Ab-initio Methodologies for Prediction of Bridge-Mediated Electronic Coupling: Through Space and Through Bond Interactions.

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ABSTRACT: A Density Functional Theory-based Green's Function Pathway Model is developed enabling further advancements towards the long-standing challenge of accurate yet inexpensive prediction of electron transfer rate. Electronic coupling predictions are demonstrated to within 0.1 eV of experiment for organic and biological systems of moderately large size, with modest computational expense. Benchmarking and comparisons are made across density functional type, basis set extent, and orbital localization scheme. The resulting framework is shown to be flexible and to offer quantitative prediction of both electronic coupling and tunneling pathways in covalently bound non-adiabatic donor-bridge-acceptor (D-B-A) systems. A new LMO-GFM Pathways adaptation enables a more intuitive understanding of electron tunneling in terms of through-bond and through-space interactions.

Electronic Supplementary Information

Table S1. Basis set study of effective Hamiltonian predictions of T_{DA} with B97-D, as a function of basis set for Set A molecules **1-5**.

	IT _{DA} I (eV)								
			Molecule						
Method/Basis:	5	4	3	2	1				
B97-D/STO-3G	0.0126	0.0458	0.0575	0.1732	0.4445				
B97-D/STO-6G	0.0127	0.0468	0.0574	0.1744	0.4417				
B97-D /Def2-SVP	0.0224	0.0419	0.0748	0.1718	0.5469				
B97-D /3-21G	0.0214	0.0475	0.0692	0.1719	0.4771				
B97-D /6-31G	0.0209	0.0509	0.0692	0.1706	0.476				
B97-D/6-31G(d)	0.0209	0.0494	0.0701	0.1727	0.4858				
B97-D /6-31G(p)	0.0209	0.0386	0.069	0.1556	0.476				
B97-D /6-31G(d,p)	0.021	0.0392	0.0697	0.1567	0.4858				
B97-D/6-31G(2d,p)	0.0205	0.0386	0.0688	0.1558	0.4847				
B97-D /6-311G	0.021	0.0401	0.0684	0.1581	0.4781				
B97-D/6-311G(d)	0.0207	0.0391	0.068	0.1584	0.4803				
B97-D /6-311G(p)	0.0213	0.0387	0.0683	0.1543	0.4761				
B97-D /6-311G(d,p)	0.0211	0.0388	0.068	0.1536	0.4817				
B97-D /6-311G(2d,p)	0.0214	0.0393	0.0695	0.1556	0.483				
B97-D /6-311G(2df,2pd)	0.0213	0.0389	0.0682	0.1531	0.4799				
B97-D /TZV(p)	0.0226	0.0408	0.0708	0.1592	0.4931				
B97-D /TZV(2p)	0.0228	0.0411	0.0713	0.1603	0.4931				
B97-D /Def2-TZVP	0.0217	0.0395	0.0684	0.1543	0.4783				
B97-D /Def2-TZVPP	0.0218	0.0397	0.0684	0.1543	0.4782				
B97-D /6-31+G(d,p)	0.0318	DNC	0.1565	0.1933	0.484				
B97-D/6-31+G(2d,p)	0.0526	0.0644	0.1439	0.2179	0.5156				
B97-D /6-311+G	DNC	DNC	0.4455	0.349	0.5354				
B97-D /6-311+G(d,p)	DNC	DNC	0.1841	0.298	0.6294				
B97-D /6-311+G(2d,p)	0.0347	DNC	DNC	0.2454	0.6529				

DNC= data not converged



Figure S1. Analogous basis set study conducted with Hartree-Fock for T_{DA} predictions of Set A molecules 1-5, yielding the same overestimation of T_{DA} when pairing to diffuse basis sets.

Table S2. Raw data from Figure S1, for Hartree-Fock basis set study, T_{DA} predictions in (eV) for Set A molecules 1-5.

	T _{DA} (eV)										
	Molecule										
Method/Basis:	1	2	3	4	5						
HF/STO-3G	0.5828	0.2392	0.0579	0.0667	0.0204						
HF/STO-6G	0.5778	0.2390	0.0571	0.0670	0.0202						
HF/Def2-SVP	0.7233	0.2275	0.0631	0.0428	0.0284						
HF/3-21G	0.6447	0.2310	0.0641	0.0536	0.0339						
HF/6-31G	0.6308	0.2169	0.0622	0.0522	0.0310						
HF/6-31G(d)	0.6281	0.2066	0.0577	0.0450	0.0264						
HF/6-31G(p)	0.6343	0.2166	0.0577	0.0440	0.0309						
HF/6-31G(d,p)	0.6287	0.2034	0.0576	0.0394	0.0267						
HF/6-31G(2d,p)	0.6302	0.2032	0.0572	0.0391	0.0263						
HF/6-311G	0.6565	0.2210	0.0651	0.0473	0.0322						
HF/6-311G(d)	0.6381	0.2059	0.0572	0.0398	0.0266						
HF/6-311G(p)	0.6542	0.2221	0.0655	0.0453	0.0314						
HF/6-311G(d,p)	0.6405	0.2052	0.0572	0.0397	0.0270						

7/6-311G(2d,p)	0.6312	0 2020	0.0570	0.0000	
(6.211C(2df 2md))	0.0512	0.2039	0.0572	0.0393	0.0270
70-5110(2a1,2pa)	0.6207	0.1990	0.0556	0.0385	0.0266
TZV(p)	0.8702	0.3424	0.1132	0.0703	0.0481
/TZV(2p)	0.8148	0.3382	0.1099	0.0656	0.0371
/Def2-TZVP	0.6209	0.1975	0.0545	0.0381	0.0262
/Def2-TZVPP	0.6173	0.1975	0.0545	0.0381	0.0381
6/6-31+G(d,p)	0.8086	0.3843	0.1073	0.0829	0.0616
6/6-31+G(2d,p)	0.8001	0.4560	0.4049	DNC	DNC
6/6-311+G	0.9116	0.3029	0.2202	0.0838	0.0515
6/6-311+G(d,p)	0.9996	0.4875	0.1269	0.0532	0.0336
6/6-311+G(2d,p)	1.2561	0.5085	0.1016	0.0833	0.0543
7/TZV(p) 7/TZV(2p) 7/Def2-TZVP 7/Def2-TZVP 7/0-31+G(d,p) 7/0-31+G(2d,p) 7/0-311+G 7/0-311+G(d,p) 7/0-311+G(d,p) 7/0-311+G(2d,p)	0.8702 0.8148 0.6209 0.6173 0.8086 0.8001 0.9116 0.9996 1.2561	0.3424 0.3382 0.1975 0.1975 0.3843 0.4560 0.3029 0.4875 0.5085	0.1132 0.1099 0.0545 0.0545 0.1073 0.4049 0.2202 0.1269 0.1016	0.0703 0.0656 0.0381 0.0381 0.0829 DNC 0.0838 0.0532 0.0833	0.0481 0.0371 0.0262 0.0381 0.0616 DNC 0.0515 0.0336 0.0543

DNC= data not converged

Table S3. Full tabulation of calculated T_{DA} (eV) coupling elements for Set B as a function of density functional type and orbital localization method, using the 6-311G(2df,2pd) basis set. MAE error presented with respect to experimental measurements of T_{DA} (photoelectron spectroscopy exeriments⁴⁰ determining IP₁ and IP₂, such that T_{DA} is $\frac{1}{2}\Delta IP$

		Pipek-Mezey Localization applied to T _{DA} (eV) predictions										
Molecule	Expt. ⁴⁰ T _{DA} (eV)	B3LYP	BLYP	PBE	PBE0	M06-L	M06	M06-2X	M06-HF	B97-D	wB97X-D	RHF
4	0.16	0.164	0.148	0.159	0.181	0.160	0.164	0.206	0.281	0.153	0.195	0.199
5	0.435	0.509	0.473	0.491	0.542	0.494	0.515	0.580	0.687	0.480	0.566	0.621
6	0.43	0.496	0.473	0.445	0.484	0.447	0.469	0.472	0.517	0.460	0.490	0.652
7	0.22	0.195	0.175	0.180	0.209	0.192	0.198	0.244	0.317	0.180	0.226	0.252
8	0.63	0.798	0.737	0.762	0.837	0.790	0.794	0.869	1.037	0.751	0.881	1.026
9	0.215	0.262	0.242	0.253	0.282	0.252	0.262	0.294	0.366	0.246	0.295	0.322
10	0.26	0.343	0.326	0.351	0.371	0.341	0.344	0.393	0.462	0.332	0.395	0.374
11	0.09	0.097	0.094	0.101	0.104	0.090	0.095	0.116	0.146	0.096	0.109	0.092
	MAE Error:	0.059	0.028	0.048	0.074	0.048	0.050	0.092	0.172	0.044	0.089	0.137
		Boys Localization applied to T _{DA} (eV) predictions										
Molecule	Expt. ⁴⁰ T _{DA} (eV)	B3LYP	BLYP	PBE	PBE0	M06-L	M06	M06-2X	M06-HF	B97-D	wB97-D	RHF
4	0.16	0.322	0.290	0.310	0.352	0.313	0.324	0.384	0.530	0.301	0.377	0.390
5	0.435	0.986	0.913	0.951	1.051	0.966	0.995	1.124	1.332	0.930	1.099	1.184
6	0.43	0.939	0.873	0.861	0.946	0.870	0.908	0.922	0.993	0.876	0.950	1.249
7	0.22	0.378	0.341	0.349	0.408	0.374	0.384	0.475	0.619	0.351	0.436	0.479
8	0.63	1.561	1.429	1.410	1.615	1.406	1.502	1.678	1.993	1.400	1.660	2.082
9	0.215	0.511	0.469	0.789	0.550	0.492	0.511	0.577	0.705	0.480	0.578	0.612
10	0.26	0.658	0.629	0.681	0.714	0.652	0.659	0.760	0.884	0.638	0.753	0.698
11	0.09	0.187	0.183	0.190	0.202	0.180	0.184	0.232	0.287	0.181	0.209	0.171
	MAE error:	0.388	0.336	0.388	0.425	0.352	0.378	0.464	0.613	0.340	0.453	0.553
				E-F	R Locali	zation a	pplied	to T _{DA} (e	V) predic	tions		
Molecule	Expt. ⁴⁰ T _{DA} (eV)	B3LYP	BLYP	PBE	PBE0	M06-L	M06	M06-2X	M06-HF	B97-D	wB97-D	RHF

4	0.16	0.305	0.275	0.298	0.357	0.550	0.309	0.389	0.550	0.305	0.364	0.366
5	0.435	0.951	0.881	0.929	1.019	1.294	0.958	1.097	1.293	0.900	1.066	1.152
6	0.43	0.915	0.852	0.846	0.926	0.972	0.890	0.905	0.972	0.858	0.932	1.219
7	0.22	0.364	0.326	0.342	0.394	0.598	0.370	0.465	0.598	0.180	0.424	0.465
8	0.63	1.388	1.285	1.336	1.464	1.836	1.385	1.560	1.836	1.295	1.537	1.754
9	0.215	0.484	0.445	0.476	0.526	0.678	0.488	0.553	0.678	0.458	0.551	0.592
10	0.26	0.626	0.637	0.683	0.684	0.909	0.629	0.730	0.909	0.644	0.769	0.671
11	0.09	0.178	0.173	0.188	0.194	0.280	0.176	0.223	0.280	0.177	0.203	0.166
	MAE Error:	0.347	0.304	0.332	0.391	0.585	0.346	0.435	0.585	0.307	0.426	0.493

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