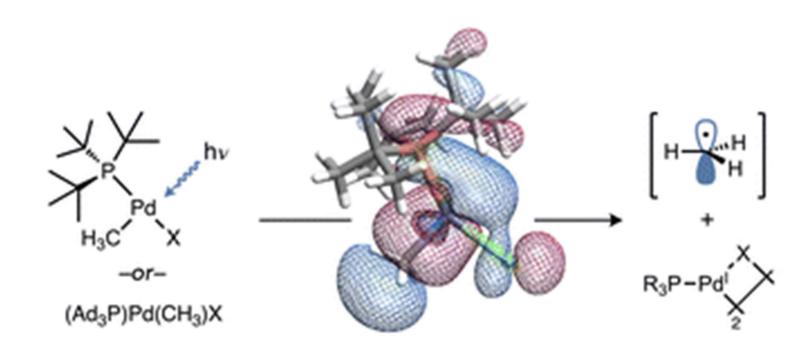
Computational and Machine Learning Exploration of Pd-C Photocleavage in T-shaped Organopalladium Complexes



Peter M. Waddell, Ph.D.



general manifold

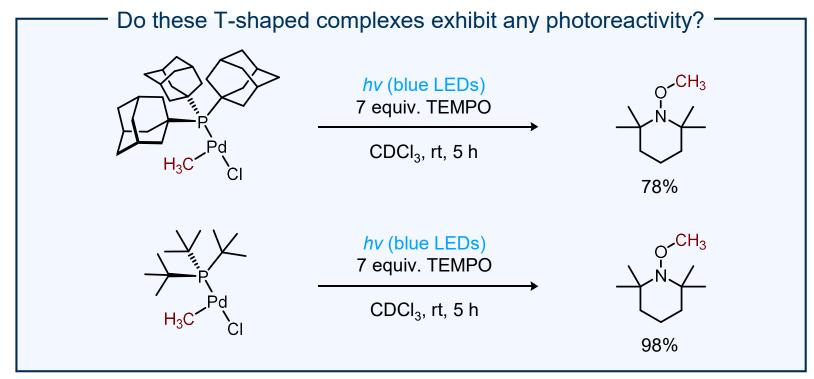
ACCESSING 1-ELECTRON MANIFOLDS WITH Pd?

thermal reactivity excited state reactivity [Pd(II)-C] [Pd(I)] + • C [Pd(0)]2-electron 1-electron catalytic cycle catalytic cycle [Pd(0)][Pd(II)] Can light energy be used to toggle between manifolds? challenging to Pd is biased to this

access



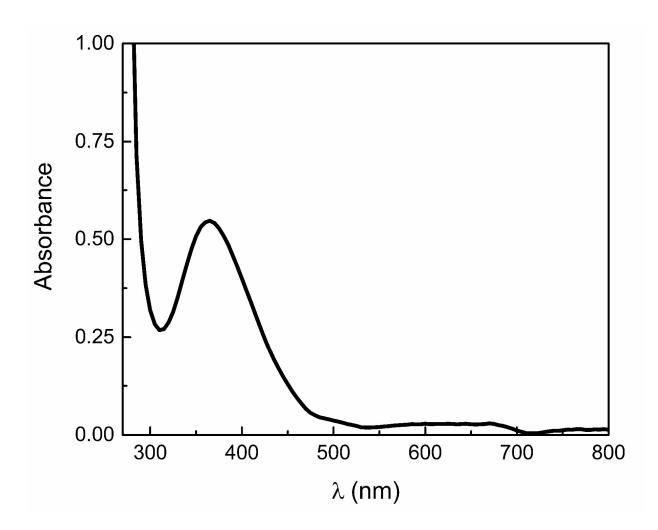
T-SHAPED COMPLEX Pd-C PHOTOCLEAVAGE WITH VISIBLE LIGHT



Visible light-induced bond weakening triggers SET chemistry in the most synthetically versatile metal and oxidation state (d⁸, Pd^{II})! Previously, this reactivity was much more limited to high-energy UV light.

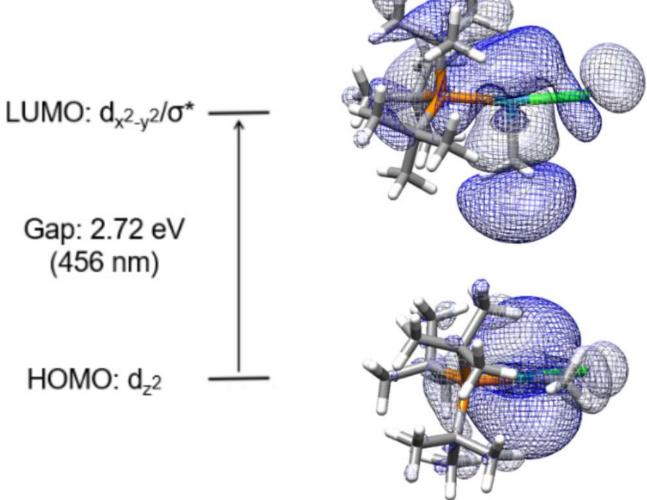


Pd-C PHOTOCLEAVAGE WITH VISIBLE LIGHT



Absorption spectrum of the T-shaped complex shows the key peak for the transition that leads to Pd-C cleavage, with a λ_{max} just under 400 nm.





LUMO shows Pd-C σ^* character, **possibly accessible with <u>visible light</u>** due to the absence of a ligand trans to C in the fourth site of the square plane.

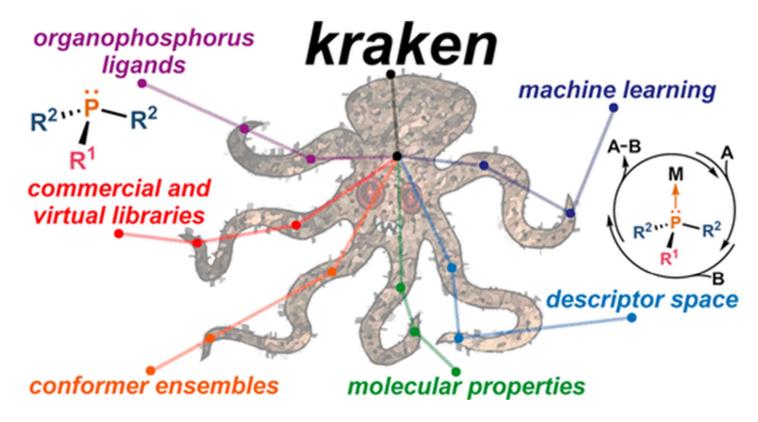


COMPUTATIONAL STUDY OBJECTIVES

- How do the steric and electronic properties of the ancillary ligand affect the UV-vis absorption spectrum of their organopalladium complexes? What characteristics cause red or blue shifts in the λ_{max} of the key peak? What is the lowest energy light that might be able to access this reactivity?
- Hypothesis: stronger bonding interaction in the fourth site will cause a blue shift in λ_{max} .
- Can we build a model with machine learning techniques to predict the spectral profile
 of a complex based only on information from its ancillary ligand?
- How conserved is the Pd-C photocleavage reactivity among a broad set of organophosphorus ligands?



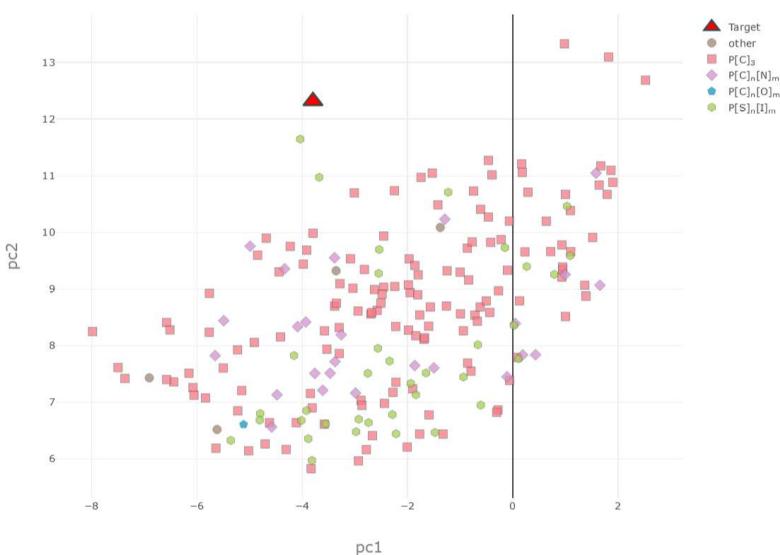
EXPLORING PHOSPHINE LIGAND SPACE WITH KRAKEN LIBRARY



The Kraken library of phosphine ligands is a perfect starting point to explore the chemical space of bulky organophosphorus ligands.



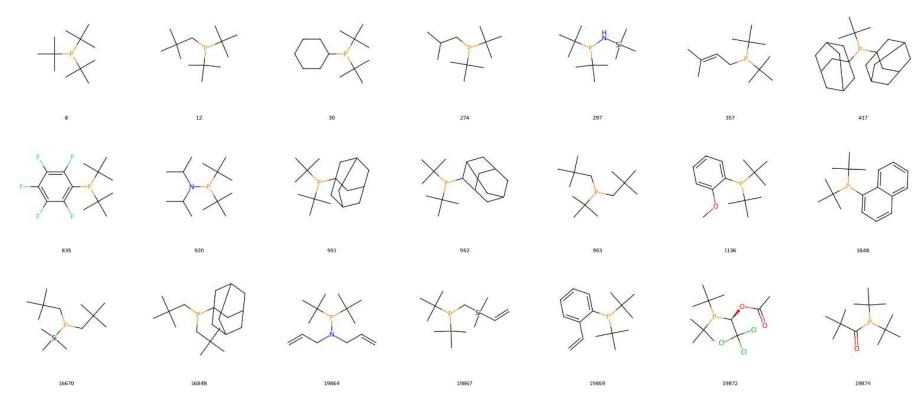
EXPLORING PHOSPHINE LIGAND SPACE WITH KRAKEN LIBRARY



To start, I used the Kraken library to find the 210 closest (in principal component space) organophosphorus ligands to our target (tri-*t*-butylphosphine)



EXPLORING PHOSPHINE LIGAND SPACE WITH KRAKEN LIBRARY

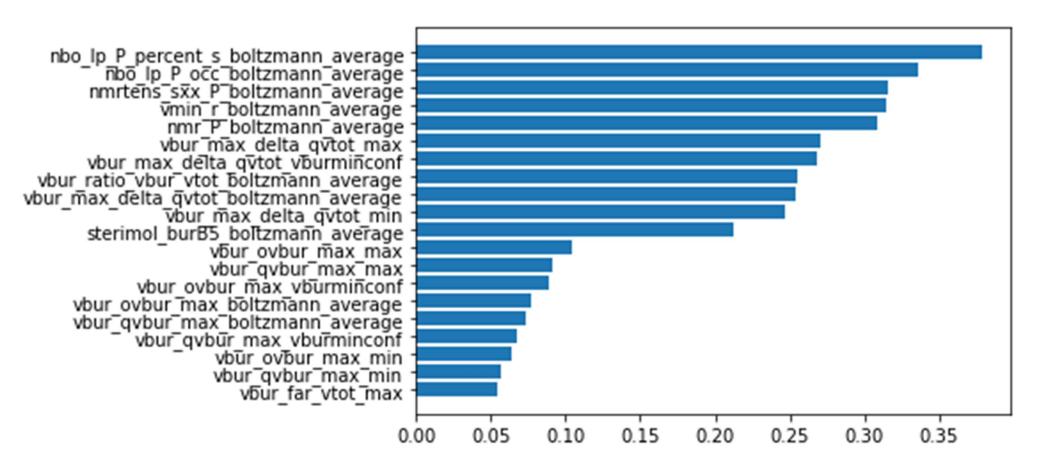


In order to ensure that the organophosphorus ligands would form T-shaped (monoligated) Pd complexes, I restricted this set to the ligands with Boltzmann-average $%V_{bur}$ of 68% or more, very close to the value for tri-t-butylphosphine.

This gave a final set of 107 ligands (small subset pictured).



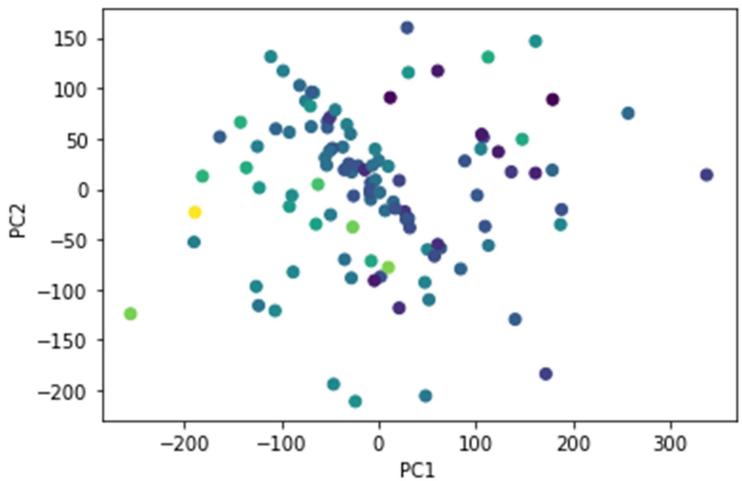
LIGAND SET PRINCIPAL COMPONENT ANALYSIS



Here are the twenty most important features for the first principal component. Notably, electronic features such as Boltzmann-average NBO P lone pair %s and NMR values rank most highly.



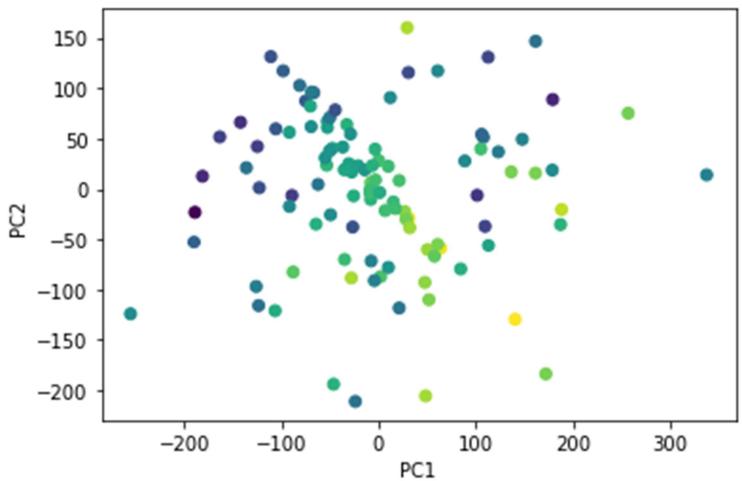
LIGAND SET PRINCIPAL COMPONENT ANALYSIS



PCA on our ligand set, colored according to Boltzmann-average NBO P lone pair %s.



LIGAND SET PRINCIPAL COMPONENT ANALYSIS



PCA on our ligand set, colored according to highest total volume difference in $%V_{bur}$ between two neighboring quadrants.



COMPUTATIONAL WORKFLOW

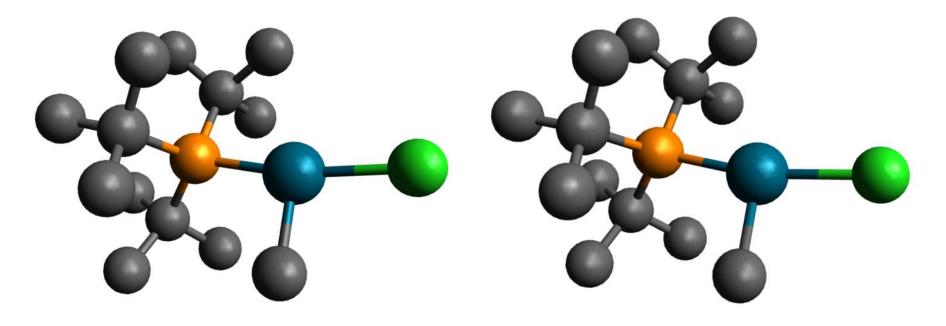
- Gather and prune ligand set from Kraken database
- Generate SMILES strings for methylpalladium chloride T-shaped complexes for each ligand
- Use RDKit to run conformer searches for each complex
- Perform geometry optimizations based on the <u>lowest energy conformer only</u> for each complex (note that currently I am neglecting all other conformers at this time, which I intend to address later with more compute time)
- Perform TDDFT calculations and simulate the UV-vis spectra for each complex, determine the λ_{max} for the relevant transition
- Find trends in λ_{max} and ligand/complex properties
- Use machine learning to build and validate models to predict λ_{max} for other organophosphorus ligands, extract insights
- See the repo at: https://github.com/pmwaddell/pd-c-photochem-ML for the source code, all steps are automated with scripts



DFT: LEVEL OF THEORY, GEOMETRY OPTIMIZATION

Literature X-ray structure

DFT geometry optimized structure



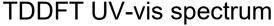
From Nozaki Organometallics 2006, 25, 4588.

(hydrogens omitted)

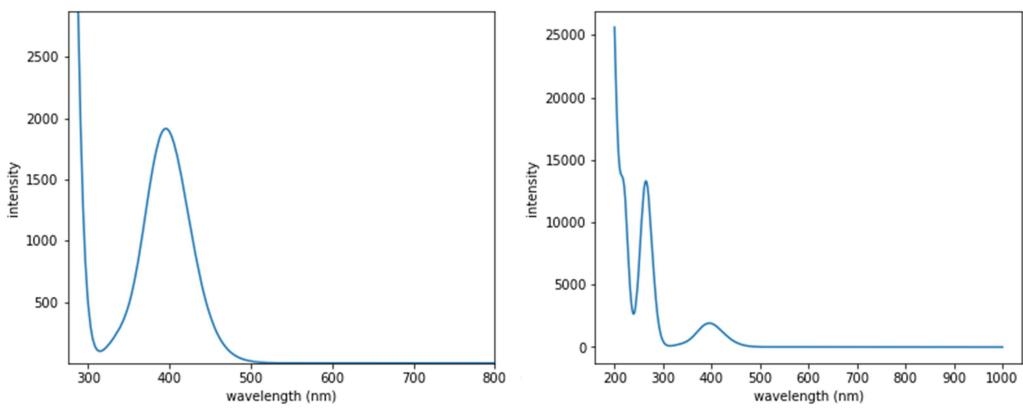
After screening various basis sets and functionals for geometry optimization, **B3LYP-D3/def2-TZVP with CPCM(CHCI₃)** was found to give good agreement (key bond lengths within 0.05 Å, angles within 1°) with the reported X-ray structure while being relatively time-efficient.



DFT: LEVEL OF THEORY, TDDFT



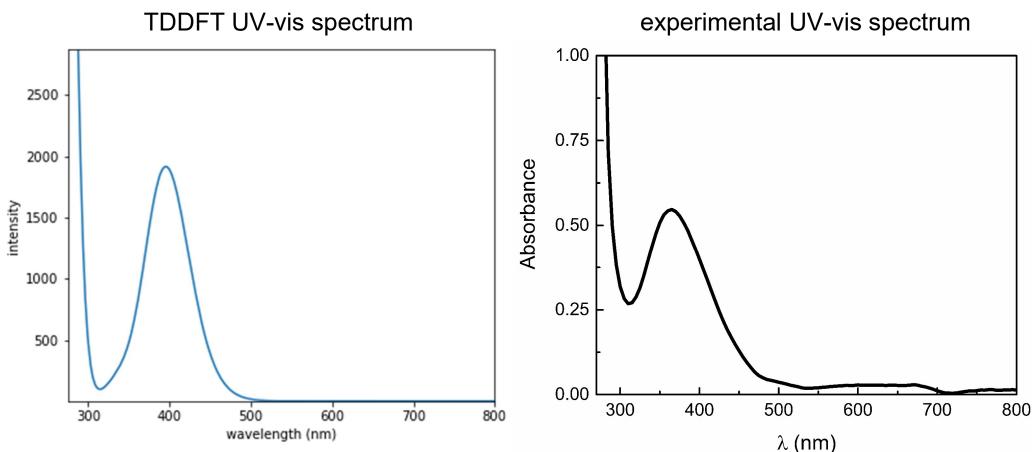
TDDFT UV-vis spectrum, full



For TDDFT calculations, agreement with the experimental UV-vis absorption spectrum benchmark performance. Similarly, **B3LYP/def2-TZVPP** used to was **CPCM(CHCI₃)** was found to give the closest agreement.

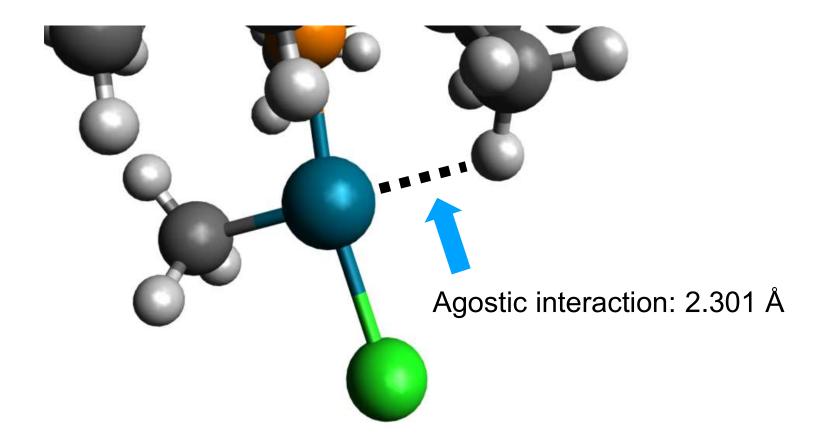


DFT: LEVEL OF THEORY, TDDFT



For TDDFT calculations, agreement with the experimental UV-vis absorption spectrum was used to benchmark performance. Similarly, **B3LYP/def2-TZVPP with CPCM(CHCI₃)** was found to give the closest agreement.

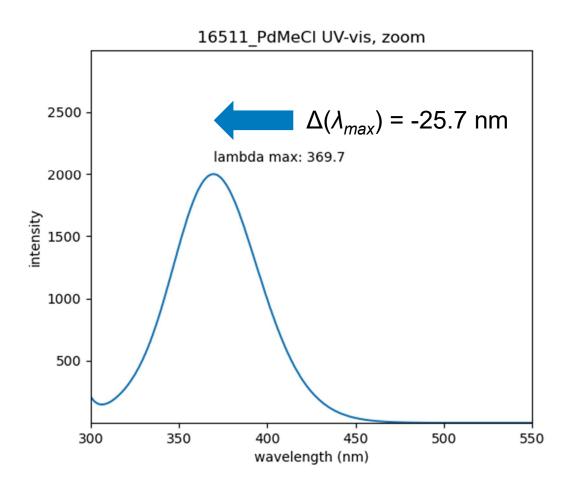


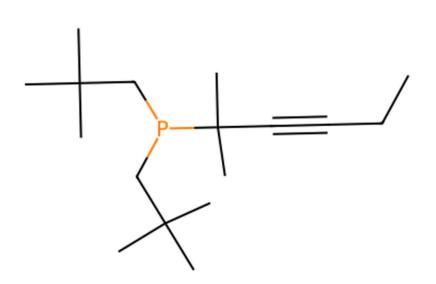


While we refer to these complexes as T-shaped, they often feature an agostic interaction in the fourth site. The distance between Pd and H correlates with the strength of the interaction.

My hypothesis is that the lack of a strong bonding interaction in this site lowers the LUMO (σ^*) energy. Thus, λ_{max} should correlate with agostic interaction strength.



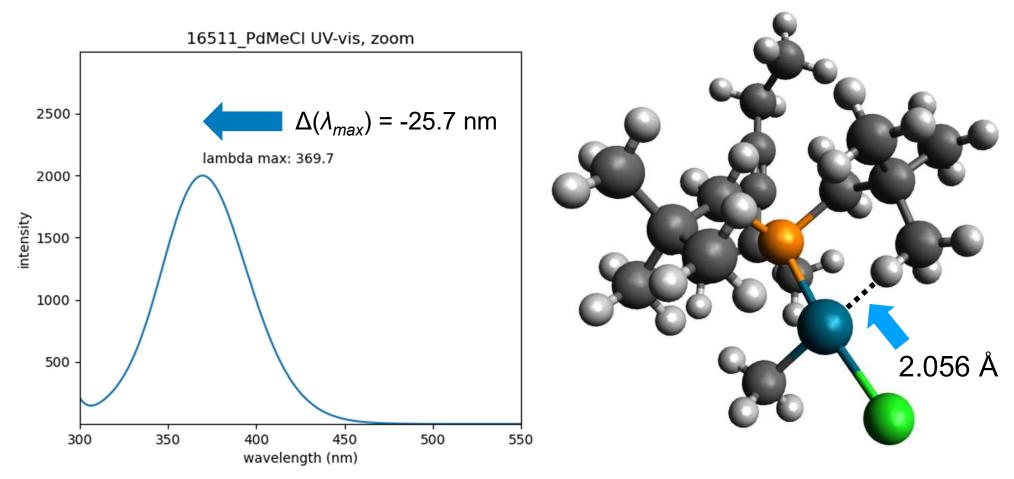




Ligand 16511 (Kraken designation)

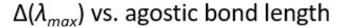
As an example, this ligand features neopentyl groups which allow the H to come in closer proximity to Pd. As a result, the stronger agostic interaction leads to a λ_{max} blueshift of over 25 nm!

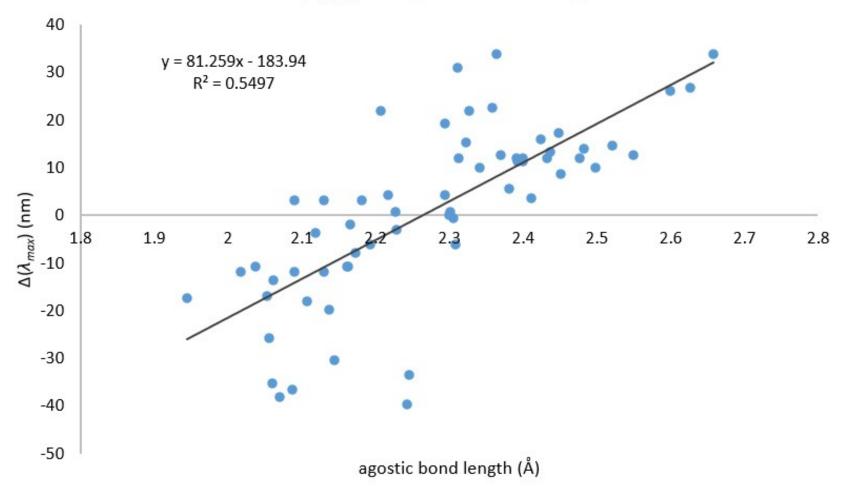




As an example, this ligand features neopentyl groups which allow the H to come in closer proximity to Pd. As a result, the stronger agostic interaction leads to a λ_{max} blueshift of over 25 nm!



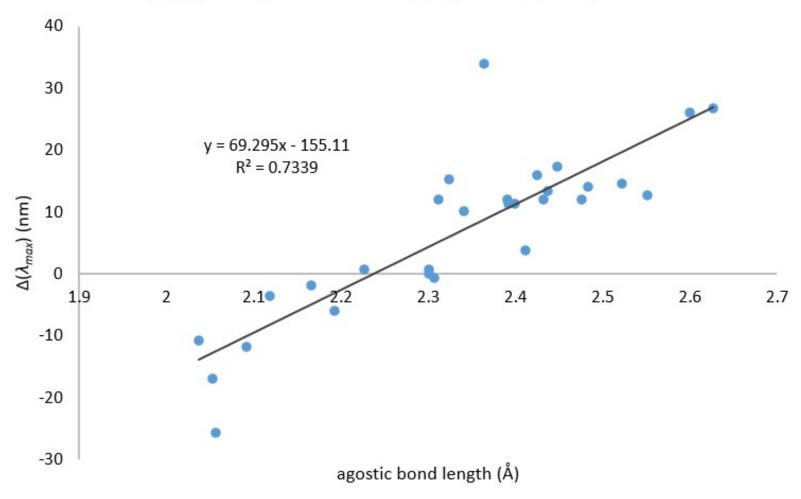




Across all ligands that apparently have an agostic interaction, the correlation between agnostic Pd-H bond length and the change in λ_{max} relative to tri-t-butylphosphine (which we will generally refer to as $\Delta(\lambda_{max})$ is pretty good.



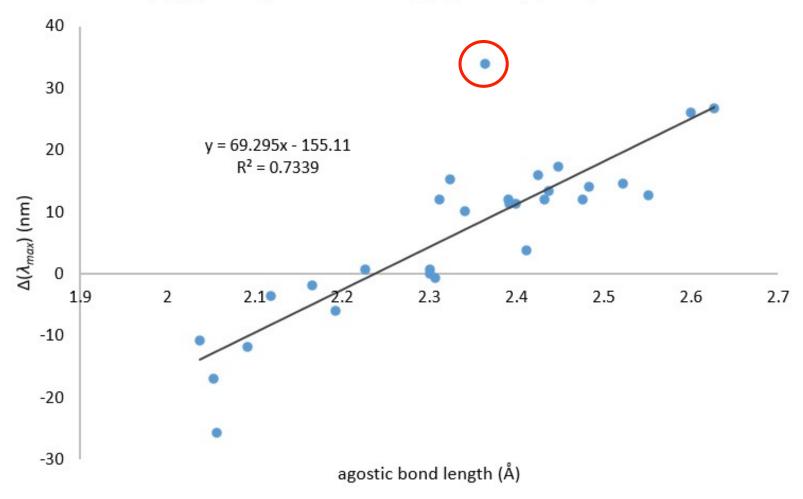
 $\Delta(\lambda_{max})$ vs. agostic bond length, trialkylphosphine-like



If we limit ourselves to trialkylphosphine-like ligands (also including Pd-Si and non-aryl P-Csp²), the correlation improves significantly.

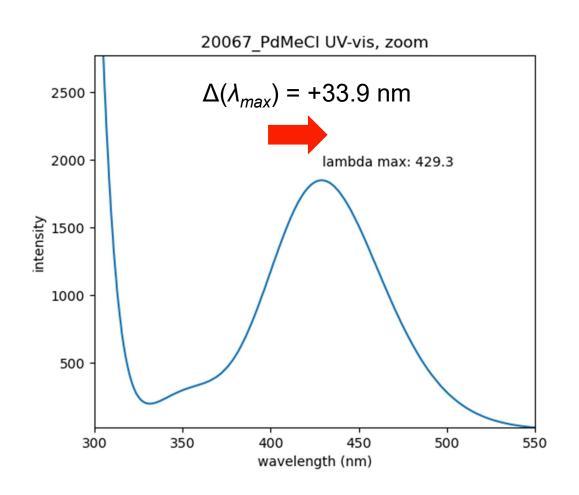


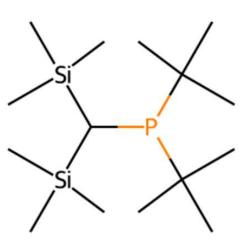
 $\Delta(\lambda_{max})$ vs. agostic bond length, trialkylphosphine-like



One particular case deviates strongly from this relationship, showing a much higher λ_{max} than expected. Can we figure out why?



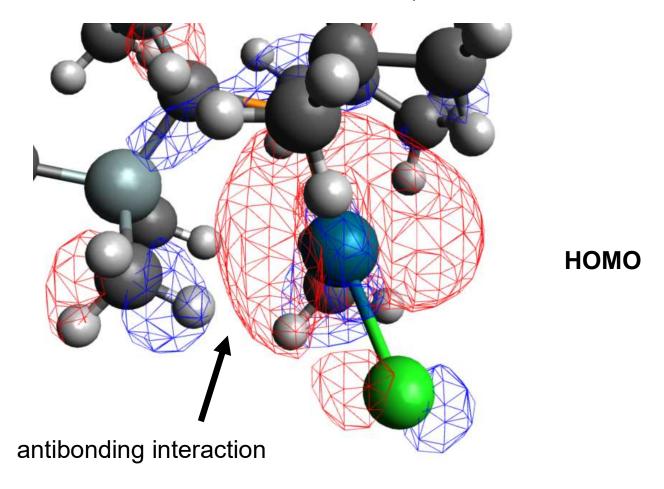




Ligand 20067

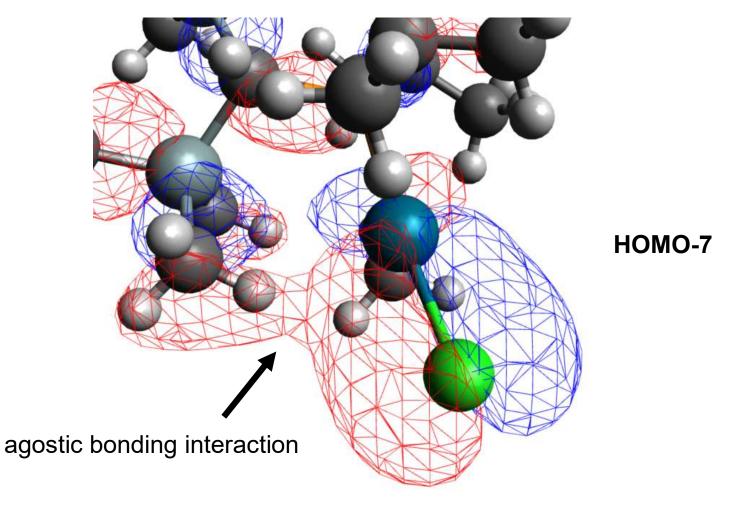
This is the ligand in question, which features large TMS groups on one substituent.





Atoms-in-molecules (AIM) analysis reveals an interaction in the apical position of the coordination sphere, suggesting an agostic interaction. Since the HOMO appears to antibonding character with respect to this interaction, a stronger apical agostic interaction should raise the HOMO energy and thus lower the HOMO-LUMO gap, redshifting λ_{max} .

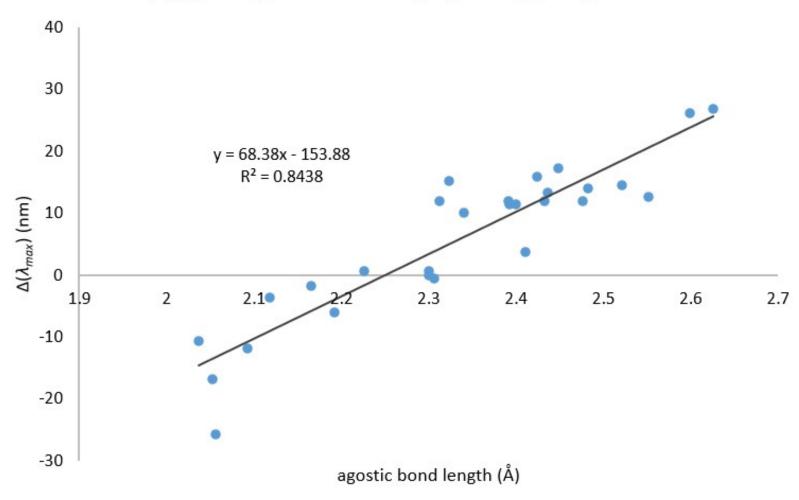




Atoms-in-molecules (AIM) analysis reveals an interaction in the apical position of the coordination sphere, suggesting an agostic interaction. Since the HOMO appears to antibonding character with respect to this interaction, a stronger apical agostic interaction should raise the HOMO energy and thus lower the HOMO-LUMO gap, redshifting λ_{max} .



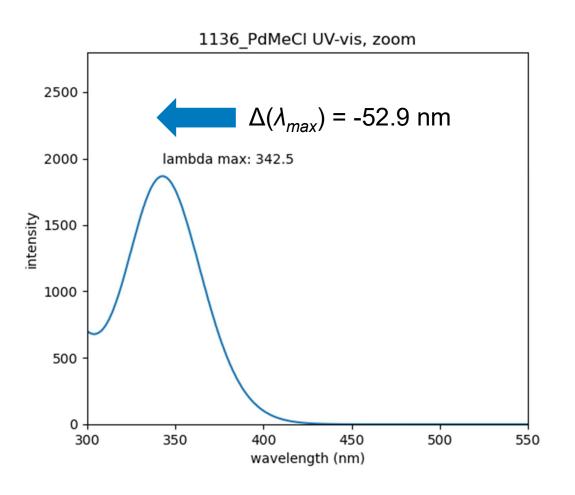
 $\Delta(\lambda_{max})$ vs. agostic bond length, trialkylphosphine-like

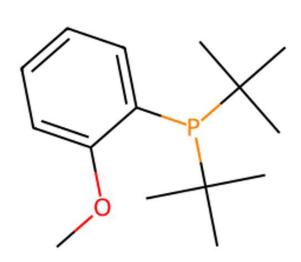


Removing this outlier results in a much stronger correlation, of course.



INITIAL OBSERVATIONS: TRENDS IN λMAX, CHELATION



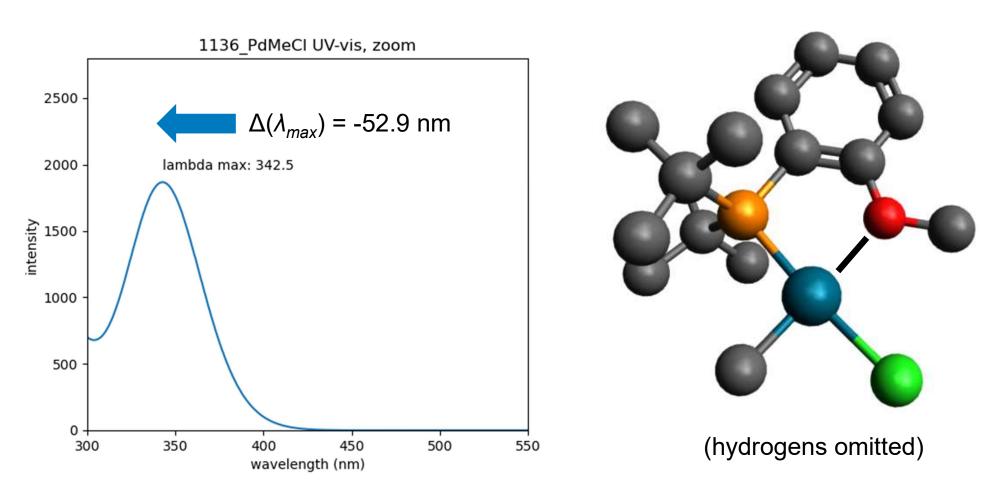


Ligand 1136

Furthermore, for ligands which have pendant heteroatoms that allow chelation, very large λ_{max} blueshifts are observed, again consistent with my hypothesis. Indeed, these complexes are in fact square planar rather than T-shaped.



INITIAL OBSERVATIONS: TRENDS IN λMAX, CHELATION

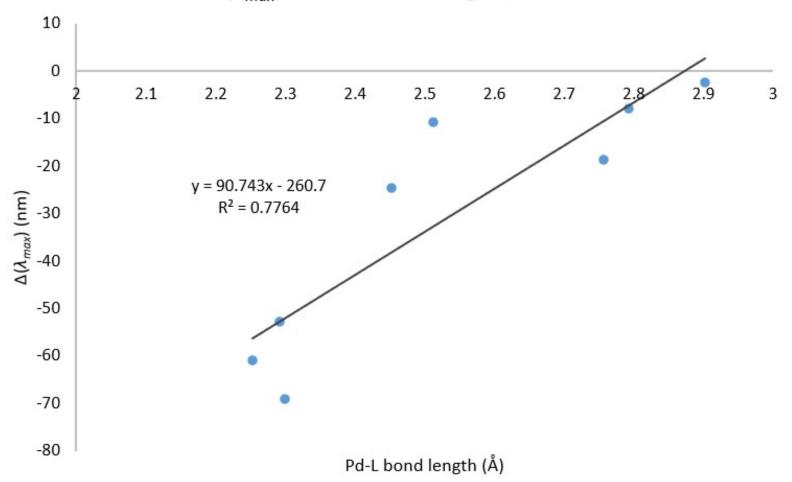


Furthermore, for ligands which have pendant heteroatoms that allow chelation, very large λ_{max} blueshifts are observed, again consistent with my hypothesis. Indeed, these complexes are in fact square planar rather than T-shaped.



INITIAL OBSERVATIONS: TRENDS IN λΜΑΧ, CHELATION

 $\Delta(\lambda_{max})$ vs. Pd-L bond length, chelates

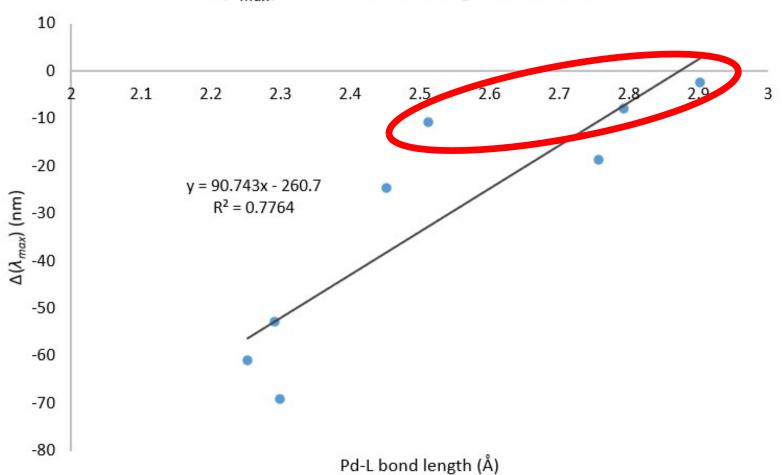


For ligands that form chelates with pendant L-type donors, the distance between Pd and the pendant donor atom correlates pretty well with λ_{max} , even across different types of donors (N, O, S, Cl).



INITIAL OBSERVATIONS: TRENDS IN λMAX, CHELATION

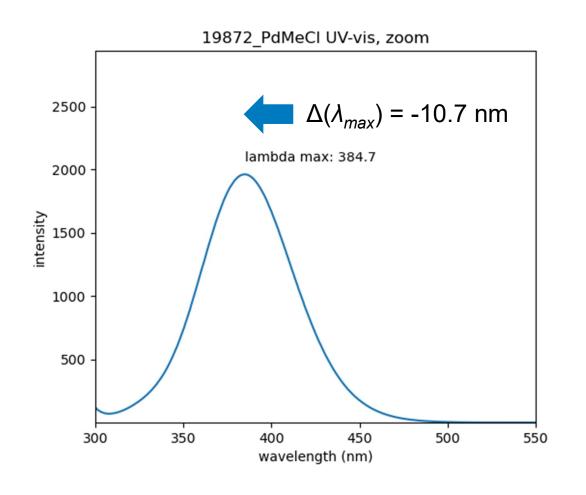
 $\Delta(\lambda_{max})$ vs. Pd-L bond length, chelates

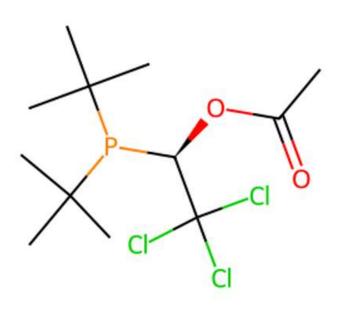


Interestingly, several of the apparently weaker chelates show a minimal blueshift in λ_{max} ! This suggests that Pd-C photocleavage could be accessible with visible light from square planar complexes!



INITIAL OBSERVATIONS: TRENDS IN λΜΑΧ, CHELATION



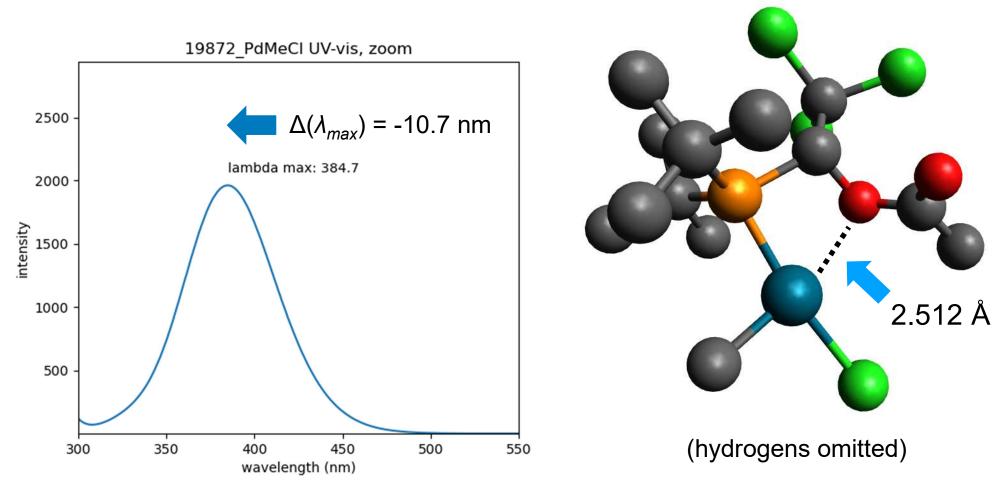


Ligand 19872

For example, consider this complex with a pendant ester has a λ_{max} which is blueshifted by only about 11 nm compared to tri-t-butylphosphine.



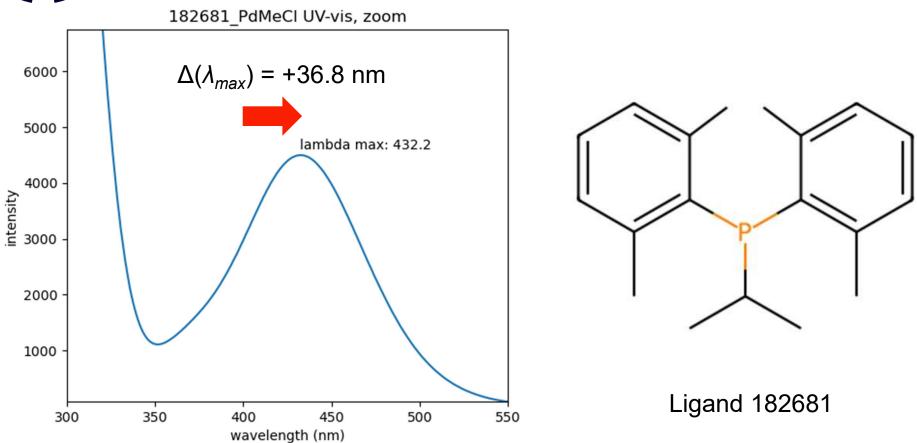
INITIAL OBSERVATIONS: TRENDS IN λMAX, CHELATION



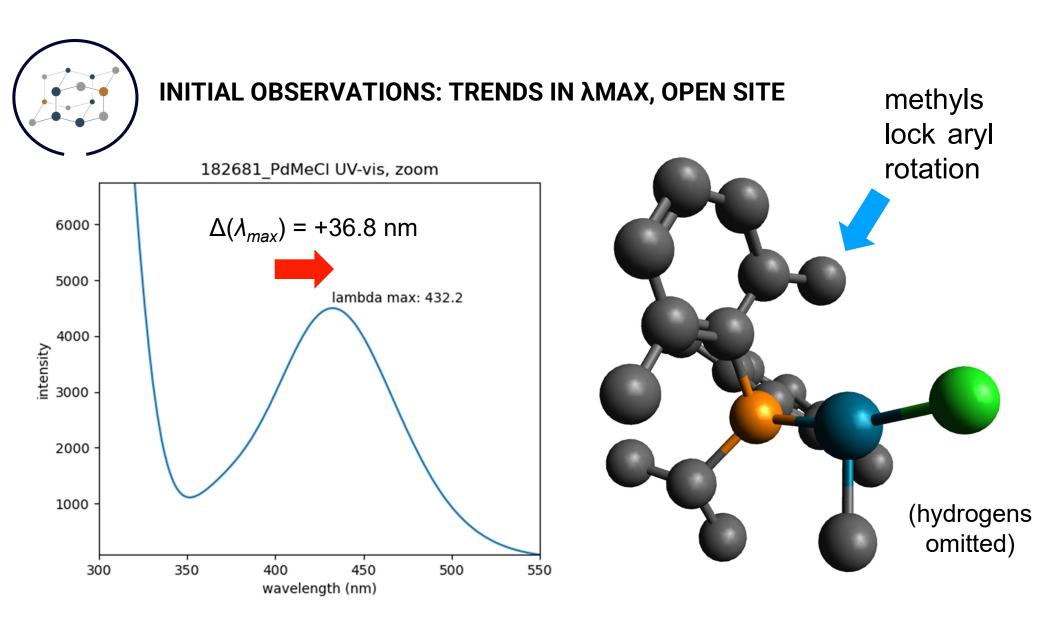
For example, consider this complex with a pendant ester has a λ_{max} which is blueshifted by only about 11 nm compared to tri-t-butylphosphine.



INITIAL OBSERVATIONS: TRENDS IN λMAX, OPEN SITE



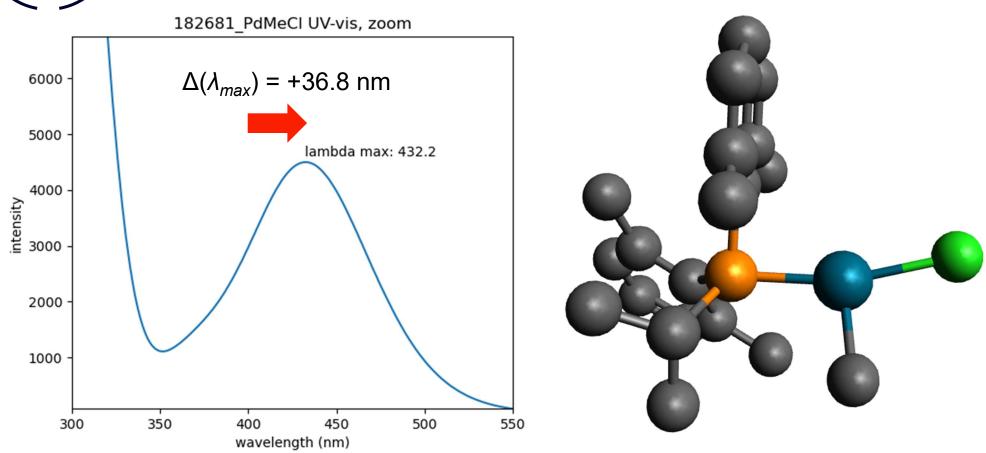
In some cases, the favored ligand conformation appears to leave the fourth site open entirely. In this limiting case, λ_{max} tends to be around 420-430 nm. However, in the condensed phase, this site would be open to occupation by solvent or e.g. bridging Cl ligand, so they may not be a good choice in practice for triggering this photochemistry with low energy light.



In some cases, the favored ligand conformation appears to leave the fourth site open entirely. In this limiting case, λ_{max} tends to be around 420-450 nm. However, in the condensed phase, this site would be open to occupation by solvent or e.g. bridging Cl ligand, so they may not be a good choice in practice for triggering this photochemistry with low energy light.



INITIAL OBSERVATIONS: TRENDS IN λMAX, OPEN SITE



In some cases, the favored ligand conformation appears to leave the fourth site open entirely. In this limiting case, λ_{max} tends to be around 420-430 nm. However, in the condensed phase, this site would be open to occupation by solvent or e.g. bridging Cl ligand, so they may not be a good choice in practice for triggering this photochemistry with low energy light.



So, my hypothesis that the strength of the bonding interaction in the fourth site strongly influences the position of the peak in the absorption spectrum corresponding to the HOMO-LUMO electronic transition (and thus, the wavelength of light that can be used to cause Pd-C homolytic cleavage) seems to be very well validated.

Now, what other factors can we find that influence λ_{max} ?



MACHINE LEARNING MODELS TO PREDICT λMAX: ELASTIC NET

- Our case is highly dimensional: each ligand has 192 features, while we have at most around 100 data points.
- To begin with, let us restrict ourselves to the top 20 features from our principal component analysis from earlier.
- Furthermore, there is significant multicollinearity in our feature set (see next slide)
- Results to come!!

For simplicity, the absolute correlation is shown here, with darker meaning more highly correlated.

nbo_lp_P_percent_s_boltzmann_average -	1	0.87	0.3	0.21	0.31	0.13	0.18	0.16	0.5	0.41	0.078	0.53	0.57	0.74	0.79	0.74	0.8	0.77	0.17
nbo_lp_P_occ_boltzmann_average -	0.87	1	0.22	0.11	0.07	0.074	0.07	0.48	0.29	0.22	0.072	0.48	0.56	0.62	0.76	0.58	0.72	0.72	0.2
nmrtens_sxx_P_boltzmann_average -	0.3	0.22	1	0.095	0.78	0.12	0.19	0.0069	0.052	0.042	0.31	0.28	0.28	0.39	0.5	0.3	0.26	0.16	0.19
vmin_r_boltzmann_average -	0.21	0.11	0.095	1	0.46	0.15	0.21	0.52	0.24	0.17		0.092	0.086	0.41	0.049	0.068	0.36		0.12
	0.31	0.07	0.78	0.46	1		0.011	0.33	0.12	0.058	0.083	0.19	0.058	0.59	0.38	0.25	0.44		0.4
nmr_P_boltzmann_average -																			2.00
vbur_max_delta_qvtot_max -	0.13	0.074	0.12	0.15	0.27	1	0.77	0.42	0.79	0.82	0.53		0.44	0.058	0.18	0.64	0.073	0.29	0.61
vbur_max_delta_qvtot_vburminconf -	0.18	0.07	0.19	0.21	0.011	0.77	1	0.23	0.85	0.87	0.65	0.43		0.15	0.15	0.58	0.26	0.51	0.39
vbur_ratio_vbur_vtot_boltzmann_average -	0.16	0.48	0.0069	0.52	0.33	0.42	0.23	1	0.13	0.1		0.31		0.026	0.44	0.26	0.12	0.2	0.33
vbur_max_delta_qvtot_boltzmann_average -	0.5	0.29	0.052	0.24	0.12	0.79	0.85	0.13	1	0.93	0.48	0.55	0.53			0.79	0.35	0.59	0.47
vbur_max_delta_qvtot_min -	0.41	0.22	0.042	0.17	0.058	0.82	0.87	0.1	0.93	1	0.43					0.8	0.41	0.61	0.35
sterimol_burB5_boltzmann_average -	0.078	0.072			0.083	0.53	0.65		0.48	0.43	1	0.36		0.15	0.12		0.22	0.36	0.43
vbur_ovbur_max_max -	0.53	0.48		0.092	0.19		0.43		0.55		0.36	1	0.74	0.37	0.55	0.58		0.52	0.4
vbur_qvbur_max_max -	0.57	0.56		0.086	0.058	0.44			0.53			0.74	1	0.43	0.57	0.63	0.43	0.49	0.74
vbur_ovbur_max_vburminconf -	0.74	0.62	0.39	0.41	0.59	0.058	0.15	0.026	0.27		0.15	0.37	0.43	1	0.75	0.61	0.96	0.83	0.0041
vbur_ovbur_max_boltzmann_average -	0.79	0.76	0.5	0.049	0.38	0.18	0.15	0.44			0.12	0.55	0.57	0.75	1	0.76	0.81	0.68	0.07
vbur_qvbur_max_boltzmann_average -	0.74	0.58	0.3	0.068	0.25	0.64	0.58	0.26	0.79	0.8	0.32	0.58	0.63	0.61	0.76	1	0.7	0.75	0.35
vbur_ovbur_max_min -	0.8	0.72		0.36	0.44	0.073	0.26	0.12	0.35	0.41	0.22	0.37	0.43	0.96	0.81	0.7	1	0.89	0.024
vbur_qvbur_max_min -	0.77	0.72	0.16	0.28	0.3	0.29	0.51	0.2	0.59	0.61	0.36	0.52	0.49	0.83	0.68	0.75	0.89	1	0.2
vbur_far_vtot_max -	_	0.2	0.19	0.12	0.4	0.61	0.39		0.47	0.35	0.43	0.4	0.74	0.0041	0.07	0.35	0.024	0.2	1
40d1_id1_400C_iiidx =	-	.		,					,					,					
	ann_avera	ann_avera	ann_avera	vmin_r_boltzmann_average	nmr_P_boltzmann_average	vbur_max_delta_qvtot_max	vburminco	ann_avera	ann_avera	vbur_max_delta_qvtot_min	ann_avera	vbur_ovbur_max_max	vbur_qvbur_max_max	vbur_ovbur_max_vburminconf	ann_avera	ann_avera	vbur_ovbur_max_min	vbur_qvbur_max_min	wbur_far_vtot_max
	s_boltzm	.c_boltzm	P_boltzm	r_boltzm	P_boltzm	max_delt	lta_qvtot_	ot_boltzm	ot_boltzm.	max_del	5_boltzm	vbur_ovb	vbur_qvb	bur_max_	x_boltzm	mz_boltzm	vbur_ovk	vbur_qvt	vpnr
	nbo_lp_P_percent_s_boltzmann_average	nbo_lp_P_occ_boltzmann_average	nmrtens_sxx_P_boltzmann_average	vmin	nmr	vbur	vbur_max_delta_qvtot_vburminconf	ibur_ratio_vbur_vtot_boltzmann_average	ur_max_delta_qvtot_boltzmann_average	ngv	sterimol_burB5_boltzmann_average			vo_ruqv	vbur_ovbur_max_boltzmann_average	vbur_qvbur_max_boltzmann_average			
	d odn	겉	Ē				ngx	⁄bur_ratio	ur_max_		ster				vbur	vbur			



To be continued...