

Supplementary materials to the paper
*Atomic charges for conformationally rich molecules
obtained through a modified principal component regression*

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The code of the Python program developed as a part of the study:

```
In [1]: %reset -f

In [2]: import os
import zipfile
import re
import numpy as np
import sys
import json

from matplotlib import pyplot as plt
%matplotlib inline

In [3]: molecules = {'ade': ('ade.json', 36, 19),      # ( json_filename, nAtoms, nIndependentAtoms )
                    'thy': ('thy.json', 36, 19),
                    'gua': ('gua.json', 37, 19),
                    'cyt': ('cyt.json', 34, 19) }

common_names = {1: "HO3'", 2: "O3'", 3: "C3'", 4: "C4'", 5: "H3'", 6: "C2'", 7: "C1'",
                8: "O4'", 9: "C5'", 10: "H1'", 11: "H2'2", 12: "H2'1", 13: "H4'",
                14: "O5'", 15: "H5'1", 16: "H5'2", 17: "P"}

atom_names = {'ade': dict(common_names.items() +
                          {18: "N9", 19: "C4", 20: "C8", 21: "N7", 22: "C5", 23: "N3",
                           24: "C2", 25: "N1", 26: "C6", 27: "N6", 28: "H2", 29: "H62",
                           30: "H61", 31: "H8",
                           32: "OP", 33: "OP1", 34: "HP1", 35: "OP2", 36: "HP2"}.items()),
              'thy': dict(common_names.items() +
                          {18: "N1", 19: "C2", 20: "C6", 21: "C5", 22: "C4", 23: "N3",
                           24: "O2", 25: "H6", 26: "C7", 27: "O4", 28: "H3", 29: "H73",
                           30: "H72", 31: "H71",
                           32: "OP", 33: "OP1", 34: "HP1", 35: "OP2", 36: "HP2"}.items()),
              'gua': dict(common_names.items() +
                          {18: "N9", 19: "C4", 20: "C8", 21: "N7", 22: "C5", 23: "N3",
                           24: "C2", 25: "N1", 26: "C6", 27: "O6", 28: "H1", 29: "N2",
                           30: "H21", 31: "H22", 32: "H8",
                           33: "OP", 34: "OP1", 35: "HP1", 36: "OP2", 37: "HP2"}.items()),
              'cyt': dict(common_names.items() +
                          {18: "N1", 19: "C2", 20: "N3", 21: "C4", 22: "C5", 23: "C6",
                           24: "H6", 25: "H5", 26: "N4", 27: "H41", 28: "H42", 29: "O2",
                           31: "OP", 30: "OP1", 34: "HP1", 32: "OP2", 33: "HP2"}.items())
              }

In [4]: # load the molecule data -- geometrical center shift method
```

Debye2eA = 0.20819434

```
def get_dd_charges_gcenter(data_list, apt_avg, nIndependentAtoms):
    """ Calculates a dipole-derived charges for a set of conformers stored
    in data_list and returns X,Y,q,q_min where q_min is the formal leasy
    squares fit (without 'zero'-th mode)
    Note that the input dipole must be in charge-center coordinate origin, and it
    is automatically translated into geometry-center coordinate origin during the
    calculations.
    """
    global vecs, vals ##

    nAtoms = len(apt_avg)
    # form the X and Y matrices
    X = []
    Y = []
    q_tot = sum(apt_avg) # the total charge
    print 'Total charge: %10.5f' % q_tot

    for R, D in zip(data_list['coords'], data_list['dipole']):
        R = np.array(R)
        gCenter = np.mean( R, axis=0)

        for mu in range(3):
            rec = []

            for ri in R:
                rec.append( ri[mu] - gCenter[mu])

            X.append(rec)
            dmu = D[mu] * Debye2eA - q_tot * gCenter[mu] # converted Debye to e*A
            Y.append(dmu)
    print 'avg |component of dipole moment| =', np.mean(np.abs(Y))

    X = np.array(X)

    nConfs = len( data_list['coords'] )

    A = X.T.dot(X)
    Y = np.array(Y)
    b = X.T.dot( Y )

    vals, vecs = np.linalg.eigh(A)
    print 'Eigenvalues of A:', vals

    q = np.array( [0.0] * nAtoms )
    q_min = np.array( [0.0] * nAtoms )

    a = np.zeros(nAtoms)

    for i in range(nAtoms):

        vec = vecs[ : , i ]
        L = vals[i]

        b_dip = vec.dot(b)
```

```

        if i != 0:
            dq_dip = b_dip / L * vec
            q_min += dq_dip

        a_apt = vec.dot(apt_avg)
        dq_apt = a_apt * vec

        q += dq_apt if i < (nAtoms - nIndependentAtoms) else dq_dip

    return X, Y, q, q_min
#-----

# Run the get_dd_charges_gcenter() for each of the nucleotides:

graph_q = { 'APT': plt.figure().gca(), 'RESP': plt.figure().gca() }
graph_evals = plt.figure().gca()
graph_evals.set_yscale("log")

# settings for plots
colors = {'ade': 'k.', 'thy': 'g.', 'gua': 'bx', 'cyt': 'rx'}
labels = {'ade': 'dAMP', 'thy': 'dTMP', 'gua': 'dGMP', 'cyt': 'dCMP'}
fit_all = {'APT': [[],[]], 'RESP': [[],[]]}
final_charges = {}

for key in sorted(molecules.keys()):
    fname, nAtoms, nIndependentAtoms = molecules[key]
    data_list = json.load(open(fname))

    print '-'*80
    nConfs = len(data_list['coords'])
    print key, '%d conformers' % nConfs
    print '-'*80

    # compute some of the 'standard' charges, averaged over all conformers
    # APT
    apt = np.array(data_list['APT']) # (num_conf, num_atoms)
    apt_avg = np.sum(apt, axis=0)/len(apt)
    #print '<apt chagres> =', apt_avg

    # RESP
    resp = np.array(data_list['RESP']) # (num_conf, num_atoms)
    resp_avg = np.sum(resp, axis=0)/len(resp)
    #print '<resp chagres> =', resp_avg

    X, Y, q, q_min = get_dd_charges_gcenter(data_list, apt_avg, nIndependentAtoms)

    idx = np.argsort(-vals)
    graph_evals.plot(range(1, len(vals)), vals[idx][: -1] / nConfs, colors[key],
                     label=labels[key], alpha=0.9)

    # estimate the fitting errors
    dy = Y - X.dot(q)
    dy_min = Y - X.dot(q_min)

    # save the results for further analysis
    final_charges[key] = {}

```

```

final_charges[key]['dd'] = q
final_charges[key]['apt'] = apt_avg
final_charges[key]['resp'] = resp_avg

print 'sum(charges) = %.5f' % sum(q)
print 'RMS(D_mu - calculated_D_mu) =', np.sqrt(dy.dot(dy)/len(dy))
print '<|D_mu - calculated_D_mu|> =', sum(np.abs(dy))/len(dy)
print 'max|D_mu - calculated_D_mu| =', np.max(np.abs(dy))

print 'lowest possible RMS(D_mu - calculated_D_mu) =', \
      np.sqrt(dy_min.dot(dy_min)/len(dy_min))
print 'lowest possible max|D_mu - calculated_D_mu| =', np.max(np.abs(dy_min))
print 'lowest possible <|D_mu - calculated_D_mu|> =', sum(np.abs(dy_min))/len(dy_min)
print

for s, lbl in zip([apt_avg, resp_avg], ['APT', 'RESP']):
    graph_q[lbl].plot(q, s, colors[key], label=labels[key] )
    fit_all[lbl][0] += list(q)
    fit_all[lbl][1] += list(s)
    graph_q[lbl].set_xlabel( '$q_{d}$ / |e|$' , fontsize=16)
    graph_q[lbl].set_ylabel( '$q_{%s}$ / |e|$' % lbl, fontsize=16)

    dy = Y - X.dot(s)
    print lbl, 'sum(charges) = %.5f' % sum(s)
    print lbl, 'max|D_mu - calculated_D_mu| =', np.max(np.abs(dy))
    print lbl, '<|D_mu - calculated_D_mu|> =', sum(np.abs(dy))/len(dy)

# fit line
def lin_fit(key, line_tmpl, label_tmpl):
    X = fit_all[key][0]
    Y = fit_all[key][1]
    ax = graph_q[key]
    fit = np.polyfit(X,Y,1)
    xr = np.linspace(min(X), max(X), num=100)
    title = label_tmpl%(fit[0], fit[1])
    line, = ax.plot(xr, fit[0]*xr + fit[1], line_tmpl, label=title)

    # Create another legend for the second line.
    ax.legend(handles=[line], loc='lower right', frameon=False, fontsize=15,
              borderaxespad=0.0)

    return line, title

graph_evals.legend(loc='best', numpoints=1, frameon=False)
graph_evals.set_xlabel(r'Eigenvalue number', fontsize=13.5)
graph_evals.set_ylabel(r'$\mathrm{Eigenvalue}$ /  $N_{\{confs\}}$', fontsize=14)
# add arrows
_ = nConfs
graph_evals.annotate('19-th', xy=(19, 1e2/_), xytext=(19, 1e3/_), ha='center',
                    arrowprops =
                    {'width': 1, 'headwidth': 4, 'color': 'black', 'headlength': 5},
                    fontsize=13 )

graph_evals.annotate('20-th', xy=(20, 1e-1/_), xytext=(20, 0.5e-2/_), ha='center',$ 
```


avg |component of dipole moment| = 0.67557455898
 Eigenvalues of A: [1.27353004e-13 2.14220338e-03 6.40311129e-03 9.77936382e-03
 1.23460236e-02 1.64111247e-02 2.57186304e-02 3.36898707e-02
 3.56176349e-02 5.57991859e-02 7.18883952e-02 1.36658422e-01
 1.81055423e-01 2.60938238e-01 1.50340110e+00 6.98302036e+00
 1.78244822e+01 2.76963876e+01 5.99354146e+01 1.52139935e+02
 1.65979923e+02 2.01393381e+02 2.76116205e+02 3.84041083e+02
 5.52597101e+02 9.73163971e+02 1.88978892e+03 2.43984577e+03
 5.13314249e+03 5.98922263e+03 6.79336807e+03 1.50127963e+04
 6.19591225e+04 1.67129687e+05]

sum(charges) = -0.00000
 RMS(D_mu - calculated_D_mu) = 0.112761622642
 <|D_mu - calculated_D_mu|> = 0.0886505890927
 max|D_mu - calculated_D_mu| = 0.343946684109
 lowest possible RMS(D_mu - calculated_D_mu) = 0.0583482032492
 lowest possible max|D_mu - calculated_D_mu| = 0.245538963823
 lowest possible <|D_mu - calculated_D_mu|> = 0.0449979828796

APT sum(charges) = -0.00000
 APT max|D_mu - calculated_D_mu| = 1.35718006804
 APT <|D_mu - calculated_D_mu|> = 0.444123955612
 RESP sum(charges) = 0.00000
 RESP max|D_mu - calculated_D_mu| = 0.546781091517
 RESP <|D_mu - calculated_D_mu|> = 0.126493292933

 gua 745 conformers

Total charge: -0.00000
 avg |component of dipole moment| = 0.720558297303
 Eigenvalues of A: [-5.85218116e-13 9.91451546e-04 2.13216000e-03 7.56943914e-03
 8.36809447e-03 1.58907254e-02 1.86571074e-02 3.04436343e-02
 3.53926258e-02 6.24959903e-02 7.07865536e-02 1.16449816e-01
 1.23348965e-01 1.47739940e-01 1.67329429e-01 2.11165690e-01
 1.59137802e+00 3.05786405e+00 1.86637082e+01 5.96235298e+01
 6.53085379e+01 1.11131354e+02 2.01383330e+02 2.17131083e+02
 2.63552365e+02 3.60281690e+02 4.96598020e+02 6.92570054e+02
 1.16626626e+03 2.46236069e+03 2.99625801e+03 6.69000037e+03
 8.06758724e+03 1.01270054e+04 4.55320709e+04 6.98270995e+04
 2.39073909e+05]

sum(charges) = -0.00000
 RMS(D_mu - calculated_D_mu) = 0.0873775873443
 <|D_mu - calculated_D_mu|> = 0.0694381438874
 max|D_mu - calculated_D_mu| = 0.276736884434
 lowest possible RMS(D_mu - calculated_D_mu) = 0.0682115296926
 lowest possible max|D_mu - calculated_D_mu| = 0.412876029072
 lowest possible <|D_mu - calculated_D_mu|> = 0.0528898168784

APT sum(charges) = -0.00000
 APT max|D_mu - calculated_D_mu| = 1.13397454397
 APT <|D_mu - calculated_D_mu|> = 0.373569556123
 RESP sum(charges) = -0.00000
 RESP max|D_mu - calculated_D_mu| = 0.450893695995
 RESP <|D_mu - calculated_D_mu|> = 0.116060722949

 thy 660 conformers

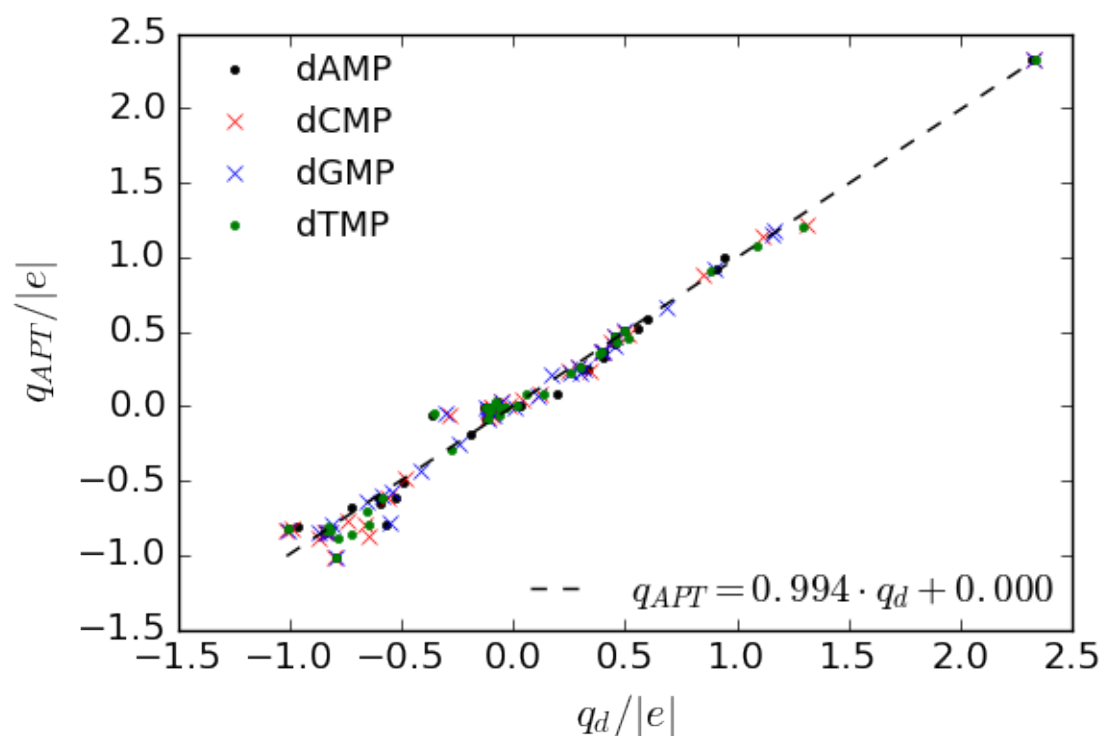
Total charge: 0.00000

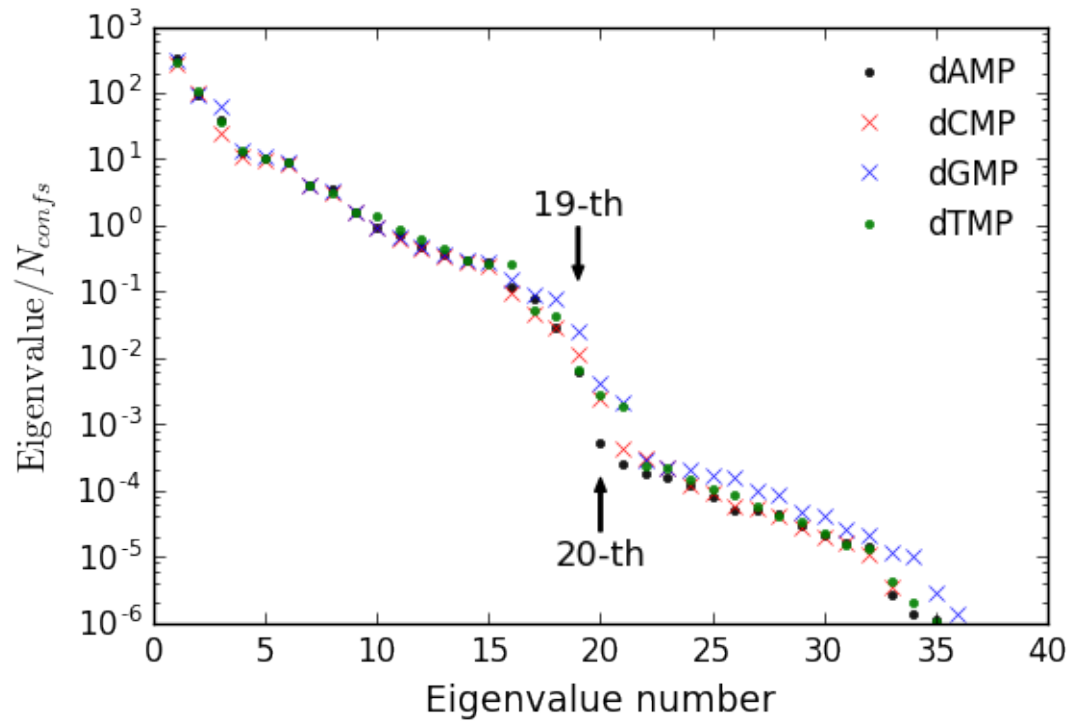
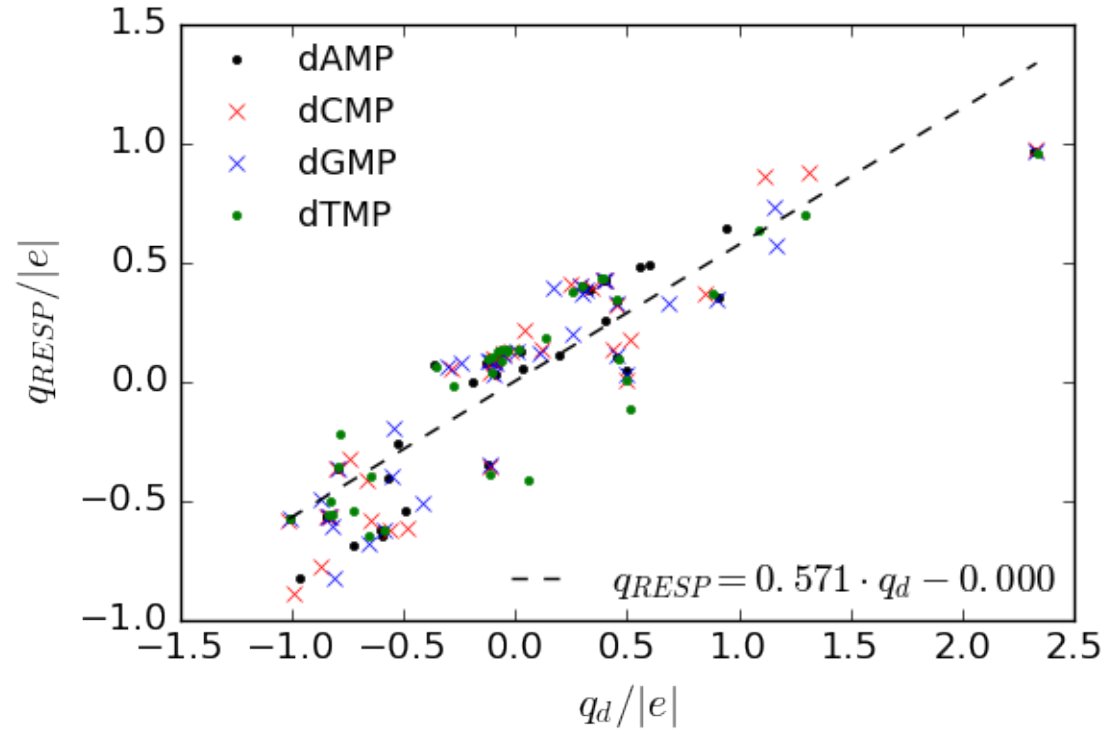
```

avg |component of dipole moment| = 0.533152481358
Eigenvalues of A: [ -2.37945476e-13   6.83756605e-04   1.35198577e-03   2.83240101e-03
 8.80661202e-03   1.01652169e-02   1.43918256e-02   2.24038844e-02
 2.66953509e-02   3.64475216e-02   5.64690382e-02   7.10660702e-02
 9.51073527e-02   1.45281704e-01   1.55610646e-01   1.21487834e+00
 1.85739478e+00   4.23827344e+00   2.80359026e+01   3.40250386e+01
 1.68708280e+02   1.74241767e+02   1.99644487e+02   2.86733801e+02
 4.11422659e+02   5.83390988e+02   8.81782052e+02   1.06294822e+03
 2.01839807e+03   2.64389501e+03   5.81506059e+03   6.62449773e+03
 8.94119714e+03   2.47662231e+04   6.94905431e+04   1.91765085e+05]
sum(charges) = 0.00000
RMS(D_mu - calculated_D_mu) = 0.0938277883159
<|D_mu - calculated_D_mu|> = 0.0737873756397
max|D_mu - calculated_D_mu| = 0.324114767921
lowest possible RMS(D_mu - calculated_D_mu) = 0.058050736819
lowest possible max|D_mu - calculated_D_mu| = 0.22356873809
lowest possible <|D_mu - calculated_D_mu|> = 0.0443742870311

APT sum(charges) = 0.00000
APT max|D_mu - calculated_D_mu| = 1.43351287103
APT <|D_mu - calculated_D_mu|> = 0.473736212581
RESP sum(charges) = -0.00000
RESP max|D_mu - calculated_D_mu| = 0.497907430054
RESP <|D_mu - calculated_D_mu|> = 0.109973277496

```





```
In [5]: # Print the tables with charges
dd_minus_apt_all = []
dd_minus_apt_mad = 0.0
```

```

dd_tot_cnt = 0

for key,rec in final_charges.items():
    q, apt_avg, resp_avg = rec['dd'], rec['apt'], rec['resp']

    print 'Here are the charges for << %s >>:' % key
    nAtoms = len(atom_names[key].items())
    print '%3s \t %7s \t %8s \t %8s \t %8s' % ('at_N', 'at_name', 'q_dd', 'q_apt', 'q_resp')
    for i in range(nAtoms):
        args = (i+1, atom_names[key][i+1], q[i], apt_avg[i], resp_avg[i])
        print '%3d \t %7s \t %8.3f \t %8.3f \t %8.3f' % args
        dff = abs(q[i] - apt_avg[i])
        dd_minus_apt_all.append( [dff, key, args] )
        dd_minus_apt_mad += dff
        dd_tot_cnt += 1

    print 'sum(charges) = %.4f' % sum(q)
    print
    print

# analyze differences w.r.t. APT charges
print '<|dd-apt|> = ', dd_minus_apt_mad / dd_tot_cnt
print 'Quantiles:'
s = sorted(dd_minus_apt_all, key=lambda x: -x[0])
nAll = len(dd_minus_apt_all)
for q in range(0,100,5):
    n = sum([ 1 if x[0] > q/100.0 else 0 for x in dd_minus_apt_all] )
    print 'N_{diff > %.2f}: %4d / %4d = %8.2f %%' % (q/100.0, n, nAll, n*100.0/nAll )

print 'sorted |dd-apt|:'
plt.hist([rec[0] for rec in dd_minus_apt_all])
plt.show()

```

Here are the charges for << gua >>:

at_N	at_name	q_dd	q_apt	q_resp
1	HO3'	0.293	0.261	0.402
2	O3'	-0.590	-0.609	-0.627
3	C3'	0.454	0.467	0.330
4	C4'	0.450	0.410	0.110
5	H3'	-0.093	-0.032	0.027
6	C2'	-0.113	-0.084	-0.351
7	C1'	0.901	0.916	0.345
8	O4'	-0.553	-0.788	-0.398
9	C5'	0.497	0.504	0.032
10	H1'	-0.307	-0.053	0.061
11	H2'2	-0.054	0.025	0.112
12	H2'1	0.009	-0.003	0.125
13	H4'	-0.090	-0.057	0.075
14	O5'	-0.792	-1.013	-0.365
15	H5'1	-0.115	-0.017	0.087
16	H5'2	-0.125	-0.010	0.086
17	P	2.329	2.330	0.966
18	N9	-0.541	-0.572	-0.195
19	C4	0.682	0.661	0.325
20	C8	0.255	0.221	0.198
21	N7	-0.411	-0.433	-0.511
22	C5	-0.247	-0.260	0.073
23	N3	-0.823	-0.847	-0.607

24	C2	1.155	1.149	0.726
25	N1	-0.659	-0.647	-0.678
26	C6	1.165	1.172	0.568
27	O6	-0.868	-0.844	-0.492
28	H1	0.168	0.209	0.391
29	N2	-0.813	-0.800	-0.823
30	H21	0.296	0.223	0.369
31	H22	0.320	0.255	0.381
32	H8	0.114	0.074	0.115
33	OP	-1.007	-0.832	-0.577
34	OP1	-0.839	-0.854	-0.570
35	HP1	0.392	0.366	0.427
36	OP2	-0.838	-0.853	-0.565
37	HP2	0.399	0.368	0.425

sum(charges) = -0.0000

Here are the charges for << ade >>:

at_N	at_name	q_dd	q_apt	q_resp
1	HO3'	0.298	0.262	0.402
2	O3'	-0.600	-0.611	-0.628
3	C3'	0.452	0.468	0.335
4	C4'	0.451	0.412	0.104
5	H3'	-0.089	-0.027	0.031
6	C2'	-0.119	-0.087	-0.347
7	C1'	0.909	0.923	0.348
8	O4'	-0.572	-0.792	-0.404
9	C5'	0.499	0.503	0.048
10	H1'	-0.366	-0.058	0.068
11	H2'2	-0.070	0.033	0.118
12	H2'1	0.023	-0.001	0.124
13	H4'	-0.080	-0.054	0.078
14	O5'	-0.793	-1.021	-0.371
15	H5'1	-0.115	-0.014	0.084
16	H5'2	-0.130	-0.012	0.081
17	P	2.319	2.329	0.966
18	N9	-0.523	-0.612	-0.264
19	C4	0.555	0.513	0.477
20	C8	0.404	0.327	0.251
21	N7	-0.495	-0.513	-0.541
22	C5	-0.193	-0.187	-0.002
23	N3	-0.600	-0.654	-0.649
24	C2	0.598	0.584	0.484
25	N1	-0.723	-0.687	-0.688
26	C6	0.946	0.997	0.643
27	N6	-0.964	-0.816	-0.824
28	H2	0.029	0.007	0.052
29	H62	0.337	0.247	0.385
30	H61	0.307	0.253	0.393
31	H8	0.198	0.081	0.109
32	OP	-1.008	-0.824	-0.575
33	OP1	-0.848	-0.848	-0.569
34	HP1	0.402	0.364	0.427
35	OP2	-0.843	-0.850	-0.567
36	HP2	0.404	0.365	0.425

sum(charges) = 0.0000

Here are the charges for << thy >>:

at_N	at_name	q_dd	q_apt	q_resp
1	HO3'	0.296	0.264	0.401
2	O3'	-0.583	-0.612	-0.626
3	C3'	0.454	0.471	0.345
4	C4'	0.461	0.426	0.094
5	H3'	-0.108	-0.033	0.034
6	C2'	-0.117	-0.082	-0.391
7	C1'	0.880	0.903	0.365
8	O4'	-0.651	-0.795	-0.403
9	C5'	0.497	0.501	0.005
10	H1'	-0.354	-0.045	0.061
11	H2'2	-0.081	0.025	0.127
12	H2'1	0.018	-0.000	0.132
13	H4'	-0.059	-0.058	0.084
14	O5'	-0.797	-1.016	-0.357
15	H5'1	-0.102	-0.013	0.099
16	H5'2	-0.126	-0.013	0.097
17	P	2.333	2.330	0.956
18	N1	-0.781	-0.882	-0.218
19	C2	1.293	1.208	0.698
20	C6	0.511	0.450	-0.114
21	C5	-0.273	-0.288	-0.023
22	C4	1.086	1.073	0.635
23	N3	-0.656	-0.710	-0.648
24	O2	-0.726	-0.856	-0.542
25	H6	0.136	0.080	0.180
26	C7	0.058	0.084	-0.416
27	O4	-0.831	-0.812	-0.505
28	H3	0.254	0.218	0.376
29	H73	-0.036	-0.006	0.128
30	H72	-0.065	-0.009	0.136
31	H71	-0.036	-0.011	0.136
32	OP	-1.012	-0.829	-0.576
33	OP1	-0.835	-0.840	-0.564
34	HP1	0.391	0.360	0.431
35	OP2	-0.819	-0.838	-0.563
36	HP2	0.382	0.353	0.429

sum(charges) = 0.0000

Here are the charges for << cyt >>:

at_N	at_name	q_dd	q_apt	q_resp
1	HO3'	0.294	0.258	0.401
2	O3'	-0.565	-0.612	-0.628
3	C3'	0.453	0.472	0.321
4	C4'	0.433	0.423	0.129
5	H3'	-0.117	-0.030	0.039
6	C2'	-0.117	-0.080	-0.360
7	C1'	0.851	0.880	0.367
8	O4'	-0.668	-0.791	-0.416
9	C5'	0.495	0.497	0.000
10	H1'	-0.284	-0.066	0.053
11	H2'2	-0.051	0.032	0.120
12	H2'1	-0.022	0.001	0.125
13	H4'	-0.098	-0.058	0.075

14	O5'	-0.800	-1.016	-0.363
15	H5'1	-0.099	-0.011	0.096
16	H5'2	-0.100	-0.011	0.095
17	P	2.326	2.329	0.968
18	N1	-0.740	-0.776	-0.328
19	C2	1.315	1.213	0.871
20	N3	-0.873	-0.887	-0.780
21	C4	1.112	1.144	0.858
22	C5	-0.484	-0.492	-0.619
23	C6	0.510	0.476	0.174
24	H6	0.120	0.085	0.129
25	H5	0.041	0.041	0.216
26	N4	-0.991	-0.826	-0.895
27	H41	0.249	0.240	0.408
28	H42	0.342	0.235	0.390
29	O2	-0.646	-0.878	-0.583
30	OP1	-0.846	-0.848	-0.567
31	OP	-1.014	-0.830	-0.582
32	OP2	-0.827	-0.847	-0.565
33	HP2	0.394	0.366	0.425
34	HP1	0.405	0.369	0.425

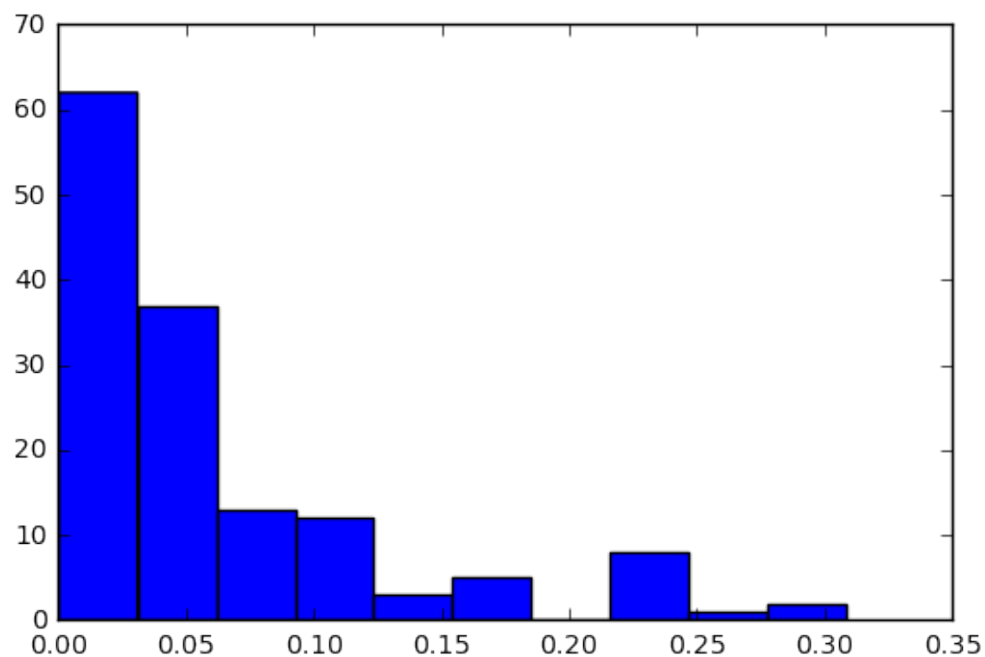
sum(charges) = -0.0000

<|dd-apt|> = 0.0615956738245

Quantiles:

N_{diff > 0.00}:	143 / 143 =	100.00 %
N_{diff > 0.05}:	53 / 143 =	37.06 %
N_{diff > 0.10}:	30 / 143 =	20.98 %
N_{diff > 0.15}:	16 / 143 =	11.19 %
N_{diff > 0.20}:	11 / 143 =	7.69 %
N_{diff > 0.25}:	3 / 143 =	2.10 %
N_{diff > 0.30}:	2 / 143 =	1.40 %
N_{diff > 0.35}:	0 / 143 =	0.00 %
N_{diff > 0.40}:	0 / 143 =	0.00 %
N_{diff > 0.45}:	0 / 143 =	0.00 %
N_{diff > 0.50}:	0 / 143 =	0.00 %
N_{diff > 0.55}:	0 / 143 =	0.00 %
N_{diff > 0.60}:	0 / 143 =	0.00 %
N_{diff > 0.65}:	0 / 143 =	0.00 %
N_{diff > 0.70}:	0 / 143 =	0.00 %
N_{diff > 0.75}:	0 / 143 =	0.00 %
N_{diff > 0.80}:	0 / 143 =	0.00 %
N_{diff > 0.85}:	0 / 143 =	0.00 %
N_{diff > 0.90}:	0 / 143 =	0.00 %
N_{diff > 0.95}:	0 / 143 =	0.00 %

sorted |dd-apt|:



```
In [6]: # Plot the distributions of approximation errors
```

```
symb2Z = {'H': 1.0, 'C': 6.0, 'N': 7.0, 'O': 8.0, 'P': 15}
```

```
distrs = {'abs': plt.figure().gca(), 'ang': plt.figure().gca() }
```

```
for g in distrs:
    #pass#
    distrs[g].set_xscale("log")
    distrs[g].tick_params(labelsize=14)
```

```
accumulated_distr = {}
```

```
for ch_type in ['dd', 'apt', 'resp']:
    d_abs_diffs = []
    d_angs = []
    for key, rec in final_charges.items():
        q = rec[ch_type]
        fname, _, __ = molecules[key]
        data_list = json.load(open(fname))

        nAtoms = len(atom_names[key].items())

        # sort atoms by their IDs and preserve their names only
        at_names = [v for (k,v) in sorted( atom_names[key].items(), key=lambda (k,v): k )]

        for R, D in zip( data_list['coords'], data_list['dipole']):
            ch_center = np.zeros(3)
            d_charges = np.zeros(3)
            geom_center = np.zeros(3)
            Ztot = 0.0
            for at_name, ri in zip(at_names, np.array(R)):
```

```

        Z = symb2Z[at_name[0]]
        ch_center += ri * Z
        Ztot += Z
    ch_center /= Ztot
    if np.linalg.norm( ch_center ) > 1e-6:
        print 'Warning: ch_center is not zero!', ch_center

    for i, ri in enumerate(np.array(R)):
        d_charges += q[i] * (ri - ch_center)
    d_charges /= Debye2eA
    D_eA = np.array(D)
    d_abs_diffs.append( np.abs(np.linalg.norm(d_charges) - np.linalg.norm(D_eA)) )
    cs = d_charges.dot(D_eA) / np.linalg.norm(d_charges)/np.linalg.norm(D_eA)
    d_angs.append( np.arccos( cs )/np.pi*180 )
print ch_type

for lbl, data in zip(['|d|-|D|', 'angle(d,D)'],
                    [d_abs_diffs, d_angs]):
    print '%s:  mean = %7.3f, median = %.5f, min = %.5f, max = %.3f' % (lbl,
                                                                    np.mean(data),
                                                                    np.median(data),
                                                                    min(data),
                                                                    max(data) )

Lbels = {'dd': 'd', 'apt': 'APT', 'resp': 'RESP'}
colors = {'dd': 'b', 'apt': 'g', 'resp': 'r'}

for k, data, bins in zip(['abs', 'ang'],
                        [d_abs_diffs, d_angs],
                        [ np.logspace(-4, 1.5, 80), np.logspace(-1, 2.3, 80) ]):

    distrs[k].set_xlim(bins[0], bins[-1])
    distrs[k].hist(data, label="$q_{%s}$" % Lbels[ch_type], alpha=0.5,
                  bins=bins, color=colors[ch_type])
    x_av = np.mean(data)
    distrs[k].axvline(x_av, color=colors[ch_type],
                    linestyle=(0,(4,1)), linewidth=1)
    ax2 = distrs[k].twinx()
    ax2.set_xlim(distrs[k].get_xlim())
    ax2.set_xscale("log")
    ax2.tick_params(labelsize=14)
    ax2.set_xticks( [x_av])
    ax2.set_xticklabels( ['%.2f' % x_av], rotation=90, ha='center' )
    #ax2.set_xlabel('Average')

accumulated_distr[ch_type] = d_abs_diffs

distrs['abs'].set_xlabel(
    r'$\left|\left|\vec{d}\right|_{\mathrm{approx}}\right| - \left|\vec{d}\right|_{\mathrm{exact}}\right|$, '+
    r'$\mathrm{Debye}$',
    fontsize=15)
distrs['ang'].set_xlabel(
    r'$\theta\left(\left|\vec{d}\right|_{\mathrm{approx}}, \left|\vec{d}\right|_{\mathrm{exact}}\right)$, $\mathrm{deg.}$',
    fontsize=15)

```

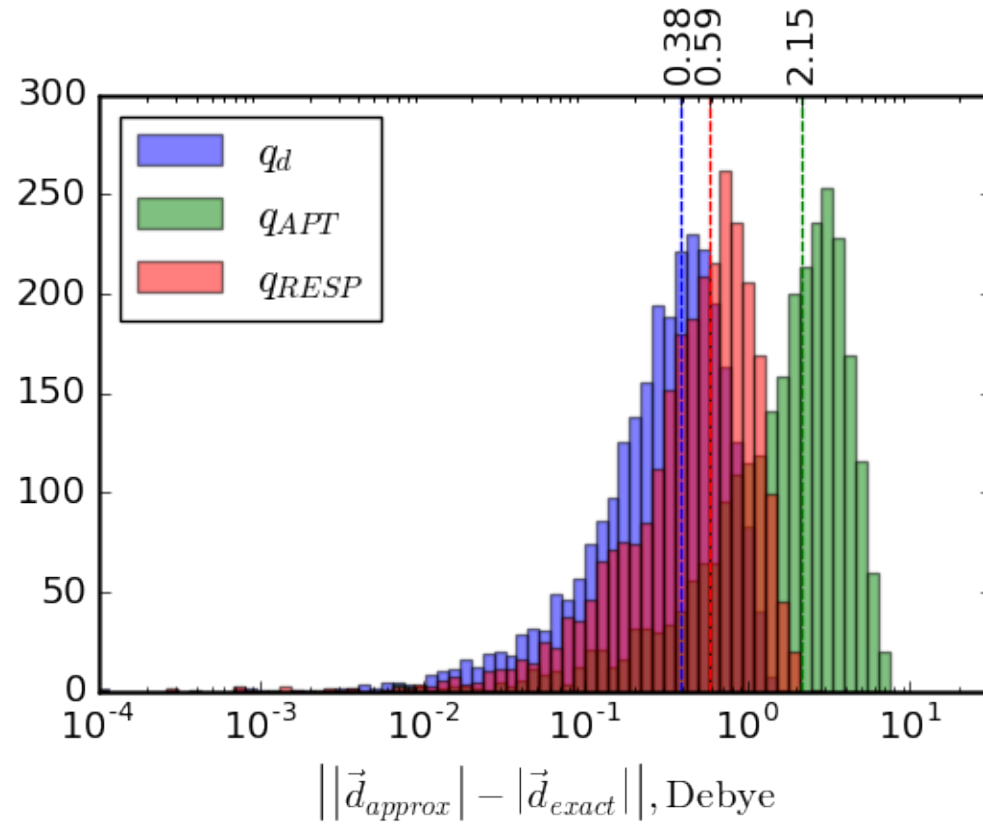
```

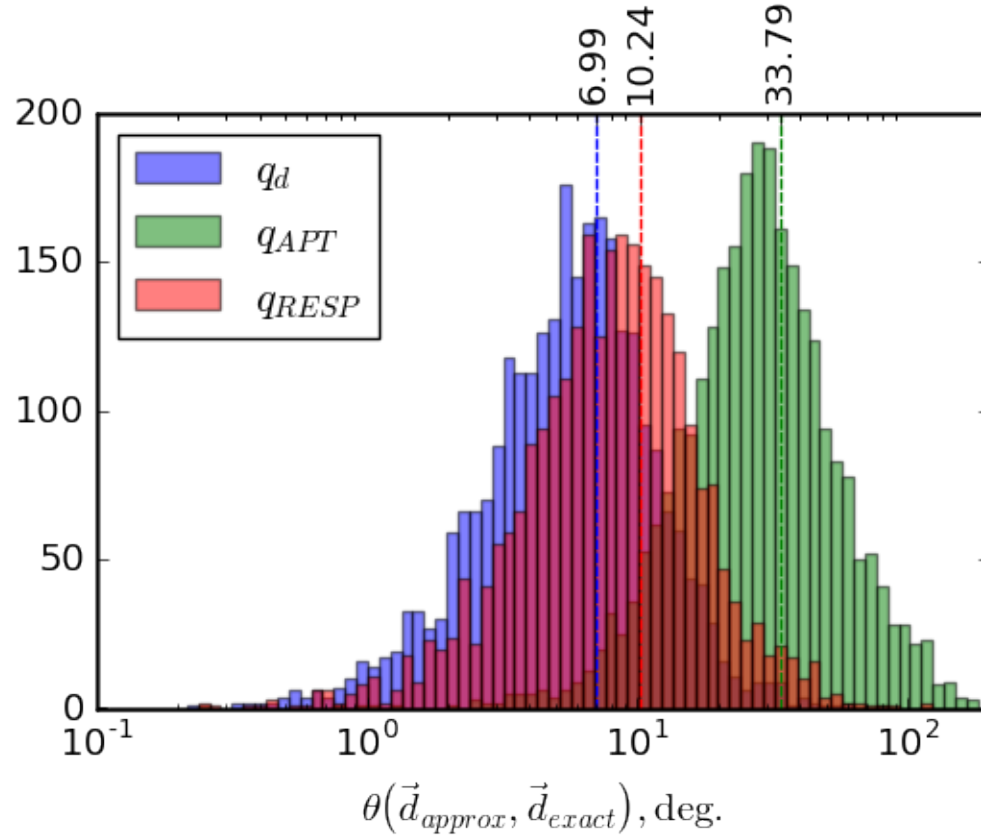
for g in distrs:
    distrs[g].legend(loc='upper left', fontsize=16)
    distrs[g].figure.savefig('distr_%.png' % g, dpi=300, bbox_inches='tight')

plt.show()

dd
||d|-|D|| : mean = 0.383, median = 0.33050, min = 0.00003, max = 1.646
angle(d,D): mean = 6.987, median = 5.70319, min = 0.23297, max = 78.070
apt
||d|-|D|| : mean = 2.153, median = 1.94872, min = 0.00038, max = 6.930
angle(d,D): mean = 33.794, median = 27.89656, min = 0.23861, max = 170.198
resp
||d|-|D|| : mean = 0.588, median = 0.53005, min = 0.00026, max = 2.805
angle(d,D): mean = 10.236, median = 8.16056, min = 0.05253, max = 122.302

```





In [7]: # Produce a similar plots for graphical abstract

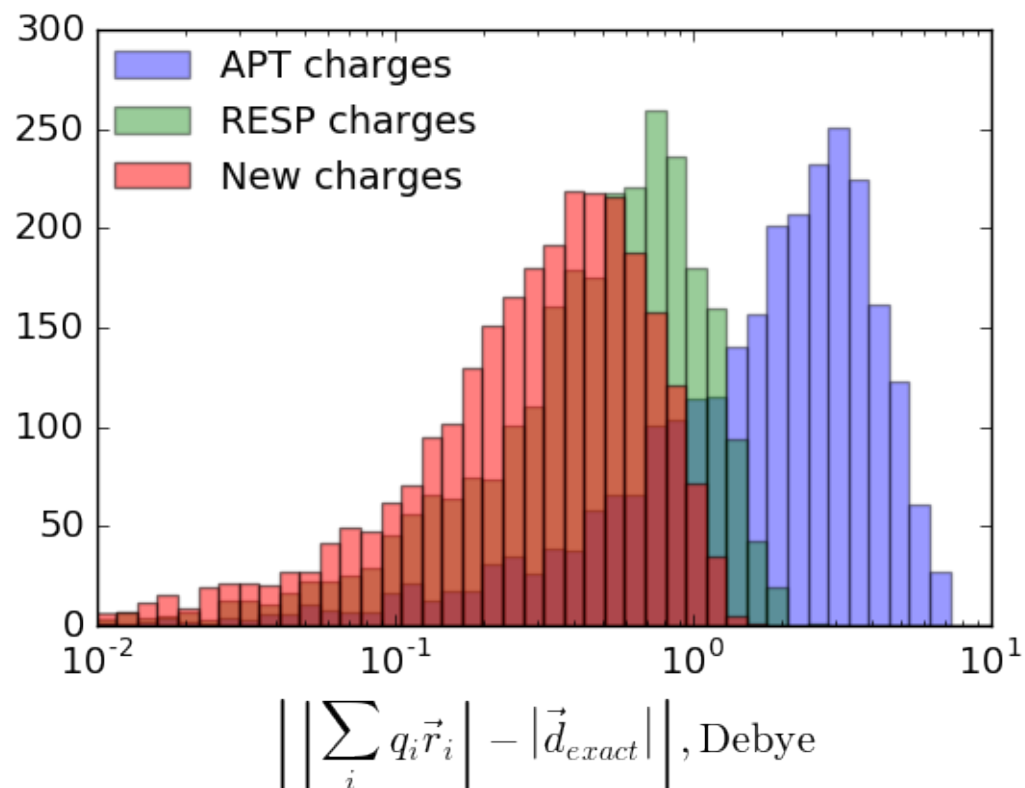
```
bins = np.logspace(-2, 1.0, 45)

plt.hist(accumulated_distr['apt'], alpha=0.4,bins=bins, label='APT charges')
plt.hist(accumulated_distr['resp'], alpha=0.4,bins=bins, label='RESP charges')
plt.hist(accumulated_distr['dd'], alpha=0.5,bins=bins, label='New charges')

plt.gca().set_xscale("log")
plt.gca().tick_params(labelsize=14)
plt.gca().set_xlabel(
    r'$\left| \left| \sum_i \vec{q}_i \right| - \left| \vec{d}_{exact} \right| \right|$, $\mathrm{deg.}$',
    fontsize=16)
plt.legend(loc='upper left', fontsize=14, frameon=False, borderaxespad=0.1)

plt.savefig('GA_template.png', dpi=300, bbox_inches='tight')

plt.show()
```



```
In [8]: def base_dipole(q, key, data_list):
    base_atoms = dict([it for it in atom_names[key].items()
                        if it[1].find('P') == -1 and
                        (it[1].find("") == -1 or it[1] == "C1" ) ])
    print 'Base atoms:', base_atoms
    base_atoms_Z = [symb2Z[x[0]] for x in base_atoms.values()]
    base_atoms_Names = base_atoms.values()
    base_atoms = [x-1 for x in base_atoms.keys()] # make them 0-based
    d_vals = []

    # find the charge which we should assign to C1'
    Q_wo_clprime = 0
    for i, nm in zip(base_atoms, base_atoms_Names):
        if nm != "C1'":
            Q_wo_clprime += q[i]
    print "Total charge without C1'", Q_wo_clprime

    for R in data_list['coords']:

        ch_center = np.zeros(3)
        Ztot = 0.0

        # calculate the charge center
        for Z, i, nm, ri in zip(base_atoms_Z, base_atoms,
                                base_atoms_Names, np.array(R)[base_atoms]):
            if nm == "C1'":
                Z = 6.0 + 3 * 1.0 # emulate methyl group
```

```

        ch_center += ri * Z
        Ztot += Z
    ch_center /= Ztot

    # calculate dipole moment
    dip_base = np.zeros(3)
    for i, nm, ri in zip(base_atoms, base_atoms_Names, np.array(R)[base_atoms]):
        at_q = q[i] if nm != "C1'" else -Q_wo_clprime
        dip_base += at_q * (ri - ch_center)
    d_vals.append( np.linalg.norm(dip_base) )

d_avg = np.mean(d_vals)
d_std = np.std(d_vals)
print '%s: %.5f +/- %.5f eA, %.5f +/- %.5f Debye' % (key,
                                                    d_avg, d_std,
                                                    d_avg/Debye2eA, d_std/Debye2eA)

print 'total base charge: %.5f' % sum( q[i] for i in base_atoms)
print

for key, rec in final_charges.items():

    fname, _, __ = molecules[key]
    data_list = json.load(open(fname))

    q, apt_avg, resp_avg = rec['dd'], rec['apt'], rec['resp']
    print key
    # analyze dipole moment of the nucleotide base
    print 'Averaged dipole moment of nucleotide base:'
    print ' - with new dipole-derived charges'
    base_dipole(q, key, data_list)
    print ' - with new <RESP>'
    base_dipole(resp_avg, key, data_list)
    print ' - with new <APT>'
    base_dipole(apt_avg, key, data_list)

gua
Averaged dipole moment of nucleotide base:
 - with new dipole-derived charges
Base atoms: {32: 'H8', 7: 'C1'', 18: 'N9', 19: 'C4', 20: 'C8', 21: 'N7', 22: 'C5', 23: 'N3', 24: 'C2',
25: 'N1', 26: 'C6', 27: 'O6', 28: 'H1', 29: 'N2', 30: 'H21', 31: 'H22'}
Total charge without C1' -0.207013582463
gua: 1.49715 +/- 0.01494 eA, 7.19112 +/- 0.07175 Debye
total base charge: 0.69397
 - with new <RESP>
Base atoms: {32: 'H8', 7: 'C1'', 18: 'N9', 19: 'C4', 20: 'C8', 21: 'N7', 22: 'C5', 23: 'N3', 24: 'C2',
25: 'N1', 26: 'C6', 27: 'O6', 28: 'H1', 29: 'N2', 30: 'H21', 31: 'H22'}
Total charge without C1' -0.160091150336
gua: 1.31254 +/- 0.01434 eA, 6.30440 +/- 0.06890 Debye
total base charge: 0.18539
 - with new <APT>
Base atoms: {32: 'H8', 7: 'C1'', 18: 'N9', 19: 'C4', 20: 'C8', 21: 'N7', 22: 'C5', 23: 'N3', 24: 'C2',
25: 'N1', 26: 'C6', 27: 'O6', 28: 'H1', 29: 'N2', 30: 'H21', 31: 'H22'}
Total charge without C1' -0.439996774497
gua: 1.60838 +/- 0.01787 eA, 7.72540 +/- 0.08583 Debye
total base charge: 0.47616

```

```

ade
Averaged dipole moment of nucleotide base:
- with new dipole-derived charges
Base atoms: {7: "C1'", 18: 'N9', 19: 'C4', 20: 'C8', 21: 'N7', 22: 'C5', 23: 'N3', 24: 'C2', 25: 'N1',
26: 'C6', 27: 'N6', 28: 'H2', 29: 'H62', 30: 'H61', 31: 'H8'}
Total charge without C1' -0.125158092584
ade: 0.55459 +/- 0.00941 eA, 2.66379 +/- 0.04521 Debye
total base charge: 0.78395
- with new <RESP>
Base atoms: {7: "C1'", 18: 'N9', 19: 'C4', 20: 'C8', 21: 'N7', 22: 'C5', 23: 'N3', 24: 'C2', 25: 'N1',
26: 'C6', 27: 'N6', 28: 'H2', 29: 'H62', 30: 'H61', 31: 'H8'}
Total charge without C1' -0.174762059229
ade: 0.47603 +/- 0.01552 eA, 2.28646 +/- 0.07456 Debye
total base charge: 0.17315
- with new <APT>
Base atoms: {7: "C1'", 18: 'N9', 19: 'C4', 20: 'C8', 21: 'N7', 22: 'C5', 23: 'N3', 24: 'C2', 25: 'N1',
26: 'C6', 27: 'N6', 28: 'H2', 29: 'H62', 30: 'H61', 31: 'H8'}
Total charge without C1' -0.460179413223
ade: 0.82920 +/- 0.01457 eA, 3.98282 +/- 0.06997 Debye
total base charge: 0.46240
thy
Averaged dipole moment of nucleotide base:
- with new dipole-derived charges
Base atoms: {7: "C1'", 18: 'N1', 19: 'C2', 20: 'C6', 21: 'C5', 22: 'C4', 23: 'N3', 24: 'O2', 25: 'H6',
26: 'C7', 27: 'O4', 28: 'H3', 29: 'H73', 30: 'H72', 31: 'H71'}
Total charge without C1' -0.0675305190885
thy: 1.01273 +/- 0.00861 eA, 4.86435 +/- 0.04136 Debye
total base charge: 0.81253
- with new <RESP>
Base atoms: {7: "C1'", 18: 'N1', 19: 'C2', 20: 'C6', 21: 'C5', 22: 'C4', 23: 'N3', 24: 'O2', 25: 'H6',
26: 'C7', 27: 'O4', 28: 'H3', 29: 'H73', 30: 'H72', 31: 'H71'}
Total charge without C1' -0.179451927273
thy: 0.88473 +/- 0.01453 eA, 4.24955 +/- 0.06980 Debye
total base charge: 0.18534
- with new <APT>
Base atoms: {7: "C1'", 18: 'N1', 19: 'C2', 20: 'C6', 21: 'C5', 22: 'C4', 23: 'N3', 24: 'O2', 25: 'H6',
26: 'C7', 27: 'O4', 28: 'H3', 29: 'H73', 30: 'H72', 31: 'H71'}
Total charge without C1' -0.459266366667
thy: 1.84764 +/- 0.02592 eA, 8.87458 +/- 0.12450 Debye
total base charge: 0.44380

```

```

cyt
Averaged dipole moment of nucleotide base:
- with new dipole-derived charges
Base atoms: {7: "C1'", 18: 'N1', 19: 'C2', 20: 'N3', 21: 'C4', 22: 'C5', 23: 'C6', 24: 'H6', 25: 'H5',
26: 'N4', 27: 'H41', 28: 'H42', 29: 'O2'}
Total charge without C1' -0.0445629429197
cyt: 1.28646 +/- 0.01314 eA, 6.17915 +/- 0.06314 Debye
total base charge: 0.80637
- with new <RESP>
Base atoms: {7: "C1'", 18: 'N1', 19: 'C2', 20: 'N3', 21: 'C4', 22: 'C5', 23: 'C6', 24: 'H6', 25: 'H5',
26: 'N4', 27: 'H41', 28: 'H42', 29: 'O2'}
Total charge without C1' -0.158119004894
cyt: 1.38063 +/- 0.01640 eA, 6.63146 +/- 0.07879 Debye
total base charge: 0.20879
- with new <APT>
Base atoms: {7: "C1'", 18: 'N1', 19: 'C2', 20: 'N3', 21: 'C4', 22: 'C5', 23: 'C6', 24: 'H6', 25: 'H5',
26: 'N4', 27: 'H41', 28: 'H42', 29: 'O2'}
Total charge without C1' -0.425615606852
cyt: 1.76089 +/- 0.03706 eA, 8.45791 +/- 0.17800 Debye
total base charge: 0.45462

```

In []:

Dipole-derived charges of and 5'-deoxycytidylic acid (dCMP) in polarizable dielectric environment (IEFPCM water, $\epsilon = 78.39$)

Computation details. Each of the 613 conformers obtained earlier in vacuum¹ was additionally optimized in the presence of a continuum polarizable dielectric environment described by IEFPCM² solvation model with the settings corresponding to a standard solvent 'water' (in particular, dielectric constant of the solvent $\epsilon = 78.39$, an optional value for the dielectric constant at infinite frequency $\epsilon_\infty = 1.776$, the solvent radius 1.385 Å). The cavity GePol encompassing the dCMP molecule was built using the UFF atomic radii³ (with the sphere radius scaling factor set to 1.0) and Hydrogen atoms having individual spheres (explicit hydrogens).

After geometry optimization, harmonic vibrational analysis was performed in order to obtain the values of APT charges in the presence of the environment. The calculations performed at this stage employed the same level of theory B3LYP/6-31G(d,p) as those performed in vacuum.

The same Python program was used for obtaining the dipole-derived charges in dielectric environment as that for vacuum case. Input data files used for the program can be found at *figshare* repository:

Nikolaienko, Tymofii (2017): Conformers of canonical 5'-deoxycytidylic acid molecule (dCMP) in continuum polarizable dielectric environment (IEFPCM water, $\epsilon = 78.39$). *figshare*.; <https://doi.org/10.6084/m9.figshare.5687419> ; Retrieved: 22:41, Dec 10, 2017 (GMT).

Results.

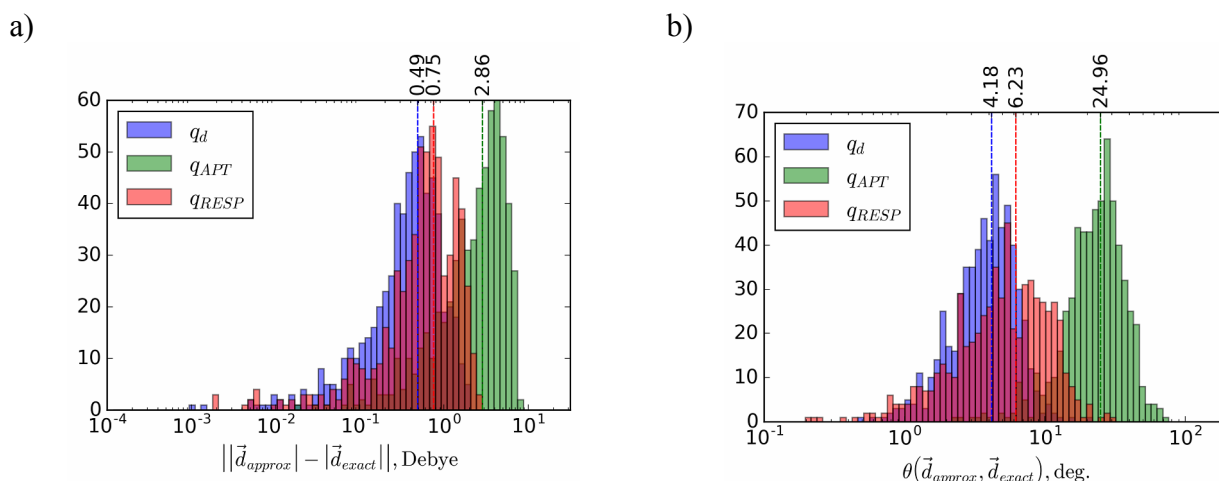


Figure SF1. The distribution of error measures for the approximation of exact dipole moment $\vec{d}_{exact}$ (obtained in polarizable continuum dielectric environment) with the value $\vec{d}_q$ calculated using the fixed RESP (q_{RESP}), APT (q_{APT}) and the dipole-derived (q_d) charges: errors in the absolute value (a) and the angle between $\vec{d}_{exact}$ and $\vec{d}_q$ (b). Note the logarithmic scale on the horizontal axis.

¹ See [T. Yu. Nikolaienko and D. M. Hovorun. *Dopov. Nac. akad. nauk Ukr.* 2010, (9), 173–184] and [T. Yu. Nikolaienko, L. A. Bulavin and D. M. Hovorun. (2017): Conformers of canonical 2'-deoxyribonucleotides, the model DNA monomers. *figshare*. <https://doi.org/10.6084/m9.figshare.5258737.v1> Retrieved: 20:42, Jul 29, 2017 (GMT)] for details

² See [J. Tomasi, B. Mennucci and R. Cammi, *Chem. Rev.* 2005, **105**, 2999–3094] for a review.

³ A. K. Rappe, C. J. Casewit, K. S. Colwell, W. A. Goddard, and W. M. Skiff. UFF, a full periodic table force field for molecular mechanics and molecular dynamics simulations. *J. Am. Chem. Soc.*, **114**:10024–10035, 1992.

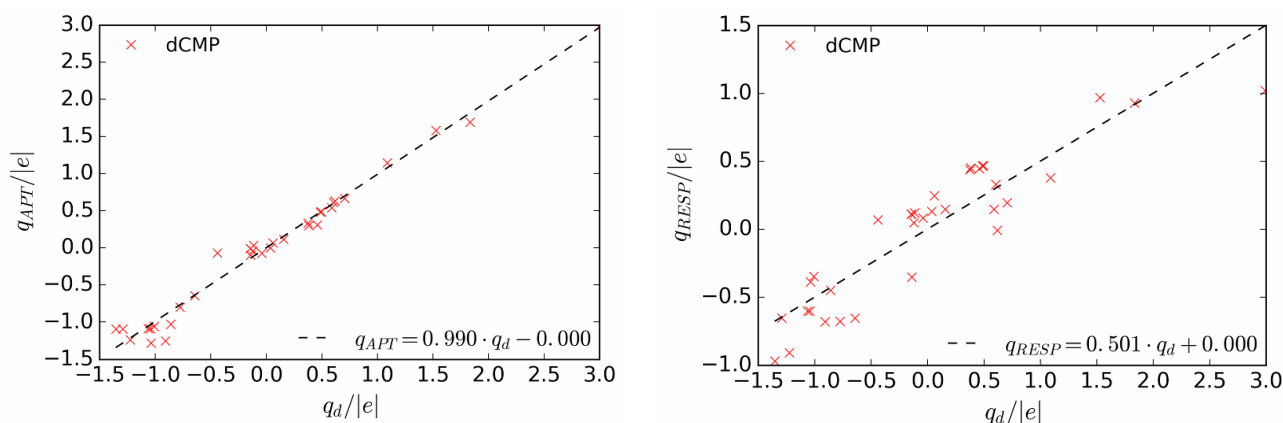


Figure SF2. Scatter plot of the effective atomic charges of 5'-deoxycytidylic acid molecule (dCMP) obtained in polarizable continuum dielectric environment by different methods: RESP (q_{RESP}), APT (q_{APT}) and the dipole-derived (q_d) charges proposed in this paper

Table ST1. Values of atomic charges of 5'-deoxycytidylic acid molecule (dCMP) in polarizable continuum dielectric environment calculated by environment by different methods: RESP (q_{RESP}), APT (q_{APT}) and the dipole-derived (q_d) charges proposed in this paper

Atom number	Atom Name	q_d	q_{APT}	q_{RESP}
1	HO3'	0.374	0.333	0.436
2	O3'	-0.778	-0.800	-0.678
3	C3'	0.602	0.612	0.331
4	C4'	0.586	0.540	0.148
5	H3'	-0.124	-0.041	0.047
6	C2'	-0.141	-0.101	-0.353
7	C1'	1.087	1.144	0.378
8	O4'	-0.861	-1.027	-0.452
9	C5'	0.616	0.630	-0.008
10	H1'	-0.442	-0.068	0.068
11	H2'2	-0.117	0.031	0.121
12	H2'1	0.036	-0.002	0.130
13	H4'	-0.041	-0.075	0.082
14	O5'	-1.039	-1.279	-0.388
15	H5'1	-0.146	-0.012	0.111
16	H5'2	-0.145	-0.012	0.108
17	P	2.991	2.980	1.021
18	N1	-1.009	-1.057	-0.347
19	C2	1.833	1.692	0.930
20	N3	-1.228	-1.236	-0.906
21	C4	1.524	1.579	0.969
22	C5	-0.646	-0.646	-0.653
23	C6	0.703	0.663	0.195
24	H6	0.156	0.115	0.147
25	H5	0.059	0.067	0.245
26	N4	-1.356	-1.092	-0.970
27	H41	0.381	0.299	0.451
28	H42	0.458	0.308	0.446
29	O2	-0.910	-1.250	-0.681
30	OP1	-1.065	-1.088	-0.604
31	OP	-1.295	-1.090	-0.654
32	OP2	-1.044	-1.085	-0.603
33	HP2	0.484	0.482	0.466
34	HP1	0.495	0.487	0.466

sum(charges) = -0.0000