

Small Representative Databases for Testing and Validating Density Functionals and Other Electronic Structure Methods

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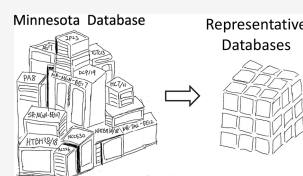
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ABSTRACT: Broad and diverse sets of accurate data provide useful metrics for assessing the performance of new theoretical methods. However, assessing methods against large databases can be an arduous task. Here, we present 17 representative energetic databases, defined as small databases whose errors and error spreads are representative of larger databases and which therefore can serve as efficient benchmarks for developing and testing electronic structure methods and density functionals. In 15 cases, the representative databases have 6 entries while being representative of larger databases with 14–107 entries, and in the other two cases, they have 14 entries while being representative of larger databases with 418–455 entries. The mean unsigned error (MUE) of 100 electronic structure methods on a given representative database is typically within about 8% of the MUE on its parent database, and the root-mean-square error (RMSE) is typically within about 11% of the RMSE on the parent database. Thus, the representative databases are quite successful in indicating accuracy while maintaining good diversity. The databases include both main-group and transition-metal compounds and reactions, and they include bond energies, reaction energies, barrier heights, noncovalent interactions, ionization potentials, and absolute energies.



1. INTRODUCTION

Testing approximate quantum mechanical methods against databases of accurate data plays a major role in validating electronic structure methods used in chemistry, and such databases can also be used during method development. Considerable effort has gone into developing large databases.^{1–13} However, especially in exploratory stages of method development or when the goal is to test a large number of methods, it is also useful to have smaller databases, provided that they are representative of the larger ones in terms of difficulty and range of chemical characteristics.^{14,15} The objective of the work reported here was to develop small databases that are representative of larger ones.

There are several major broad databases that have been used for developing or testing density functionals.^{6,7,9–11,16} The current work starts with Minnesota Database 2019, which has been used to develop Minnesota density functionals. Minnesota Database 2019 is diverse in that it involves many subdatabases, including several that go beyond the main group; it involves main-group bond energies, transition-metal bond energies, reaction barrier heights, noncovalent interactions, ionization potentials, electron affinities, proton affinities, isomerization energies, atomic energies, excitation energies, and geometries. Most of the reference values of Minnesota Database 2019 come from experimental values, and, where relevant, the spin–orbit coupling and zero-point energies have been removed so that the data can be directly compared to energetic electronic structure calculations without computing frequencies or spin–orbit couplings.

2. METHODS

2.1. Parent Databases. We consider a major subset of Minnesota Database 2019⁹; the subset involves 34 subdatabases that are listed in Table 1. Subdatabases 1–25 have been used for both training and testing the revM11 Minnesota functional, and subdatabases 26–34 were used only for testing; the subdatabases were named previously,¹⁰ and we retain those names. The naming convention for each subdatabase is AAM, where AA is an abbreviation describing the type of data and M is the number of data points, for example HTBH38 denotes the Hydrogen-Transfer Barrier Heights database, which has 38 data points; however, if the given database has been updated without changing the number of data points, we use AAM/YY, where YY denotes the last two digits of the year of the update; for example, HTBH38/18 denotes the version updated in 2018. A special situation occurs when the number of data points is given by a product, for example, SIE4 × 4 has 16 data points. Detailed descriptions of Minnesota Database 2019, including citations for the reference data, can be found in ref 10.

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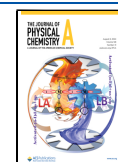


Table 1. All Databases Used in this Work

no.	database	description
1	SR-MGM-BE8	single-reference main-group metal bond energies
2	SR-MGN-BE107	single-reference main-group nonmetal bond energies
3	SR-TM-BE15	single-reference transition-metal bond energies
4	MR-MGM-BE4	multireference main-group metal bond energies
5	MR-MGN-BE17	multireference main-group nonmetal bond energies
6	MR-TML-BE12	multireference transition-metal ligand bond energies
7	MR-TMD-BE3	multireference transition-metal dimer bond energies
8	HTBH38/18	hydrogen-transfer barrier heights
9	NHTBH38/18	non-hydrogen-transfer barrier heights
10	NCCE30/18	noncovalent complexation energies
11	NGD21/18	noble gas dimer weak interactions
12	IP23	ionization potentials
13	EA13/03	electron affinities
14	PA8	proton affinities
15	2pIsoE4	2p isomerization energies
16	4pIsoE4	4p isomerization energies
17	IsoL6/11	isomerization energies of large molecules
18	π TC13	thermochemistry of π systems
19	AE17	atomic energies
20	HC7/11	hydrocarbon chemistry
21	SMAE3/19	sulfur molecule atomization energies
22	DC9/19	difficult cases
23	3dAEE8	3d transition-metal atomic excitation energies
24	4dAEE5	4d transition-metal atomic excitation energies
25	pAEE5	p-block atomic excitation energies
26	Al2 \times 6	dimerization energies of aluminum compounds
27	BHDIV10	barrier heights of diverse reactions
28	BHPERI26	barrier heights of pericyclic reactions
29	BHROT27	barrier heights for rotation around single bonds
30	DIPCS10	double-ionization potentials of closed-shell systems
31	HeavySB11	dissociation energies in heavy-element compounds
32	PX13	proton-exchange barriers in H ₂ O, NH ₃ , and HF clusters
33	SIE4 \times 4	self-interaction-errors
34	YBDE18	ylide bond-dissociation energies

The representative databases developed in the present work are representatives of parent databases, which are either combined subdatabases of Minnesota Database 2019 or a single subdatabase of Minnesota Database 2019. In this work, we consider 17 parent databases, which are listed in Table 2. Parent databases 1–8 are combined subdatabases of Minnesota Database 2019, and parent databases 9–17 are single subdatabases of Minnesota Database 2019.

All data in the databases have units of energy and correspond to calculations done with a fixed set of reference geometries. The reference geometries for the full set of databases are available in ref 8. The reference geometries of the representative databases are repeated in the Supporting Information (SI) of the present paper for the convenience of users.

The 8 parent databases obtained by combining subdatabases of Minnesota Database 2019 are as follows (where the naming convention is the same as already explained): 27 transition-metal bond energies (TMBE27), 139 barrier heights (BH139), 40 transition-metal data points (TM40), 14 isomerization energies (IsoE14), 174 main-group bond energies (MGBE174), 33 ionization potentials (SDIP33), 418

Table 2. Parent Databases and Their Composition

no.	parent database	description and constituents
1	TMBE27	transition-metal bond energies: SR-TM-BE15 + MR-TML-BE12
2	BH139	barrier heights: HTBH38/18 + NHTBH38/18 + BHDIV10 + BHPERI26 + BHROT27
3	TM40	transition metal data: SR-TM-BE15 + MR-TML-BE12 + 3dAEE8 + 4dAEE5
4	IsoE14	isomerization energies: 2pIsoE4 + 4pIsoE4 + IsoL6/11
5	MGBE174	main-group bond energies: MR-MGM-BE4 + MR-MGN-BE17 + SR-MGN-BE107 + SR-MGM-BE8 + SMAE3/19 + Al2 \times 6 + HeavySB11 + YBDE18
6	SDIP33	single and double-ionization potentials: IP23 + DIPCS10
7	EMNT418	energetic portion of Minnesota training database: databases 1–25 in Table 1
8	EMNTT555	energetic portion of Minnesota training and testing database: databases 1–34 in Table 1
9	AE17	one constituent: AE17
10	HTBH38/18	one constituent: HTBH38/18
11	NHTBH38/18	one constituent: NHTBH38/18
12	SR-MGN-BE107	one constituent: SR-MGN-BE107
13	NCCE30	one constituent: NCCE30
14	NGD21	one constituent: NGD21
15	BHPERI26	one constituent: BHPERI26
16	BHROT27	one constituent: BHROT27
17	IP23	one constituent: IP23

Minnesota training data points (EMNT418), and 555 Minnesota training and testing data points (EMNTT555). The EMNTT555 database contains all the data considered in the current work. Notice that in BH139, unlike some barrier height databases, not every reaction included has both a forward and a reverse barrier height; therefore, the number of barrier heights can be odd and is odd.

Each of the 555 data points is computed with Hartree–Fock theory (HF), 42 Kohn–Sham local density functionals, and 57 hybrid density functionals, making a total of 100 electronic structure methods. The 99 considered density functionals are listed in Table 3. All energies are Born–Oppenheimer electronic energies; that is, they do not include vibrational zero-point energy or thermal contributions.

The basis sets used for the various approximate calculations with the 100 electronic structure methods are specified in previous papers presenting subdatabases of Minnesota Database 2019. We do not repeat this kind of detail here since it is irrelevant to the usage of the representative databases, which may be used with any method and any basis set.

2.2. Representative Databases. All equations in this section refer to a given parent database with M data points. Denote a reference datum as $Q_{i,\text{ref}}$ (where $i = 1, 2, \dots, M$), and denote a value calculated by electronic structure method α (where $\alpha = \text{HF}$ or a density functional theory with one of the 99 density functionals) as $Q_{i,\alpha}$. For that method, we define the mean unsigned error (MUE), mean signed error (MSE), and root-mean-square error (RMSE) for the given parent database as

$$\text{MUE}_\alpha = \frac{1}{M} \sum_{i=1}^M [Q_{i,\alpha} - Q_{i,\text{ref}}] \quad (1)$$

Table 3. Density Functionals

no.	type ^a	functional	X ^b	year	ref	no.	type ^a	functional	X ^b	year	ref
local						nonlocal					
1	LSDA	GKSVWN5	0	1980	18–21	57		X3LYP	21.8	2004	65
2		GKSVWN3	0	1980	18–21	58		MPW3LYP	21.8	2004	66
3	GGA-SO (second-order exchange)	SOGGA	0	2008	22	59		MPWLYP1M	5	2005	38
4		PBEsol	0	2008	23	60		B97–3	26.93	2005	67
5		SOGGA11	0	2011	24	61		SOGGA11-X	35.42	2011	68
6	GGA	B86P86	0	1986	25, 26	62	global-hybrid GGA + MM	B3LYP-D3(BJ)	20	2011	
7		B86LYP	0	1987	25, 27	63	RS-hybrid GGA	CAM-B3LYP	19–65	2004	69
8		BP86	0	1988	26, 28	64		LC- <i>ω</i> PBE	0–100	2006	70–73
9		BLYP	0	1988	27, 28	65		HSE06	25–0	2006	74, 75
10		BR89LYP	0	1989	27, 29	66		HISS	0–60–0	2008	76
11		B86PW91	0	1991	25, 30	67		<i>ω</i> B97	0–100	2008	77
12		PW91	0	1991	30	68		<i>ω</i> B97X	15.77-	2008	77
13		BPW91	0	1991	28, 30	69	RS-hybrid NGA	N12-SX	25–0	2012	78
14		PBE	0	1996	31	70	RS-hybrid GGA + MM	<i>ω</i> B97X-D	22.2–100	2008	79
15		mPW	0	1997	32	71	global-hybrid meta-GGA	TPSSH	10	2002	80
16		revPBE	0	1997	33	72		<i>τ</i> -HCTHhyb	15	2002	45
17		RPBE	0	1999	34	73		BB1K	42	2004	28, 58, 81
18		HCTH407	0	2001	2	74		MPWB1K	44	2004	66
19		OLYP	0	2001	27, 35	75		MPW1B95	31	2004	66
20		OPBE	0	2001	31, 35, 36	76		BMK	42	2004	82
21			MPWLYP1W	0	2005	37	77		TPSS1KCIS	13	2005
22		PBE1W	0	2005	37	78		MPWKCIS1K	41	2005	40
23		PBELYP1W	0	2005	37	79		MPW1KCIS	15	2005	40
24		MOHLYP	0	2005	38	80		PBE1KCIS	22	2005	84
25		B97-D	0	2006	39	81		PWB6K	46	2005	3
26		MOHLYP2	0	2009	40	82		PW6B95	28	2005	3
27		OreLYP	0	2009	27, 35, 41	83		M05	28	2005	85
28	NGA	N12	0	2012	42	84		M05-2X	56	2005	86
29		GAM	0	2015	43	85		M06-HF	100	2006	87
30	meta-GGA	VSXC	0	1998	44	86		M06	27	2008	88
31		<i>τ</i> -HCTH	0	2002	45	87		M06-2X	54	2008	88
32		TPSS	0	2003	46	88		M08-HX	52.23	2008	89
33		TPSSLYP1W	0	2005	37	89		M08-SO	56.79	2008	89
34		M06-L	0	2006	47	90		MGGA_MS2H	9	2013	50
35		revTPSS	0	2009	48	91		revM06	40.41	2018	90
36		M11-L	0	2011	49	92	global-hybrid meta-GGA + MM	PW6B95-D3(BJ)	28	2005	3, 91
37		MGGA_MS0	0	2013	50	93	RS-hybrid meta- GGA	M11	42.8–100	2011	92
38		MGGA_MS1	0	2013	50	94		revM11	22.5–100	2019	10
39		MGGA_MS2	0	2013	50	95		M06-SX	33.5–0	2019	11
40	revM06-L	0	2017	51	96	RS-hybrid meta- NGA	MN12-SX	25–0	2012	78	
41	meta-NGA	MN12-L	0	2012	52	97	global-hybrid meta-NGA	MN15	44	2015	93
42		MN15-L	0	2015	53	98	RS-hybrid meta- GGA + rung- 3.5 correlation	M11plus	42.8–100	2019	94
nonlocal						99	meta-GGA + Rung-3.5 correlation	M11pz	0	2023	95
43	global-hybrid GGA	HFLYP	100	1987	27, 54	^a GGA, generalized-gradient approximation; NGA, nonseparable gradient approximation; meta-GGA, GGA plus local kinetic energy density; meta-NGA, NGA plus local kinetic energy density; global- hybrid \Rightarrow exchange part of the functional involves a constant percentage of nonlocal HF exchange; RS, range-separated \Rightarrow exchange part of the functional involves a percentage of nonlocal HF exchange that depends on interelectronic distance; MM, molecular mechanics term. ^b X is percentage of HF exchange. A single value indicates a local functional if X = 0 or a global-hybrid functional if X > 0.					
44		HFPW91	100	1991	30, 54						
45		B3PW91	20	1992	28, 55						
46		B3LYP	20	1994	27, 28, 55, 56						
47		PBE0	25	1996	57						
48		B1B95	28	1996	58						
49		mPW1PW	25	1997	32						
50		B1LYP	25	1997	59						
51		B98	21.98	1998	60						
52		B97–1	21	1998	61						
53	MPW1K	42.80	2000	62							
54	O3LYP	11.61	2001	36							
55	B97–2	21	2001	63							
56	B3LYP*	15 ^c	2001	64							

^aGGA, generalized-gradient approximation; NGA, nonseparable gradient approximation; meta-GGA, GGA plus local kinetic energy density; meta-NGA, NGA plus local kinetic energy density; global-hybrid \Rightarrow exchange part of the functional involves a constant percentage of nonlocal HF exchange; RS, range-separated \Rightarrow exchange part of the functional involves a percentage of nonlocal HF exchange that depends on interelectronic distance; MM, molecular mechanics term. ^bX is percentage of HF exchange. A single value indicates a local functional if X = 0 or a global-hybrid

Table 3. continued

functional if $X \neq 0$. A range of X values indicates that X depends on interelectronic separations. For a range specified by two values, the short-range limiting percentage comes before the long-range limiting percentage. For a range specified by three values, the values are listed

in the order of short-range, medium-range, and long-range. ‘B3LYP*’ is the name given by Reiher et al.⁶⁴ to a functional, that is, like B3LYP except that the percentage of Hartree–Fock exchange is reduced from 20 to 15%.

Table 4. Parent Databases, Representative Databases, DMUE, DPMUE, and P%

no.	parent database	rep. database	DMUE (kcal/mol)	PMUE (kcal/mol)	P%
1	TMBE27	rTMBE6	5.68	0.92	16.2
2	BH139	rBH6	3.83	0.21	5.5
3	TM40	rTM6	6.98	0.98	14.0
4	IsoE14	rIsoE6	2.68	0.20	7.5
5	MGBE174	rMGBE6	3.87	0.49	12.7
6	SDIP33	rSDIP6	5.55	0.52	9.4
7	EMNT418	rEMNT14	5.51	0.38	6.9
8	EMNTT555	rEMNTT14	5.54	0.35	6.3
9	AE17	rAE6	32.97	0.52	1.6
10	HTBH38/18	rHTBH6	5.14	0.14	2.7
11	NHTBH38/18	rNHTBH6	4.74	0.25	5.3
12	SR-MGN-BE107	rSR-MGN-BE6	1.88	0.21	11.2
13	NCCE30	rNCCE6	1.28	0.11	8.6
14	NGD21	rNGD6	0.20	0.01	5.0
15	BHPER126	rBHPER6	3.79	0.22	5.8
16	BHROT27	rBHROT6	0.59	0.04	6.8
17	IP23	rIP6	5.32	0.56	10.5

$$\text{MSE}_\alpha = \frac{1}{M} \sum_{i=1}^M (Q_{i,\alpha} - Q_{i,\text{ref}}) \quad (2)$$

$$\text{RMSE}_\alpha = \sqrt{\frac{1}{M} \sum_{i=1}^M (Q_{i,\alpha} - Q_{i,\text{ref}})^2} \quad (3)$$

Notice, in eqs 1–3, that all data points have the same weight. (For a very small number of cases, due to SCF convergence issues, certain data may be unavailable for a given electronic structure method; in such a case we simply omit that data in calculating the means. The list of missing data points is provided in the SI. Notice that only 15 data points are missing, as compared to a total of 55,485 data points included, and the effect of missing data on the representative databases should be negligible.)

We consider various subsets of the data in the given parent data set; these are trial representative databases with N_R data drawn from the M data in the parent database. We calculate the mean errors for that subset of data by equations analogous to eqs 1–3, and we call these MUE_α^R , MSE_α^R , and RMSE_α^R .

We then define the privation of the selected subset of data as

$$\text{Pr} = \langle |\text{MUE}^R - \text{MUE}| + |\text{MSE}^R - \text{MSE}| + |\text{RMSE}^R - \text{RMSE}| \rangle \quad (4)$$

where, for any quantity Q_α

$$\langle Q \rangle = \frac{1}{100} \sum_{\alpha=1}^{100} Q_\alpha \quad (5)$$

Our goal is to find a representative subset, which we define as a subset with a small Pr . To find the best representative database for a given parent database, we use a genetic algorithm to sample many different subsets of a given size N_R for that parent database. We use the Distributed Evolutionary

Algorithms in Python (DEAP) package¹⁷ to maximize the fitness function that is taken as the negative of the privation:

$$\text{fitness} = -\text{Pr} \quad (6)$$

The genetic-algorithm pool size is equal to the size of the parent database; the crossover and mutation probabilities are set to 0.5 and 0.2, respectively; and we use 100 generations of optimization for each of 200 random initial guesses. The result with the smallest P is taken as the representative database.

We use $N_R = 6$ for all parent databases except EMNT418 and EMNTT555; for those two we use $N_R = 14$.

Notice that the privation shown in eq 4 has three components, namely,

$$\text{PMUE} = \langle |\text{MUE}^R - \text{MUE}| \rangle \quad (7)$$

$$\text{PMSE} = \langle |\text{MSE}^R - \text{MSE}| \rangle \quad (8)$$

$$\text{PRMSE} = \langle |\text{RMSE}^R - \text{RMSE}| \rangle \quad (9)$$

We combine these as a privation array:

$$P \equiv (\text{PMUE}, \text{PMSE}, \text{PRMSE}) \quad (10)$$

The averages in eqs 1–3 are averages over data points in a parent database, and the averages in eqs 4 and 5 are averages over both data points and method. For tabulation, we need additional notation for averages only over methods for a given datum; we call these difficulties and define them as

$$\text{DMUE}_i \equiv \langle |Q_i - Q_{i,\text{ref}}| \rangle = \frac{1}{100} \sum_{\alpha=1}^{100} |Q_{i,\alpha} - Q_{i,\text{ref}}| \quad (11)$$

$$\text{DMSE}_i \equiv \langle Q_i - Q_{i,\text{ref}} \rangle = \frac{1}{100} \sum_{\alpha=1}^{100} (Q_{i,\alpha} - Q_{i,\text{ref}}) \quad (12)$$

$$\text{DRMSE}_i \equiv \sqrt{\langle (Q_i - Q_{i,\text{ref}})^2 \rangle}$$

$$= \sqrt{\frac{1}{100} \sum_{\alpha=1}^{100} (Q_{i,\alpha} - Q_{i,\text{ref}})^2} \quad (13)$$

The three difficulties are called MUE difficulty, MSE difficulty, and RMSE difficulty, respectively. We combine these as a difficulty array:

$$D_i \equiv (\text{DMUE}_i, \text{DMSE}_i, \text{DRMSE}_i) \quad (14)$$

Similarly, one defines the difficulty for the whole parent database as

$$D \equiv (\text{DMUE}, \text{DMSE}, \text{DRMSE}) \quad (15)$$

where

$$\text{DMUE} = \frac{1}{M} \sum_{i=1}^M \text{DMUE}_i \quad (16)$$

$$\text{DMSE} = \frac{1}{M} \sum_{i=1}^M \text{DMSE}_i \quad (17)$$

$$\text{DRMSE} = \frac{1}{M} \sum_{i=1}^M \text{DRMSE}_i \quad (18)$$

Notice that averaging over methods to provide difficulties shows how difficult it is for a data set to be described by a density functional—averaged over all density functionals (including HF). This is useful in the following way. If, for example, the DMUE for a database is 10 kcal/mol, and the privation is 1 kcal/mol, then the privation is only 10% of the difficulty. This is useful way to look at the privation, and therefore, we define the MUE privation percentage as

$$P\% = \frac{\text{PMUE}}{\text{DMUE}} \quad (19)$$

3. DISCUSSION

A complete difficulty array (DMUE, DMSE, DRMSE) for each parent database is provided in Table S1 in SI, and a complete privation array (DMUE, DMSE, DRMSE) is provided in Table S2. Tables S3–S11 in the SI provide complete difficulty arrays (DMUE_i, DMSE_i, DRMSE_i) for all data in all the representative databases.

Because we draw the same conclusions when we consider the entire 3-member arrays, we simplify the discussion in the following to the MUE components of these arrays. The size, MUE difficulty (DMUE), MUE privation (PMUE), and MUE privation percentage (*P*%) of each of the parent databases is given in Table 4. The average of the last column is 8.3%; it means that the MUE calculated from the subset would typically differ from the MUE calculated for the whole database by only 8.0%, indicating that we have met our objective. Similarly, the RMSE reproduces, on average, the RMSE of the parent database within 10.7%. Thus, the representative databases maintaining good diversity while being successful in indicating accuracy.

In the following, we provide the content of the representative databases. To label the representative database, we use the notation rAAN_R. For example, a representative database for HTBH38/18 with 6 data points is denoted as

Table 5. Barrier Heights and Reference Values of BH6 and rHTBH6^a

<i>i</i>	<i>Q</i> _{i,ref} (kcal/mol)
BH6, PMUE = 0.28 kcal/mol	
OH + CH ₄ → \ddagger (→ CH ₃ + H ₂ O)	6.30
CH ₃ + H ₂ O → \ddagger (→ OH + CH ₄)	19.50
H + OH → \ddagger (→ O + H ₂)	10.90
O + H ₂ → \ddagger (→ H + OH)	13.20
H + H ₂ S → \ddagger (→ H ₂ + HS)	3.90
H ₂ + HS → \ddagger (→ H + H ₂ S)	17.20
rHTBH6, PMUE = 0.14 kcal/mol	
H ₂ O + CH ₃ → \ddagger (→ OH + CH ₄)	19.50
OH + C ₂ H ₆ → \ddagger (→ H ₂ O + C ₂ H ₅)	3.50
O + CH ₄ → \ddagger (→ OH + CH ₃)	14.40
H ₂ + PH ₂ → \ddagger (→ H + PH ₃)	24.70
H + HO → \ddagger (→ H ₂ + O)	10.90
<i>s-trans cis</i> -C ₅ H ₈ → \ddagger (→ <i>s-trans cis</i> -C ₅ H ₈) ^b	39.70

^aFor barriers, the products are shown only to identify the reaction; their energy is not used in the representative database. ^b[1,5] sigmatropic rearrangement of *s-trans cis*-1,3-pentadiene.

Table 6. Barrier Heights, Subdatabases from which Selected, and Reference Values of rBH6^a

<i>i</i>	subdatabase	<i>Q</i> _{i,ref} (kcal/mol)
rBH6, PMUE = 0.21 kcal/mol		
H + H ₂ → \ddagger (→ H ₂ + H)	HTBH38/18	9.70
H ₂ O + NH ₂ → \ddagger (→ OH + NH ₃)	HTBH38/18	13.70
F [−] ⋯CH ₃ F → \ddagger (→ FCH ₃ ⋯F [−])	NHTBH38/18	13.40
1,3-pentadiene sigmatropic shift	BHPERI26	39.70
formonitrile ylide + ethylene: 1,3-dipolar cycloaddition	BHPERI26	4.70
N ₂ H ₄ N–N bond rotation barrier	BHROT27	8.41

^aWhen products are identified, they are shown only to identify the reaction; their energy is not used in the representative or parent database.

rHTBH6, and a representative database for EMNT418 with 14 data points is denoted as rEMNT14.

3.1. HTBH38/18. We start by considering HTBH38/18. This is an interesting case because we have previously presented a representative database for barrier heights, namely, BH6.¹⁴ The BH6 representative database involves three selected reactions, and for each reaction, both forward and reverse barrier heights are included. The three chemical reactions in BH6 are given in Table 5. The HTBH38/18 has DMUE = 5.1 kcal/mol, and BH6 representative database has PMUE = 0.28 kcal/mol.

Table 5 shows the genetic-algorithm-optimized representative database, rHTBH6, which has a PMUE of only 0.14 kcal/mol. Notice that the better performance is obtained in part because of greater flexibility in that BH6 is restricted to the forward and reverse barrier heights of three chemical reactions, whereas rHTBH6 selects six data points without the requirement that if a reaction is chosen, both its forward and reverse barriers are used. Notice that the older BH6 set, because both forward and backward barriers are chosen, involves 9 individual calculations (3 reactants, 3 products, and 3 transition states), whereas the new set involves 12 calculations (6 reactants and 6 transition states).

Table S3 in SI shows a complete difficulty array for BH6 and rHTBH6.

Table 7. Barrier Heights and Reference Values of rNHTBH6, rBHPER6, rBHROT6^a

<i>i</i>	<i>Q_{i,ref}</i> (kcal/mol)
rNHTBH6, PMUE = 0.25 kcal/mol	
H + HF → \ddagger (→ FH + H)	42.10
CH ₃ F + Cl → \ddagger (→ CH ₃ + FCl)	59.80
Cl [−] + CH ₃ Cl → \ddagger (→ ClCH ₃ + Cl [−])	2.50
OH [−] ...CH ₃ F → \ddagger (→ HOCH ₃ ...F [−])	11.00
HN ₂ → \ddagger (→ H + N ₂)	10.90
H + C ₂ H ₄ → \ddagger (→ CH ₃ CH ₂)	2.00
rBHPER6, PMUE = 0.22 kcal/mol	
<i>cis</i> -1,3,5-hexatriene electrocyclic ring closing barrier	30.80
1,5-hexadiene sigmatropic shift barrier	35.80
fulminic acid + ethylene: 1,3-dipolar cycloaddition barrier	11.80
formazomethine imine + ethylene: 1,3-dipolar cycloaddition barrier	5.90
phosphole + ethylene: Diels–Alder cycloaddition barrier	21.30
thiophene + ethylene: Diels–Alder cycloaddition barrier	31.30
rBHROT6, PMUE = 0.04 kcal/mol	
(CH ₃) ₂ CHC–CH(CH ₃) ₂ C–C bond rotation barrier	3.72
NH ₂ OH NO bond rotation barrier	6.91
NH ₂ OH NO bond rotation barrier	2.68
bithiophene C–C bond rotation barrier	1.78
butadiene C–C bond rotation barrier	6.30
ethylthiourea C–N bond rotation barrier	10.24

^aWhen products are identified, they are shown only to identify the reaction; their energy is not used in the representative or parent database.

3.2. BH139, NHTBH38/18, BHPER126, and BHROT27.

Additional parent databases composed of barrier heights are BH139 constructed in the current work and NHTBH38/18, BHPER126, and BHROT27 from the previous work. The optimized representative databases, namely, rBH6, rNHTBH6, rBHPER6, and rBHROT6 are shown in Tables 6 and 7.

Database rBH6 involves 2 reactions from HTBH38/18, 1 reaction from NHTBH38/18, 2 reactions from BHPER126, and 1 reaction from BHROT27. Therefore, rBH6 involves barrier heights of diverse chemical reactions, and it has a PMUE of only 0.21 kcal/mol.

The PMUEs for rNHTBH6, rBHPER6, and rBHROT6 are 0.25, 0.22, and 0.04 kcal/mol, respectively. These may be

Table 9. Isomerization Energies, Subdatabases from which Selected, and Reference Values of rIsoE6

<i>i</i>	subdatabase	<i>Q_{i,ref}</i> (kcal/mol)
rIsoE6, PMUE = 0.20 kcal/mol		
C(CH ₃) ₄ → CH ₃ CH ₂ CH ₂ CH ₂ CH ₃	2pIsoE4	3.80
CH ₃ CH ₂ CF ₃ → CH ₂ FCHFCH ₂ F	2pIsoE4	26.90
PhAsH ₂ → C ₆ H ₆ AsH	4pIsoE4	33.00
C ₄ SeH ₈ → C ₄ H ₇ SeH	4pIsoE4	20.80
NH ₂ C ₆ H ₄ –C ₆ H ₄ NH ₂ → C ₆ H ₅ NHNHC ₆ H ₅	IsoL6/11	33.50
C ₆ H ₄ OHCOCH(CH ₃)COCH ₃ → C ₆ H ₄ (OCOCH ₃)COCH ₂ CH ₃	IsoL6/11	5.30

compared to DMUEs of 4.74, 3.79, and 0.59 kcal/mol for the parent databases. The privation percentages are only 5.3, 5.8, and 6.8% for rNHTBH6, rBHPER6, and rBHROT6, respectively. Tables S4 and S5 in SI show complete difficulty arrays for rNHTBH6, rBHPER6, and rBHROT6.

3.3. Transition-Metal Parent Databases: TM40 and TMBE27. The optimized representative databases rTM6 and rTMBE6 are shown in Table 8. Database rTM6 involves 4 multireference transition-metal–ligand bond energies and 2 transition-metal excitation energies. The rTMBE6 representative database involves 3 single-reference transition-metal bond energies and 3 multireference transition-metal–ligand bond energies. The PMUEs of rTM6 and rTMBE6 are 0.98 and 0.92 kcal/mol. The DMUEs for TM40 and TMBE27 are 6.98 and 5.68 kcal/mol. Dividing these yields P% for rTM6 and rTMBE6 of 14 and 16%, respectively. Table S6 in SI shows complete difficulty arrays for rTM6 and rTMBE6.

3.4. Isomerization Parent Database: IsoE14. The optimized representative database rIsoE6 is shown in Table 9. Database rIsoE6 involves two 2p isomerization energies, two 4p isomerization energies, and two isomerization energies of large molecules. The DMUE of IsoE14 is 2.68 kcal/mol, and PMUE and P% for rIsoE6 are 0.20 kcal/mol and 7.5%. Table S7 in SI shows a complete difficulty array for rIsoE6.

3.5. Main-Group Bond Energy Databases: MGBE174 and SR-MGN-BE107. The optimized representative databases rMGBE6 and rSR-MGN-BE6 are shown in Tables 10 and 11. Database rMGBE6 involves 4 single-reference main-group nonmetal bond energies, 1 multireference main-group non-metal bond energy, and 1 dissociation energy of a heavy-

Table 8. Bond Energies, Subdatabases from which Selected, and Reference Values of rTM6 and rTMBE6

<i>i</i>	broken bonds ^a	subdatabase	<i>Q_{i,ref}</i> (kcal/mol)
rTM6, PMUE = 0.98 kcal/mol			
TiCl → Ti + Cl	1	MR-TML-BE12	101.70
Co(CO) ₄ H → Co + 4C + 4O + H	9	MR-TML-BE12	136.68
NiCH ₂ ⁺ → Ni ⁺ + CH ₂	1	MR-TML-BE12	76.30
CuCl → Cu + Cl	1	MR-TML-BE12	90.20
Fe excitation energy	N/A	3dAEE8	34.24
Ru ⁺ excitation energy	N/A	4dAEE5	26.17
rTMBE6, PMUE = 0.96 kcal/mol			
FeCl ₂ → Fe + 2Cl	2	SR-TM-BE15	95.15
CuAg → Cu + Ag	1	SR-TM-BE15	40.70
Pd(PH ₃) ₂ –C ₁₀ H ₁₂ → Pd(PH ₃) ₂ + C ₁₀ H ₁₂	1	SR-TM-BE15	17.30
CrCl → Cr + Cl	1	MR-TML-BE12	90.15
Fe(CO) ₅ → Fe + 5CO	5	MR-TML-BE12	29.48
VO → V + O	1	MR-TML-BE12	151.00

^aWhen an entry is a molecular atomization, the atomization energy is divided by the number of bonds broken to yield the average bond energy of the molecule, and the average bond energy is the datum used for that molecule and is given in the last column. N/A denotes not applicable.

Table 10. Bond Energies, Subdatabases from which Selected, and Reference Values of rMGBE6

<i>i</i>	broken bonds ^a	subdatabase	<i>Q_{i,ref}</i> (kcal/mol)
rMGBE6, PMUE = 0.49 kcal/mol			
SO (<i>M</i> = 3) → S + O	1	MR-MGN-BE17	125.69
CH ₃ CH ₂ OCH ₃ → CH ₃ CH ₂ + OCH ₃	1	SR-MGN-BE107	95.26
C ₄ H ₁₀ (isobutane) → 4C + 10H	13	SR-MGN-BE107	100.23
C ₄ H ₈ (cyclobutene) → 4C + 8H	12	SR-MGN-BE107	96.55
C ₅ H ₈ (spiropentane) → 5C + 6H	14	SR-MGN-BE107	91.73
Te ₂ (CH ₃) ₂ → 2TeMe	1	HeavySB11	52.91

^aIn each case, the energy of the reaction shown is divided by the number of bonds broken to yield the average bond energy of the bonds broken, and that average bond energy is the datum used for that molecule, as listed in the last column.

Table 11. Bond Energies and Reference Values of rSR-MGN-BE6

<i>i</i>	broken bonds ^a	<i>Q_{i,ref}</i> (kcal/mol)
rSR-MGN-BE6, PMUE = 0.21 kcal/mol		
tert-butyl-H → tert-butyl + H	1	103.86
PH ₂ → P + 2H	2	76.60
Cl ₂ → 2Cl	1	58.07
SiF ₄ → Si + 4F	4	143.59
C ₄ H ₈ (cyclobutene) → 4C + 8H	12	96.55
C ₅ H ₈ (spiropentane) → 5C + 6H	14	91.73

^aIn each case, the energy of the reaction shown is divided by the number of bonds broken to yield the average bond energy of the bonds broken, and that average bond energy is the datum used for that molecule, as listed in the last column.

Table 12. Ionization Potentials, Subdatabases from which Selected, and Reference Values of rSDIP6

<i>i</i>	subdatabase	<i>Q_{i,ref}</i> (kcal/mol)
rSDIP6, PMUE = 0.52 kcal/mol		
Cl → Cl ⁺	IP23	299.10
OH → OH ⁺	IP23	299.10
S ₂ → S ₂ ⁺	IP23	216.00
Cr → Cr ⁺	IP23	156.01
Zn → Zn ⁺	IP23	216.63
C ₂ H ₄ → C ₂ H ₄ ²⁺	DIPCS10	655.80

Table 13. Ionization Potentials and Reference Values of rIP6

<i>i</i>	<i>Q_{i,ref}</i> (kcal/mol)
rIP6, PMUE = 0.56 kcal/mol	
C → C ⁺	259.70
SH → SH ⁺	238.90
S ₂ → S ₂ ⁺	216.00
Cu → Cu ⁺	178.17
Rh → Rh ⁺	172.11
Sc → Sc ⁺	151.32

element compound. Databases rMGBE6 and rSR-MGN-BE6 have PMUEs of 0.49 and 0.21 kcal/mol, respectively. This may be compared to the difficulties (DMUEs) of MGBE174 and SR-MGN-BE107, which are 3.87 and 1.88 kcal/mol, respectively. The success of the representation is shown by the small *P*% for rMGBE6 and rSR-MGN-BE6, namely, 12.7 and 11.2%, respectively. Tables S8 and S9 in SI shows complete difficulty arrays for rMGBE6 and rSR-MGN-BE6.

3.6. Ionization Potential Energy Databases: SDIP33 and IP23. The optimized representative databases rSDIP6 and rIP6 are shown in Tables 12 and 13. Database rSDIP6 involves

Table 14. Noncovalent Complexation and Dimerization Energies and Reference Values of rNCCE6 and rNGD6

<i>i</i> ^a	<i>Q_{i,ref}</i> (kcal/mol)
rNCCE6, PMUE = 0.11 kcal/mol	
NH ₃ ...H ₂ O → NH ₃ + H ₂ O	6.38
HCN...ClF → HCN + ClF	4.80
NH ₃ ...Cl ₂ → NH ₃ + Cl ₂	4.85
(H ₂ S) ₂ → 2H ₂ S	1.62
parallel-displaced (C ₆ H ₆) ₂ → 2C ₆ H ₆	2.59
parallel-displaced (CO ₂) ₂ → 2CO ₂	1.49
rNGD6, PMUE = 0.01 kcal/mol	
Ne ₂ → 2Ne	0.08
HeAr → He + Ar	0.06
HeHe (<i>r</i> = 3.274 Å) → He + He	0.02
ArAr (<i>r</i> = 3.457 Å) → Ar + Ar	0.14
KrKr (<i>r</i> = 4.311 Å) → Kr + Kr	0.34
HeNe (<i>r</i> = 2.731 Å) → He + Ne	0.01

^a*r* denotes separation distance.

Table 15. Absolute Energies and Reference Values of rAE6

<i>i</i>	<i>Q_{i,ref}</i> (kcal/mol)
rAE6, PMUE = 0.52 kcal/mol	
He	−1822.11
B	−15,470.55
N	−34,255.21
Na	−101,816.22
Al	−152,074.30
S	−249,817.61

five ionization potentials and one double-ionization potential. Databases rSDIP6 and rIP6 have PMUEs of 0.52 and 0.56 kcal/mol. The DMUEs for SDIP33 and IP23 are 5.55 and 5.32 kcal/mol, respectively, and *P*% for rSDIP6 and rIP6 are 9.4 and 10.5% respectively. Tables S10 and S11 in SI show a complete difficulty array for rSDIP6 and IP6 databases.

3.7. Noncovalent Interaction Databases: NCCE30 and NGD21. The optimized representative databases rNCCE6 and rNGD6 are shown in Table 14. Databases rNCCE6 and rNGD6 have PMUEs of 0.11 and 0.01 kcal/mol, respectively. The DMUEs of NCCE30 and NGD21 are 1.28 and 0.20 kcal/mol, respectively, so *P*% for rNCCE6 and rNGD6 are 8.6 and 5.0%, respectively. Table S12 in SI shows a complete difficulty array for rNCCE6 and rNGD6 databases.

3.8. Atomic Energy Database: AE17. The optimized representative database rAE6 is shown in Table 15. Database rAE6 involves one element from first row, two elements from the second row, and three elements from the third row. The DMUEs for AE17 is 32.97 kcal/mol. Database rAE6 has a

Table 16. Data, Subdatabases from which Selected, and Reference Values of rEMNT14 and rEMNTT14

$i^{a,b}$	broken bonds ^c	subdatabase	$Q_{i,ref}$ (kcal/mol)
rEMNT14, PMUE = 0.44 kcal/mol			
N	N/A	AE17	−34,255.21
OH + NH ₃ → \ddagger (→ H ₂ O + NH ₂)	N/A	HTBH38/18	3.40
O ₂ → O ₂ ⁺	N/A	IP23	278.90
P → P ⁺	N/A	IP23	241.90
PH → PH ⁺	N/A	IP23	234.10
CN → C + N	1	MR-MGN-BE17	181.27
VF ₅ → V + 5F	5	MR-TML-BE12	112.83
(CH ₄) ₂ → 2CH ₄	N/A	NCCE30	0.53
He ₂ → 2He	N/A	NGD21	0.02
HeNe → He + Ne	N/A	NGD21	0.04
NeNe ($r = 2.791$ Å) → Ne + Ne	N/A	NGD21	0.01
HNC → \ddagger (→ HCN)	N/A	NHTBH38/18	33.00
H ₂ S → H ₃ S ⁺	N/A	PA8	173.70
tert-butyl−OH → tert-butyl + OH	1	SR-MGN-BE107	115.02
rEMNTT14, PMUE = 0.37 kcal/mol			
C	N/A	AE17	−23,748.08
Al ₂ (CH ₃) ₄ → 2Al(CH ₃) ₂	N/A	Al2x6	38.40
cis-1,3,5-hexatriene electrocyclic ring closing barrier	N/A	BHPERI26	30.80
H ₂ S ₂ S−S bond rotation barrier	N/A	BHROT27	8.03
O ₂ → O ₂ ⁺	N/A	IP23	278.90
Si → Si ⁺	N/A	IP23	187.90
Zn → Zn ⁺	N/A	IP23	216.63
ClO → Cl + O	1	MR-MGN-BE17	64.84
T-shaped (C ₆ H ₆) ₂ → 2C ₆ H ₆	N/A	NCCE30	2.63
He ₂ → 2He	N/A	NGD21	0.02
HeHe ($r = 3.274$ Å) → He + He	N/A	NGD21	0.02
H + FCH ₃ → \ddagger (→ HF + CH ₃)	N/A	NHTBH38/18	30.50
HN ₂ → \ddagger (→ H + N ₂)	N/A	NHTBH38/18	10.90
tert-butyl−OH → tert-butyl + OH	1	SR-MGN-BE107	115.02

^aWhen products are identified after a transition state, they are shown only to identify the reaction; their energy is not used in the representative database, and the barrier height is the datum for that reaction, as listed in the last column. ^b r denotes separation distance. ^cIn each case where bonds are broken, the energy of the reaction shown is divided by the number of bonds broken to yield the average bond energy of the bonds broken, and that average bond energy is the datum used for that molecule, as listed in the last column. N/A denotes not applicable.

PMUE of 0.52 kcal/mol and a P% of 2.0%. Table S13 in SI shows a complete difficulty array for the rAE6 database.

3.9. Minnesota Databases: EMNT418 and EMNTT555.

Next, we consider two very big databases, namely, the energetic portion (EMNT418) of Minnesota training database and the energetic portion (EMNTT555) of the Minnesota training and testing database (the geometric portions of these databases are not included). We used 14 as the size of our optimized representative database size for these larger databases; this results in representative databases rEMNT14 and rEMNTT14. The energetic portions of databases EMNT418 and EMNTT555 involve 25 and 34 subdatabases, respectively. Both the optimized rEMNT14 and rEMNTT14 databases involve systems from 10 subdatabases, which makes them very diverse. The involved systems and the databases from which they are taken are shown in Table 13. The DMUEs for EMNT418 and EMNTT555 are 5.51 and 5.54 kcal/mol. The PMUEs of optimized rEMNT14 and rEMNTT14 are 0.38 and 0.35 kcal/mol, which results in 6.9 and 6.3% for P%. Table S14 in SI shows a complete difficulty array for the rEMNT14 and rEMNTT14 databases.

4. SUMMARY AND CONCLUSIONS

In this work, we have optimized representative databases formed from various subdatabases of Minnesota Database

2019. The optimizations were achieved by using a genetic algorithm that maximizes the correspondence between the representative database and the parent database in terms of MUE, MSE, and RMSE. The inclusion of the RMSE in the optimizations is important because it means the representative databases include the diversity of the data as well as its difficulty.

Our goal in producing representative databases involves more than just statistics; we try to keep the databases small enough to be very convenient, but large enough to have appropriate diversity. We consider two big parent databases, namely, the energetic portion of the Minnesota training database and the energetic portion of the Minnesota training and testing database. The energetic portion of the Minnesota training database is called EMNT418, and it has 418 data points. The energetic portion of the Minnesota training and testing database is called EMNTT555, and it has 555 data points. For these two large parent databases, we considered representative databases with sizes of 14 data points each. These are called rEMNT14 and rEMNTT14 (see Table 16). We also consider representative databases of smaller parent databases, which are either combined subdatabases of Minnesota Database 2019 or a single subdatabase of Minnesota Database 2019. In particular, we consider 15 such smaller parent databases, which are listed in Table 2. Parent

databases 1–8 are combined subdatabases of Minnesota Database 2019, and parent databases 9–17 are single subdatabases of Minnesota Database 2019.

The 17 parent databases considered here cover a variety of chemical and physical properties of transition-metal and main-group molecules and reactions. The size of the representative databases is 6 for 15 of them and is 14 for the two biggest parent databases, namely, the energetic portion of the Minnesota training database and the energetic portion of the Minnesota training and testing database. On average, our optimized representative databases deviate from parent databases by 8.0% in terms of MUE averaged over 100 electronic structure methods (HF method and Kohn–Sham density functional theory with 99 density functionals). We also achieved success in representing the error spread. The low deviations in errors and error spreads indicate that our current optimization strategy is successful in producing representative databases that adequately reproduce the MSEs, MUEs, and RMSEs of larger databases. The representative databases allow one to gain a quick understanding of a method's accuracy in a modest time and with modest expense.

■ ASSOCIATED CONTENT

■ Supporting Information

The Supporting Information is available free of charge at <https://pubs.acs.org/doi/10.1021/acs.jpca.4c03137>.

Difficulties of parent databases and difficulties and privations of representative databases; reference data and geometries for representative databases (PDF)

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Notes

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