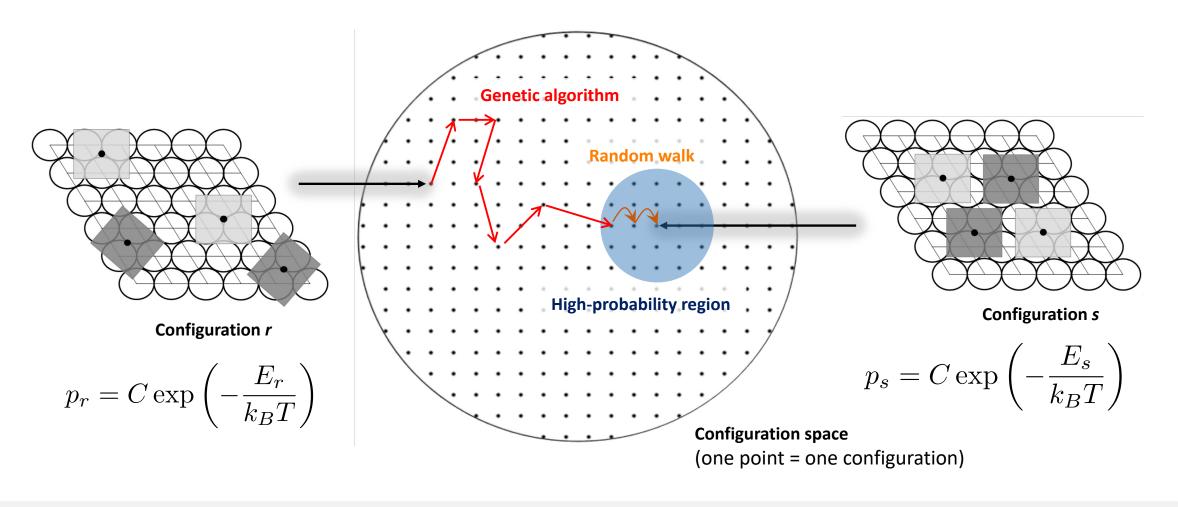
Markov chain Monte Carlo (MCMC)



In MCMC, we simulate a random walk over the configuration space. It is simulated in such a way that, after a long length of time, the number of visits to configuration s is proportional to p_s (the formation probability).

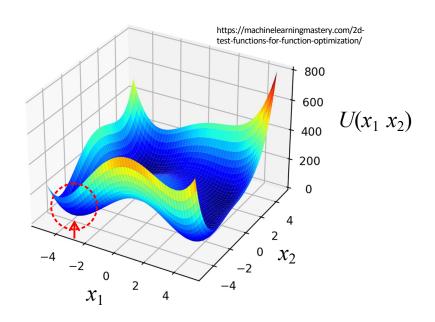
Problem: MCMC can be very inefficient. The configuration space is huge. The high-probability region (where the molecules are closely packed) is very small. Long simulation times are usually required to reach it.

Our solution: genetic algorithm + Markov chain Monte Carlo



The genetic algorithm makes large steps in the configuration space, quickly bringing us to the high-probability region (coarse search)

Markov chain Monte Carlo (random walk) makes short steps, thoroughly exploring the high-probability region. (fine search)



Genetic algorithm (general concept)

Task: Find the values of $x_1, x_2, ..., x_n$ which minimize the objective function $U(x_1, x_2, ..., x_n)$

Initial setup: N vectors of random numbers (x_{ij})

$$\mathbf{v}_1 = (x_{11}, x_{12}, \dots, x_{1n})$$
 $\mathbf{v}_2 = (x_{21}, x_{22}, \dots, x_{2n})$ \dots $\mathbf{v}_N = (x_{N1}, x_{N2}, \dots, x_{Nn})$

These vectors are called *chromosomes*. The elements x_{ij} are called *genes*.

Make new population with

N - k high-fitness

Algorithm:

Population of chromosomes	Calculate objective function	Calculate fitness	Create <i>k</i> new chromosomes by random mixing	chromosomes from original population and the <i>k</i> new ones	chro adding
\mathbf{v}_1	U_1	f_1	V =	\mathbf{v}_1	
\mathbf{v}_{2}	U_2	f_2	$\mathbf{v}_{12} = (x_{11}, x_{22},, x_{2n})$	\mathbf{v}_{12}	$y_{12}' = (x_{11} +$
:	:	:		:	
\mathbf{v}_{N}	U_N	f_{N}		\mathbf{v}_N	

Mutate all romosomes by ng small random numbers

 \mathbf{v}_1 ,

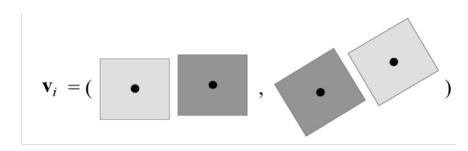
 $+ w_1, x_{22} + w_2, ..., x_{2n} + w_n$

 \mathbf{v}_N '

As algorithm is iterated, $\min(U_1, U_2, ..., U_N)$ converges to the global minimum.

Genetic algorithm implementation

Chromosomes: Vector of molecular clusters



Clusters correspond to farseparated groups of molecules

Closest interatomic distance > $r_{\rm cut}$, negligible interaction

Objective function: a free energy function

$$U\left(\mathbf{v}_{i}\right) = E\left(\mathbf{v}_{i}\right) - JS\left(\mathbf{v}_{i}\right) \qquad S\left(\mathbf{v}_{i}\right) = k_{B}\ln W\left(\mathbf{v}_{i}\right)$$

$$\uparrow \qquad \uparrow \qquad \uparrow$$
Energy Pseudo- Configuration Number of unitemperature entropy can be placed

$$S(\mathbf{v}_i) = k_B \ln V$$
Configuration Numeropy can

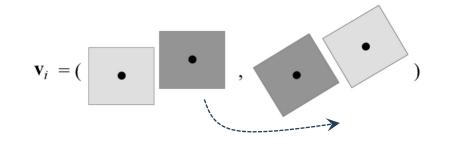
Number of unique ways molecular clusters can be placed on the surface (approximate formula: R. Soc. Open. Soc. 3, 2016, 150681)

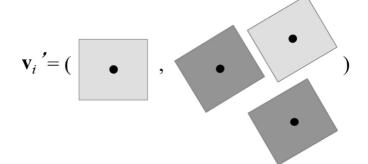
Chromosome mixing:

As before, but with conditions (to ensure that number of molecules n_1 , n_2 , is constant)

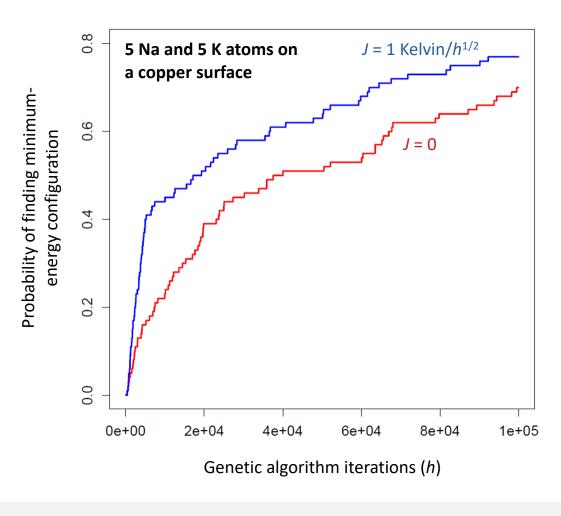
Chromosome mutations:

Random shift of a molecule between clusters



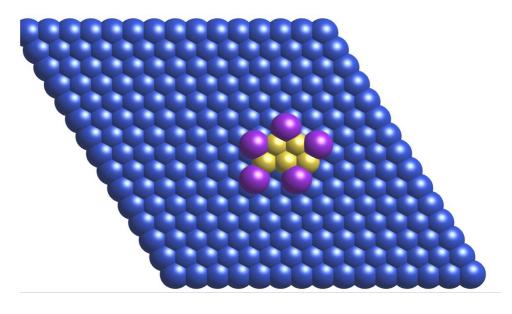


Special feature of our genetic algorithm: simulated annealing



Minimum-energy configuration

(yellow = Na atom, purple = K atom)

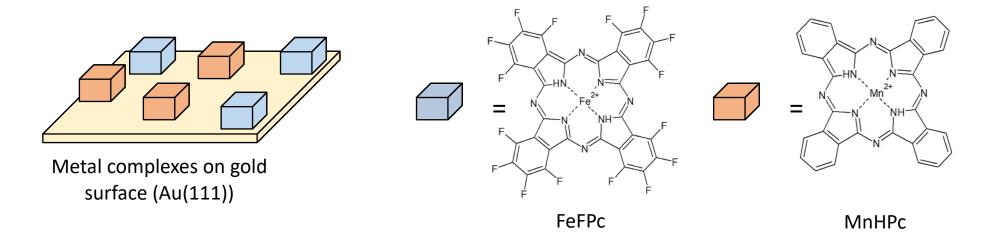


We gradually decrease the pseudo-temperature *J* as the algorithm proceeds. This helps the algorithm move out of local energy minima, improving performance.

Note: *J* is just a parameter to control the algorithm, and not the true surface temperature.

$$U\left(\mathbf{v}_{i}\right) = E\left(\mathbf{v}_{i}\right) - JS\left(\mathbf{v}_{i}\right)$$

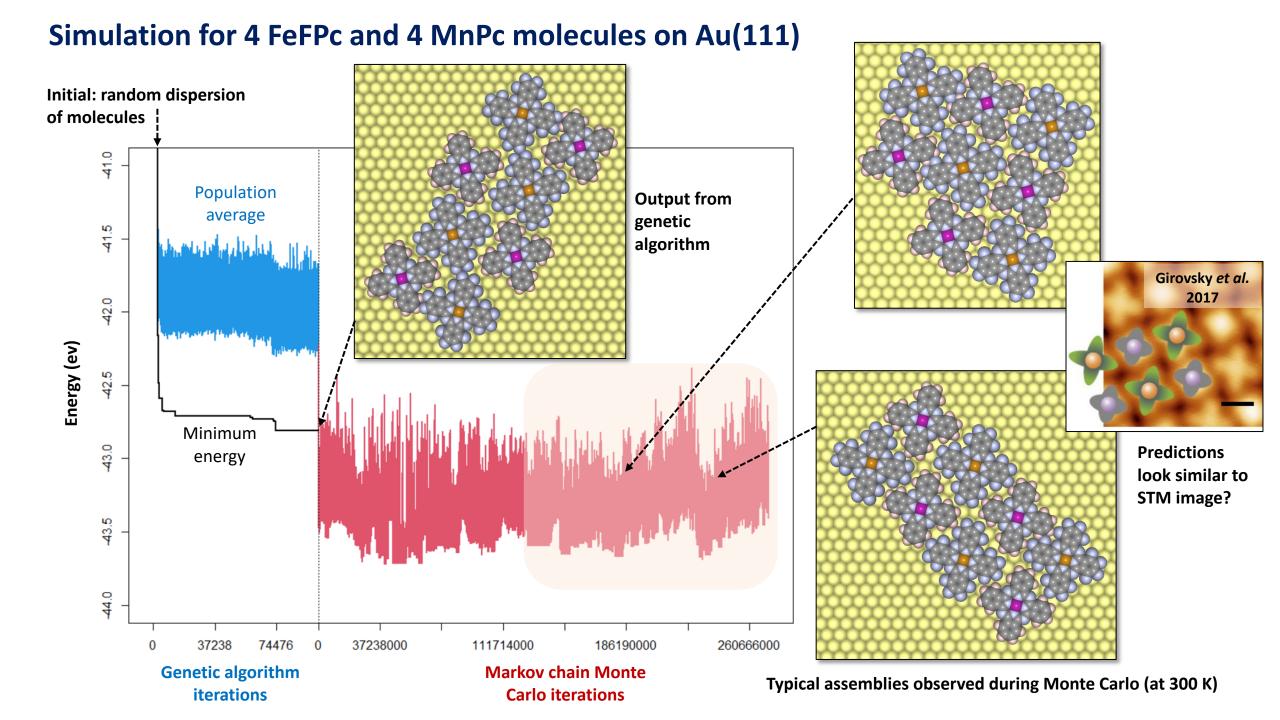
Q1. How to build a simplified model for the system?



Q2. How to obtain predictions from the model?



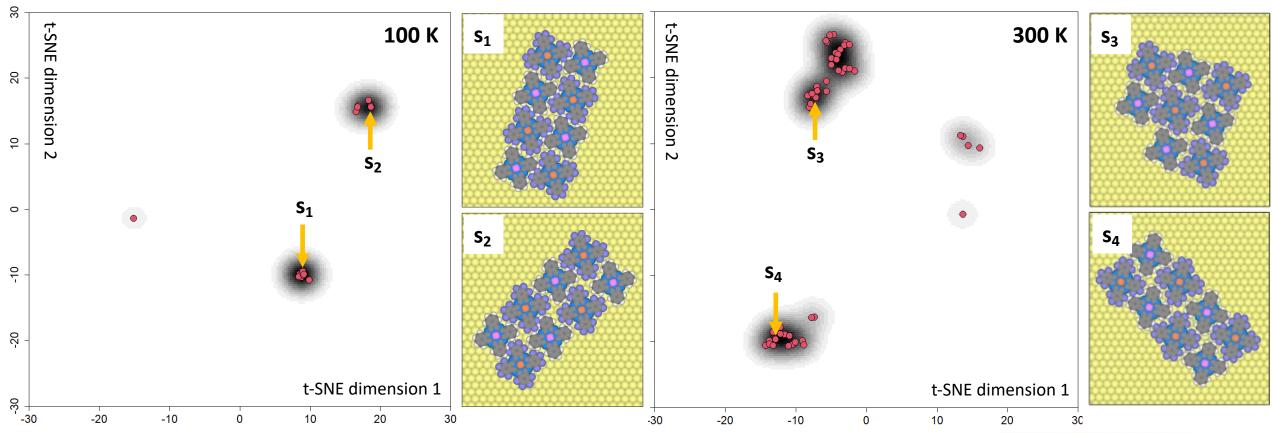
Results...



Visualization of equilibrium distribution of molecular configurations (300 K) Population average 50 configurations dimension from MCMC 42.0 Energy (ev) t-SNE 9 Minimum 43.0 energy 44.0 74476 37238000 111714000 186190000 260666000 **Genetic algorithm** Markov chain Monte iterations **Carlo iterations** MCMC gives us a sample of configurations that appear at t-SNE dimension 1 thermodynamic equilibrium.

- We apply t-distributed stochastic neighborhood embedding (tSNE) to visualize the MCMC sample in 2D. The configurations (red points) are arranged according to their structures.
- The configurations sampled by MCMC are mostly located in two clusters. Within these clusters, the configurations are mostly identical.

t-SNE dimension 1 10 20 30 Interpretation. At 300 K, are the predominantly two types of configurations on the surface.

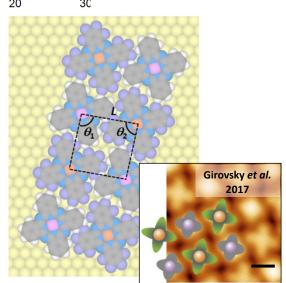


To compare with experiment, we consider simulations performed at low temperature (100 K).

Two types of configurations are also seen at 100 K, although different from the ones at 300 K.

Configuration s_1 achieves quantitative agreement with cryogenic STM images. Another phase also reported experimentally (perhaps s_2 ?).

	Calculation (mean ± st err)	Experiment (mean ± st err)
L	14.14 ± 0.07	14.05 ± 0.08
$ heta_1$	95.27 ± 1.86	95.84 ± 1.26
θ_2	84.73 ± 1.87	84.84 ± 0.79



Predicting magnetic properties

The spin directions of the Mn / Fe ions are very difficult to predict from first-principles. We therefore use a classical Ising model:

$$H = \sum_{i \neq j} J_{ij} \mathbf{S}_i \cdot \mathbf{S}_j$$

 S_i = spin vector for spin i

 J_{ij} = Exchange constant

For the case of RKKY interactions between spins*:

$$J_{ij} = Qg(2k_F r_{ij}) \quad g(x) = \left(\frac{2}{x}\right)^4 (\sin x - x \cos x)$$

Q = System-dependent constant

 r_{ii} = Distance between spins i and j

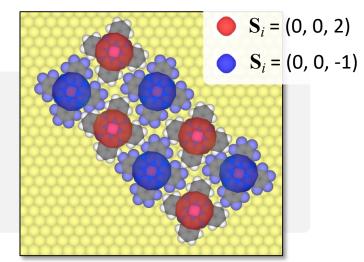
 k_F = Fermi vector for surface (about 0.18 Å⁻¹ for Au(111)*)



Result:

This model correctly predicts an antiferromagnetic ground state for the molecular assembly!

(a direct calculation of the spin orientations using density functional theory would be preferred for studying the magnetic ordering in more detail)



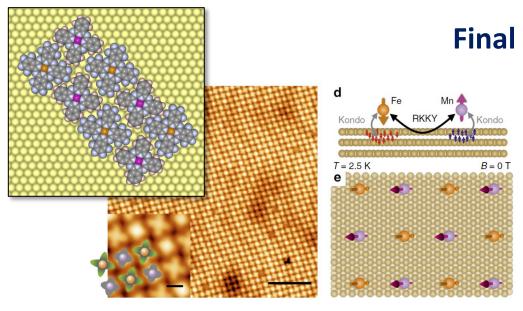
Metal ion electron

Surface electrons

Metal ion

S₂

^{*}Patterson and Bailey. Solid-State Physics. 2018. Springer



Final comments for part 1

- We succeeded to create a method that can predict how molecules assemble on metal surfaces.
- It combines a machine-learned interaction potential with genetic algorithms and Monte Carlo sampling.

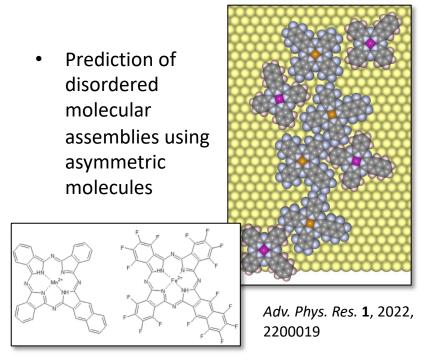
References: *Nat. Commun.* **8**, 2017, 14463;

Adv. Phys. Res. **1**, 2022, 2200019 <- this one is better!

We have done some other things with this method:

• Discovery of connection between single-molecule properties and molecular assembly shape.

Nat. Commun. 9, 2018, 2469



Lecture topics

Simulation of on-surface molecular self-assembly

Machine learning for organic photovoltaic materials

April 2021

iCeMS-MacDiarmid Institute Online Workshop



Te Mana

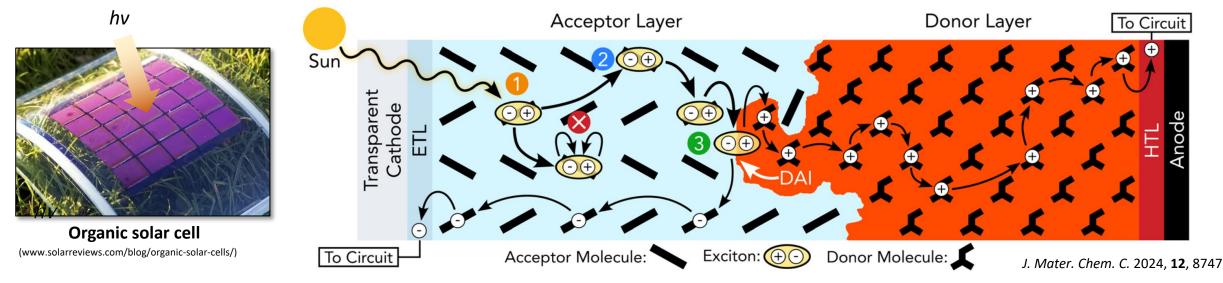
Tangata Whakawhanake

MacDiarmid

Institute
Advanced Materials

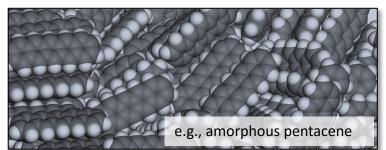


Organic solar cells and exciton diffusion (Hodgkiss group)



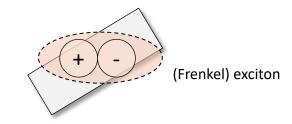
Acceptor layer is an organic semiconductor (crystal or amorphous solid of organic molecules)

Donor layer is another semiconductor (can be organic or inorganic)

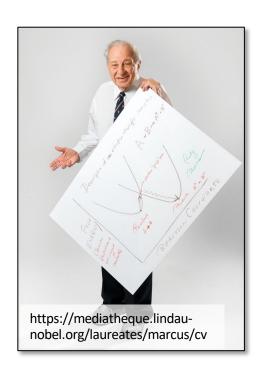


Light absorption by the acceptor layer results in Frenkel excitons

- tightly-bound electron-hole pairs localized to single molecules.



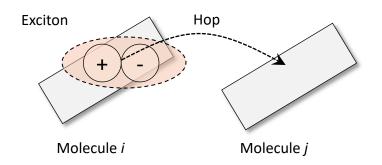
Excitons hop between molecules to the donor-acceptor interface (DAI), where they dissociate into electron and hole pairs and generate electricity. However, if the exciton moves too slowly, it will die by electron-hole recombination.



Exciton hopping

About 60 years ago, Rudolf Marcus showed that the rate of exciton hopping between molecules is approximately

$$k_{ij} = \left(\frac{\pi}{\lambda k_B T}\right)^{\frac{1}{2}} \frac{v_{ij}^2}{\hbar} \exp\left(-\frac{\lambda}{4k_B T}\right)$$
 Temperature

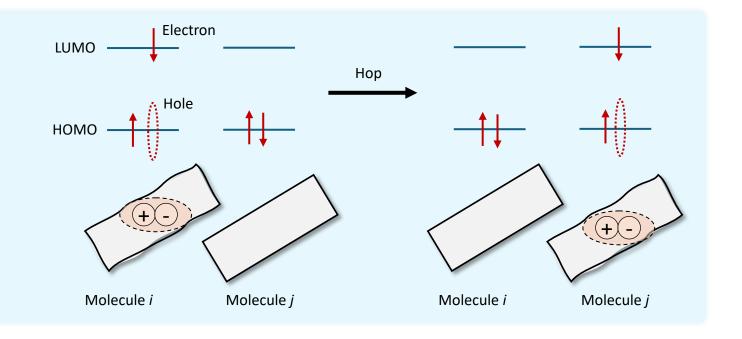


 $1/k_{ij}$ is the (average) time taken for the exciton to hop from molecule i to molecule j.

Important parameter 1. Reorganization energy (λ)

The exciton distorts the shape (conformation) of the molecule.

The reorganization energy measures the energy required to change the shapes of the molecules as the exciton shifts.



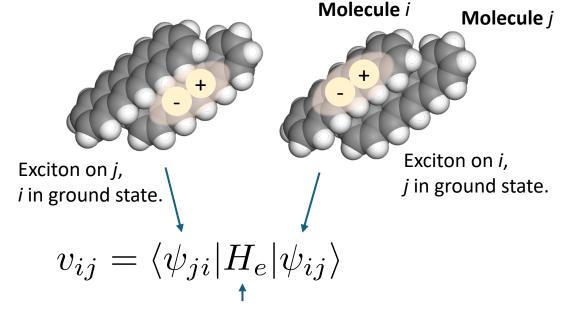
Important parameter 2.

Exciton coupling

$$k_{ij} = \left(\frac{\pi}{\lambda k_B T}\right)^{\frac{1}{2}} \frac{v_{ij}^2}{\hbar} \exp\left(-\frac{\lambda}{4k_B T}\right)$$
 Exciton coupling energy hope energy hope more than the property of t

The exciton coupling v_{ij} is a quantum mechanical parameter. Its interpretation is somewhat abstract:

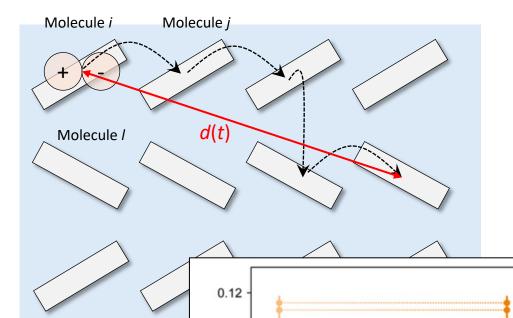
- Start with $|\psi_{ij}\rangle$. This is the wavefunction for the two molecules together, with the exciton on molecule i (initial state, before the hop).
- Electron-electron interactions between molecules perturbs $|\psi_{ij}\rangle$. The perturbed wavefunction is represented as $H_e|\psi_{ij}\rangle$.
- Now consider $\langle \psi_{ji}|$. This is the final wavefunction, with the exciton on molecule j (final state, after the hop).
- Finally, $\langle \psi_{ji}|H_e|\psi_{ij}\rangle$ tells us the overlap between the perturbed initial wavefunction and the final wavefunction.



Electron-electron interaction operator

Both of these parameters can be calculated from firstprinciples (time-dependent DFT / TDDFT). However, these calculations are very time consuming!

Kinetic Monte Carlo (kMC) simulation of exciton diffusion



Once the hopping rates are calculated, the hopping process can be simulated using the kinetic Monte Carlo (kMC) method.

Roughly, the exciton hops to its neighbor j with probability proportional to k_{ij} . This results in a random walk-type motion through the crystal*.

Mean-square displacement

Exciton diffusion coefficient can be estimated as:

$$D = \lim_{t \to \infty} \frac{1}{6} \frac{\overline{d(t)^2}}{t}$$

compared to spectroscopic measurements (crystalline materials)

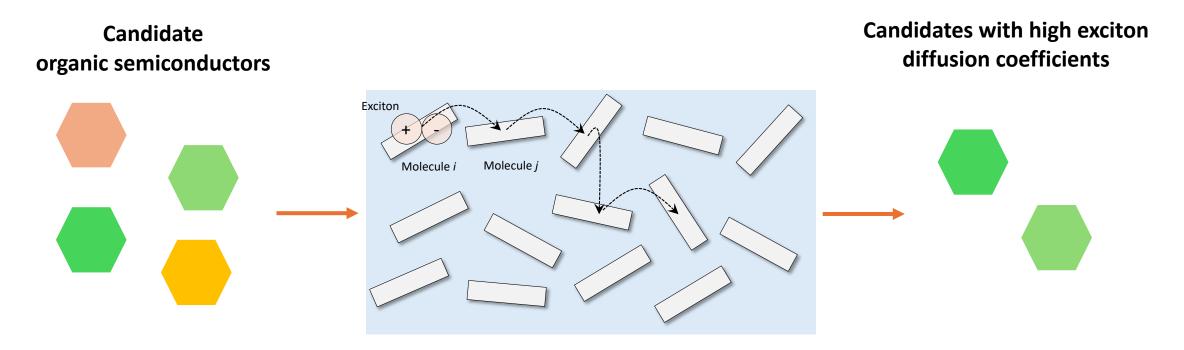
J. Mater. Chem. C. 24, 2024, 8747

0.10 D_{kMC} (cm²s⁻¹) 00 99 IDIC (Chandrabose) IDIC (Firdaus) ITIC-4F 0.04 × ITIC-2CI (δ) ITIC-2Cl (average) ITIC-2CI (y) 0.02 ITIC **EH-IDTBR** 0.00 0.10 0.02 0.04 0.06 0.08 0.12 0.00 D_{Expt} (cm²s⁻¹)

kMC simulations yield reasonable predictions of diffusion coefficients.

Could we discover new organic materials with large diffusion coefficients by high-throughput kMC simulations?

Kinetic Monte Carlo (kMC) for materials discovery?



Looks feasible – kMC can be done quite quickly on a laptop (minutes per candidate).

Problem: kMC has a big computational overhead!

For each candidate, couplines and reorganization energies need to be pre-computed from TDDFT before kMC can start.

Can we use machine learning to predict these parameters quickly?

$$k_{ij} = \left(\frac{\pi}{\lambda k_B T}\right)^{\frac{1}{2}} \frac{v_{ij}^2}{\hbar} \exp\left(-\frac{\lambda}{4k_B T}\right)$$

2021 - 2022

First attempt at machine learning for exciton couplings

Dr. Chayanit Wechwithayakhlung





Data science

Prof. Justin Hodgkiss

Dr. Paul Hume

Dr. Geoff Weal

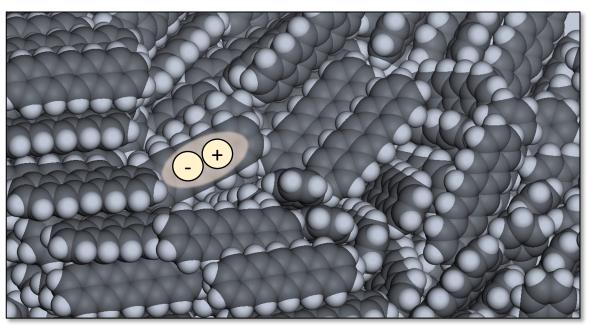


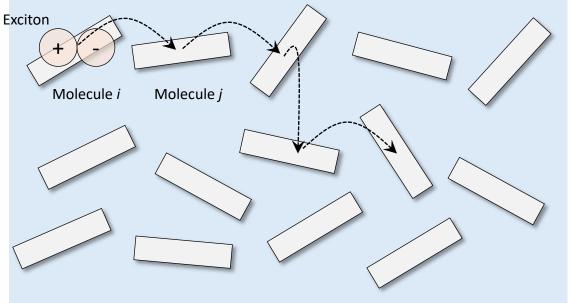




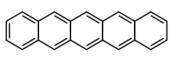
Ultrafast spectroscopy Excited state quantum chemistry

First target - exciton diffusion in amorphous pentacene





Pentacene molecule:





$$k_{ij} = \left(rac{\pi}{\lambda k_B T}
ight)^{rac{1}{2}} rac{v_{ij}^2}{\hbar} \exp\left(-rac{\lambda}{4k_B T}
ight)$$

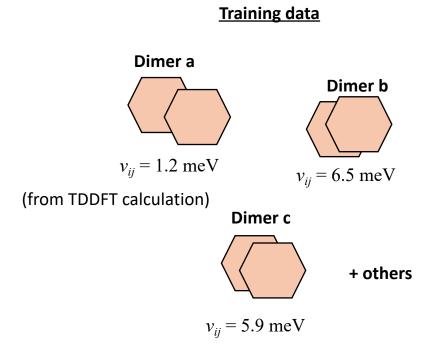
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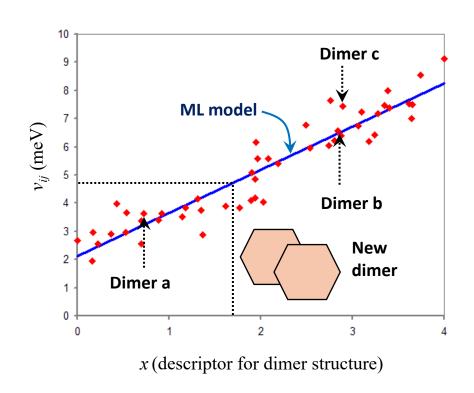


Amorphous pentacene is an organic semiconductor which can be used in organic solar cells.

Simple and relevant molecule, good starting point.

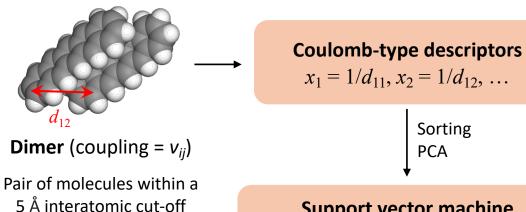
Machine learning concept





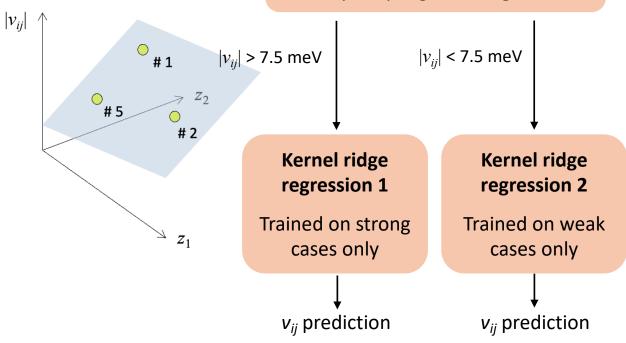
Again, we aim to fit a model which predicts coupling from dimer structure (x). With the fitted model, couplings for new dimers can be quickly predicted.

ML model for exciton couplings



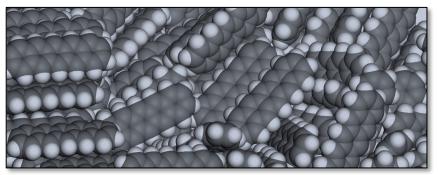
Support vector machine

Classify coupling as strong or weak

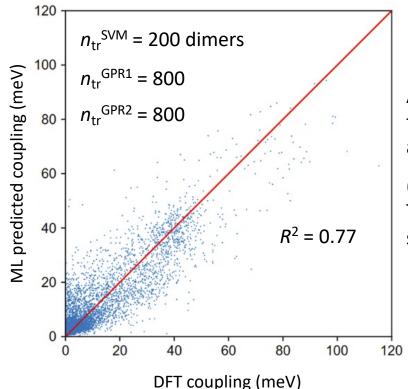




Amorphous pentacene (generated by **Dr. Yu Kaneko (DAICEL)**)



Performance on 4127 dimers



Average prediction time around 7 ms on an office workstation*

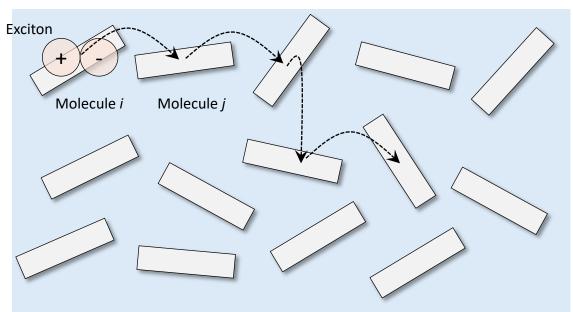
(cf. 7.4 hours for TDDFT on supercomputer**)

^{*} Single 3.50 GHz Intel Xeon E5-1620 core

^{** 64} cores (128 threads), 2.0 - 3.35 GHz AMC Epyc 7702 processors.

Kinetic Monte Carlo simulation in amorphous pentacene

DFT couplings



Molecule <i>i</i> Molecule <i>j</i>		listan	200 - ML coupli	ngs		
			0 20	0	400 time (ps)	600
			DFT couplings			
)	•		*	
			200 ps	400 ps	600 ps	800 ps
			ML couplings		9.00	alka d
			- •			
	Ab initio couplings	Model-predicted coupling	gs			
Diffusion coefficient ($\times 10^{-3} \text{ cm}^2 \text{ s}^{-1}$)	1.630 ± 0.011	1.547 ± 0.005	200 ps	400 ps	600 ps	800 ps
,						

(Statistics from 10⁴ trials)

1000 ps

1000 ps

800

400 Å

400 Å

Mean square distance (10³ A²)

Diffusion tensor eigenvalues ($\times 10^{-3} \text{ cm}^2 \text{ s}^{-1}$) Major 1.815 ± 0.014 1.686 ± 0.017 Middle 1.551 ± 0.016 1.492 ± 0.007 Minor 1.525 ± 0.012 1.462 ± 0.014

(Experimental diffusion coefficient for multicrystalline pentacene: 0.5 x 10⁻³ cm² s⁻¹)

Good start, but a serious problem remains:

Coupling model restricted to only one type of molecule (pentacene). Cannot use this for virtual screening!

2023 - 2024 General exciton coupling model

Dr. Geoff Weal



Data science

Prof. Justin Hodgkiss

Dr. Paul Hume

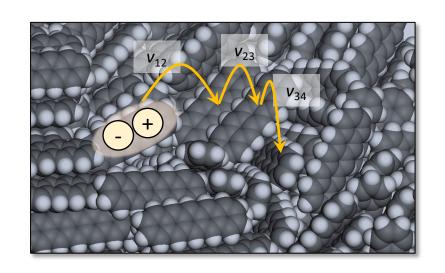


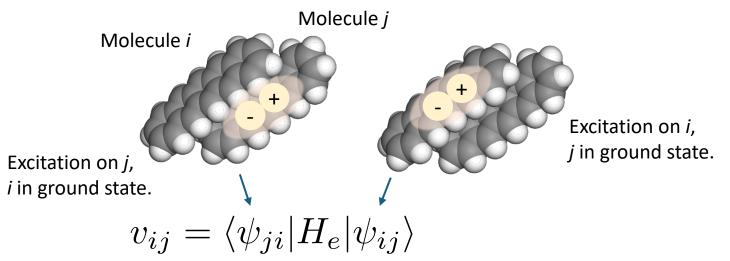


Ultrafast spectroscopy Excited state quantum chemistry

JSPS Postdoctoral Fellowship

Towards a new coupling model that works for all types of molecules?





Longuet-Higgins showed that v_{ij} can be approximated as a sum over simple, Coulomb-like terms*:

 Q_{α}^{i} is the **atomic transition charge** (ATC) for atom α .

It measures the change in the electron density on atom α when molecule i transitions from the ground to the excited state $(\rho_{\rm tr}{}^i({\bf r})$ is called the transition density)

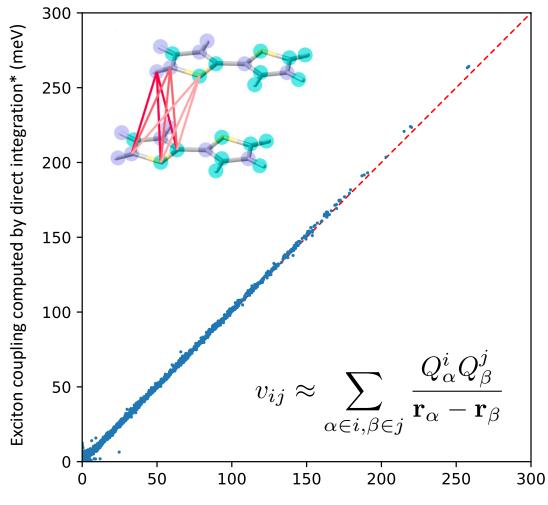
This is known as the **ATC approximation**. It has never been tested extensively, so we put it to work...

$$v_{ij} pprox \sum_{lpha \in i, eta \in j} rac{Q_{lpha}^{i} Q_{eta}^{\jmath}}{\mathbf{r}_{lpha} - \mathbf{r}_{eta}}$$

$$Q_{\alpha}^{i} = \int_{\mathbf{r} \text{ on atom } \alpha} \rho_{\text{tr}}^{i}(\mathbf{r}) d\mathbf{r}$$

*Longuet-Higgins. Proc. Roy. Soc. 235, 1956, 537

Towards a new coupling model that works for all types of molecules?



Exciton coupling computed from ATC approximation* (meV)

We tested the ATC approximation for molecular dimers extracted from 1989 organic crystals in the CCDC database (Cambridge Crystal Data Center)

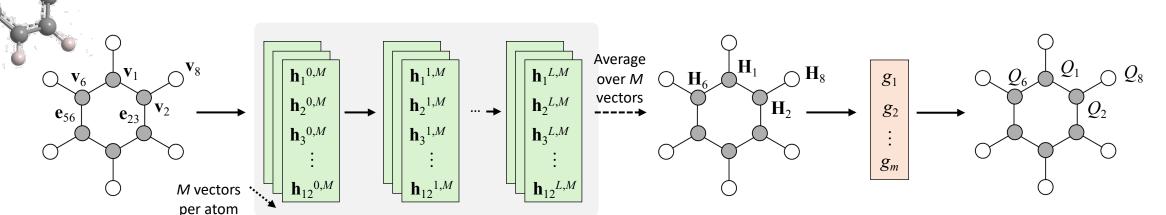
Good agreement, with only small deviations for strong coupling cases (ATC approximation neglects some closerange quantum effects)

=> Instead of creating an ML model for couplings directly, let's make an ML model for atomic transition charges (Q_{α}) .

We could then compute v_{ij} for any type of molecule using the ATC approximation.

^{*} TDDFT with ω -B97XD xcf with 6-31+G(d,p) basis set as implemented in Gaussian 16.

Graph neural network to predict atomic transition charges (ATCs)

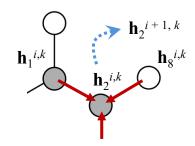


Molecular graph

Initial atom descriptors \mathbf{v}_i Initial bond descriptors \mathbf{e}_{ij}

Iterative feature embedding

Message parsing between atoms



Molecular graph

Final atom descriptors

Graph readout

Atom readout

ATC predictions

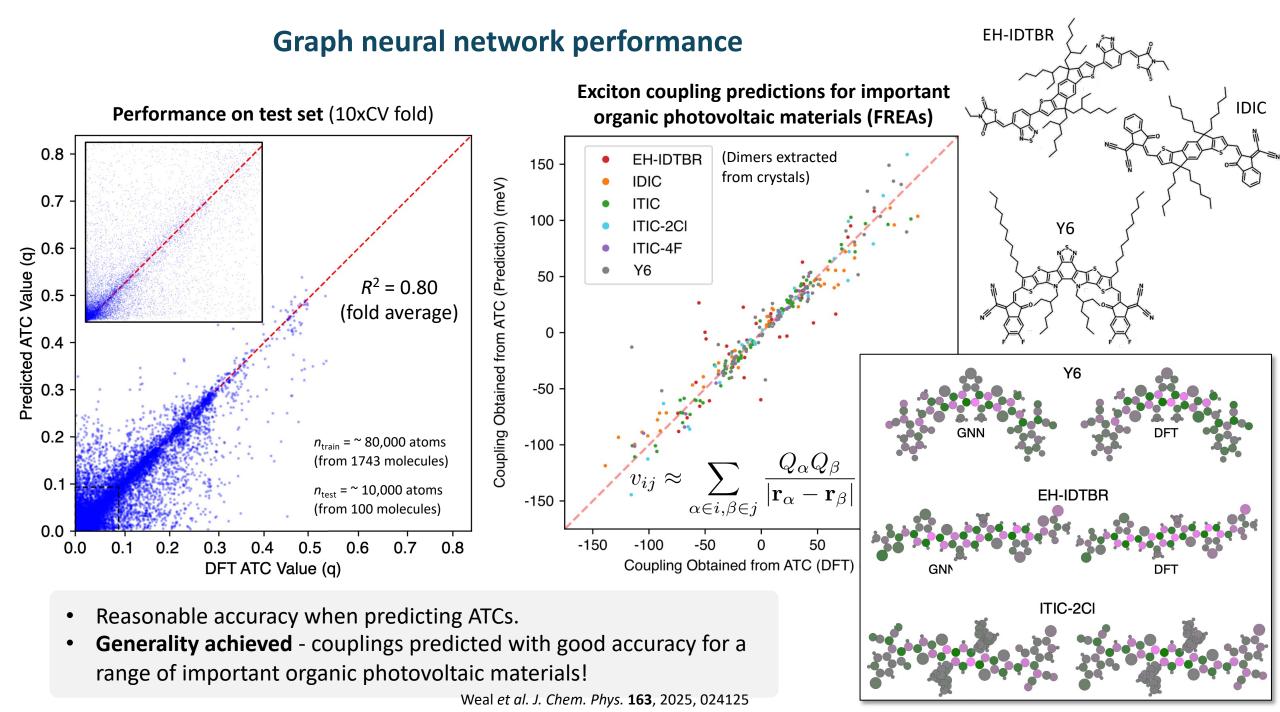
Neural networks / non-linear transformations

Implementation

SOAP (Smooth Overlap of Atomic Positions) descriptors used for \mathbf{v}_i . An integer-valued descriptor corresponding to hybridization state also incorporated (sp, sp2, sp3).

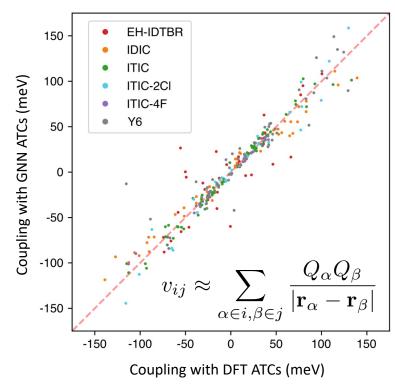
Integer-valued descriptor for bond type (single, double, etc) used for e_{ij} .

Other settings and training procedure followed Han et al. Phys. Chem. Chem. Phys. 24, 2022, 26870.

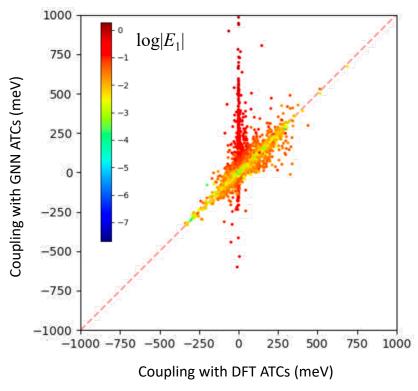


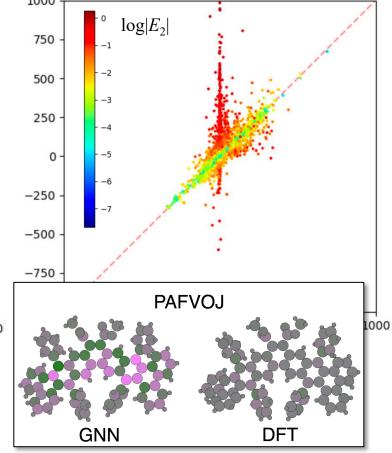
How general? Error propagation limits accuracy for weakly coupled cases

Coupling predictions for important organic photovoltaic materials (FREAs)



Couplings for dimers extracted from 1000 organic crystals



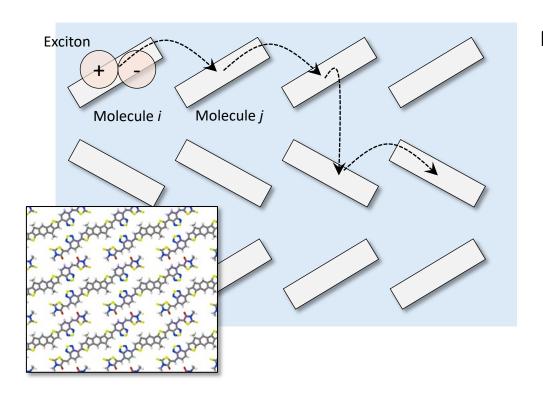


Let ε_{α} be the error of the Q_{α} prediction (ε_{α} = Q_{α} - $Q_{\alpha}^{\rm GNN}$).

Then
$$v_{ij} = v_{ij}^{\text{GNN}} + E_1 + E_2$$
, where $E_1 = \sum \varepsilon_{\alpha} Q_{\beta}^{\text{GNN}} / |\mathbf{r}_{\alpha} - \mathbf{r}_{\beta}|$ and $E_2 = \sum \varepsilon_{\alpha} \varepsilon_{\beta} / |\mathbf{r}_{\alpha} - \mathbf{r}_{\beta}|$.

First- and second-order errors can be large for dimers where coupling is in fact weak ($|v_{ij}|$ less than about 75 meV). For other cases, the method seems reliable.

Kinetic Monte Carlo simulations using GNN-predicted ATCs

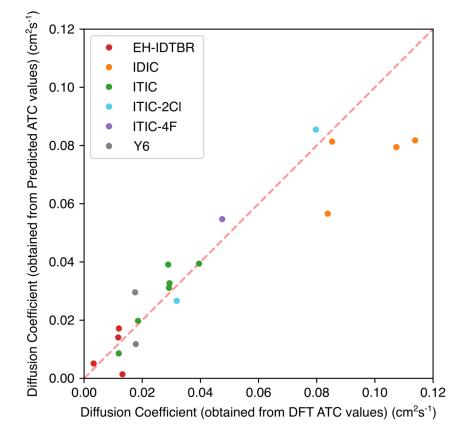


Marcus hopping rates:

GNN-predicted exciton coupling

Reorganization energy (TDDFT-calculated)

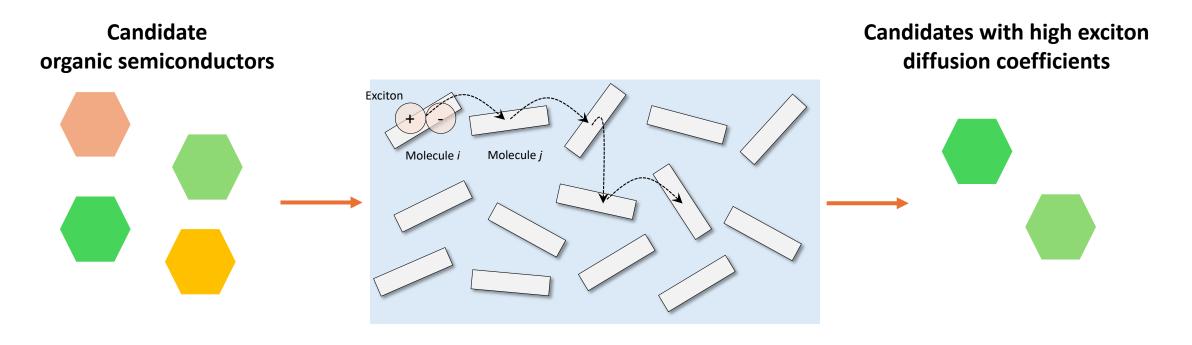
$$k_{ij} = \left(\frac{\pi}{\lambda k_B T}\right)^{\frac{1}{2}} \frac{v_{ij}^2}{\hbar} \exp\left(-\frac{\lambda}{4k_B T}\right)$$



Weal *et al. J. Chem. Phys.* **163**, 2025, 024125

Good predictions of diffusion coefficient obtained for multiple materials!

Closer to high-throughput kinetic Monte Carlo (kMC)?



Computational overhead remains!

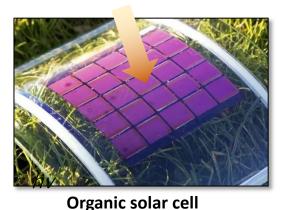
We succeeded to create a general ML scheme to predict couplings.

But reorganization energies still require expensive timedependent DFT calculations. We still have work to do! GNN-predicted exciton coupling

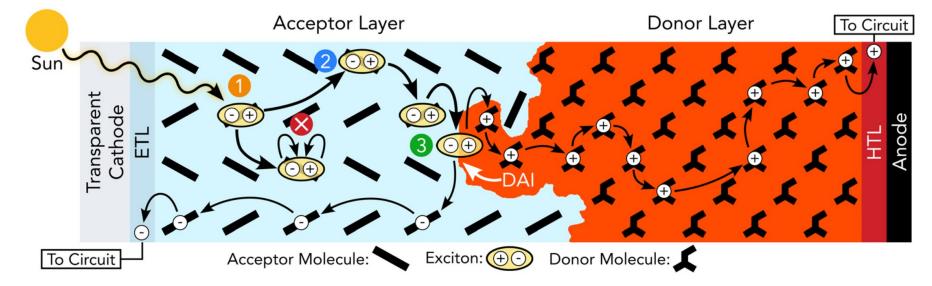
$$k_{ij} = \left(\frac{\pi}{\lambda k_B T}\right)^{\frac{1}{2}} \frac{v_{ij}^2}{\hbar} \exp\left(-\frac{\lambda}{4k_B T}\right)$$

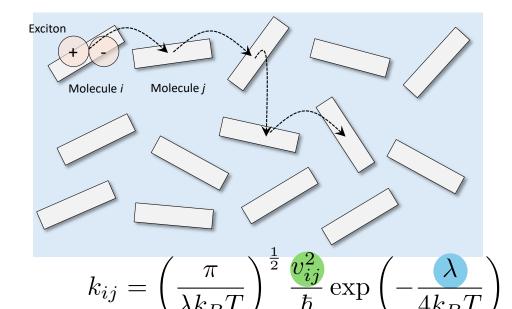
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Summary of part 2



(www.solarreviews.com/blog/organic-solar-cells/)





- Kinetic Monte Carlo simulations *might* be used for screening organic semiconducting materials. However, the computational times required for exciton hopping rates need to be significantly reduced first.
- We created a new method for quickly computing exciton coupling parameters. It combines the atomic transition charge approximation and a graph neural network.
- The method generalizes widely across different molecule types.

References: Wechwithayakhlung et al. J. Chem. Phys. 158, 2023, 204106 Weal et al. J. Mater. Chem. C. 24, 2024, 8748 Weal et al. J. Chem. Phys. 163, 2025, 024125

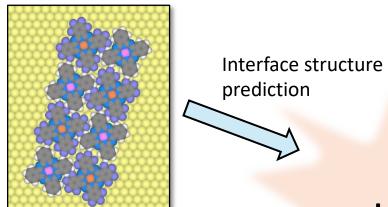
Lecture topics

Simulation of on-surface molecular self-assembly

Machine learning for organic photovoltaic materials

What's next?

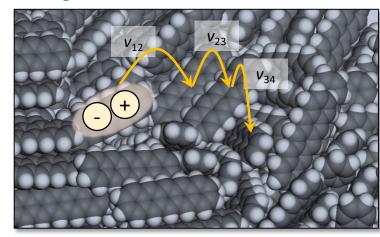
Molecular self-assembly research

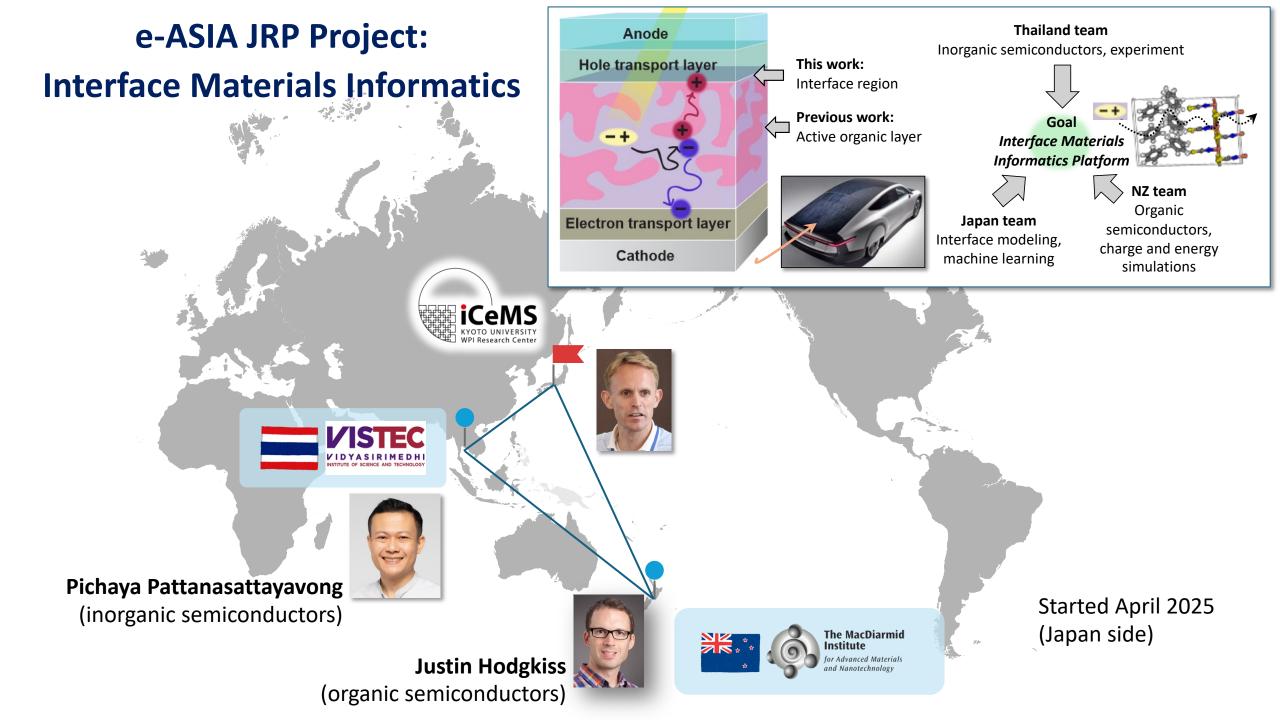


New challenge!

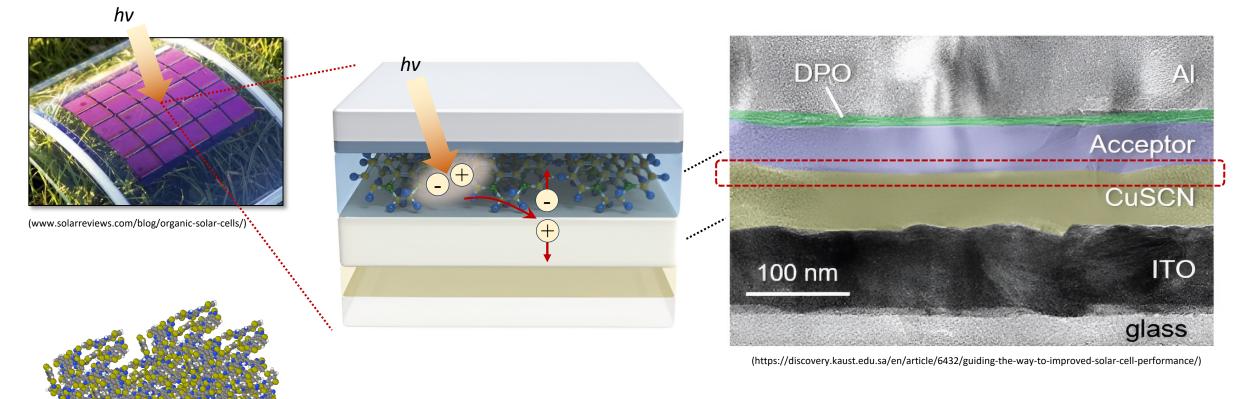
Exciton transport simulation

Organic semiconductor research



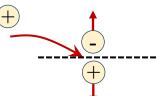


Project focus: organic-inorganic interface in organic solar cells



Can we predict the atomic-level structure of the interface?

Can we simulate charge separation at the interface?



Can we use these simulations to guide experimental solar cell fabrication?

Can experiment guide simulations?



(https://www.solar.fau.de/research/devices/)

Group members (2025)

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Chio Hayashi

Dr. Bandon Meza

Dr. Maryam Nurhuda

Dr. Shreya Rastogi

Dr. James Scott



Dr. Geoff Weal

Dr. Chayanit Wechwithayakhlung

Collaborators (on-surface self-assembly)

Dr. Patrick Han

Prof. Taro Hitosugi

Collaborators (organic photovoltaics)

Dr. Yu Kaneko (DAICEL)

Dr. Paul Hume (MacDiarmid Institute)

Dr. Joshua Sutton (MacDiarmid Institute)

Prof. Justin Hodgkiss (MacDiarmid Institute)



2024



2022

Chayanit Wechwithayakhlung

Funding (on-surface self-assembly, organic photovoltaics)

JST PRESTO (2014 – 2018)

JSPS Kakenki Kiban C (21K05003)

JSPS Kakenhi Shingakujyutsu Koubo (19H04574)

JSPS Kakenhi Wakate (18K14126)

JSPS Kakenhi Shingakujyutsu Koubo (16H00879)

JSPS Bilateral Projects / MBIE CATALYST

JSPS Postdoctoral Fellowship for Foreign Researchers