

# MCCE Data Analysis

## MCCE data analysis tools

### fitpka.py

*Fit the titration curve of an ionizable residue.*

#### Syntax:

```
fitpka.py [-h] RES [RES ...]
```

Fit a titration of charged residues

positional arguments:

RES        Charged residue names to plot, as in sum\_crg.out or pK.out

optional arguments:

-h, --help show this help message and exit

#### Required input file

- sum\_crg.out

#### Example:

Find the residue IDs:

```
$ cat sum_crg.out
pH          0      1      2      3      4      5      6      7      8      9     10     11     12
13    14
NTR+A0001_  1.00  1.00  1.00  1.00  0.99  0.96  0.70  0.20  0.03  0.00  0.00  0.00  0.00
0.00  0.00
LYS+A0001_  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  0.97  0.78  0.27  0.04  0.00
0.00  0.00
ARG+A0005_  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  1.00  0.97  0.80
0.38  0.08
GLU-A0007_ -0.00 -0.01 -0.07 -0.38 -0.84 -0.98 -1.00 -1.00 -1.00 -1.00 -1.00 -1.00 -1.00
-1.00
```

[illegible]

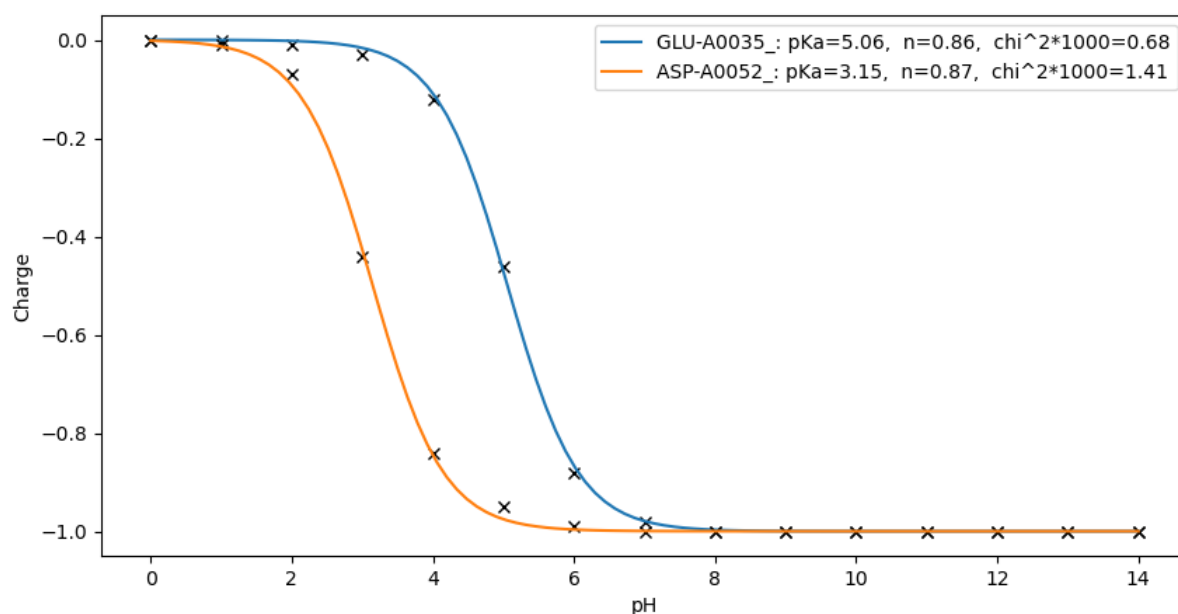
```

ASP-A0101_ -0.00 -0.00 -0.01 -0.09 -0.51 -0.91 -0.99 -1.00 -1.00 -1.00 -1.00 -1.00 -1.00 -1.00
-1.00
ARG+A0112_ 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 0.98 0.87
0.43 0.09
ARG+A0114_ 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 0.99 0.94
0.63 0.17
LYS+A0116_ 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 0.97 0.75 0.27 0.05 0.01
0.00 0.00
ASP-A0119_ -0.00 -0.00 -0.03 -0.19 -0.71 -0.96 -1.00 -1.00 -1.00 -1.00 -1.00 -1.00 -1.00 -1.00
-1.00
ARG+A0125_ 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 0.99 0.90
0.55 0.13
ARG+A0128_ 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 1.00 0.99 0.97
0.79 0.31
CTR-A0129_ -0.00 -0.04 -0.29 -0.75 -0.96 -0.99 -1.00 -1.00 -1.00 -1.00 -1.00 -1.00 -1.00 -1.00
-1.00
-----
Net_Charge 18.93 18.34 16.22 13.47 11.05 9.70 8.68 7.57 7.01 6.38 4.53 1.82 -0.64 -4.61
-9.32
Protons 18.93 18.34 16.22 13.47 11.05 9.70 8.68 7.57 7.01 6.38 4.53 1.82 -0.64 -4.61
-9.32
Electrons 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.00
0.00 0.00

```

Fit the titration curves of residue GLU-A0035\_ and ASP-A0052\_:

```
fitpka.py GLU-A0035_ ASP-A0052_
```



## mfe.py

Analyze ionization free energy of a residue. It tells you why a residue has that pKa and what factors played a role.

### Syntax

```
mfe.py [-h] [-p pH/Eh] [-x TS_correction] [-c cutoff] residue
```

- residue: residue ID as in pK.out
- pH/Eh: pH value at which ionization energy is calculated. Default is the pKa (midpoint) where  $dG = 0$ .
- cut\_off: Report only pairwise interaction bigger than this value.
- TS\_correction: "t" to include entropy in G, "f" not to include, "r" (default) will look for run.prm. If entropy correction was turned on in step 4, mfe should not include this term as entropy has been "removed".

### Required files:

- run.prm
- head3.lst
- extra.tpl for scaling factors that are not equal to 1.
- energies/\*.opp for pairwise interactions

### Example:

Check titration result in pKa.out:

```
cat pK.out
...
ASP- A0052_      3.152
...
```

ASP-A0052\_ is the residue\_ID. Its calculated pKa is 3.152. At this point, the free energy of reaction from ASP neutral to ASP ionized should be close to 0.

Run

```
$ mfe.py ASP- A0052_ -c 0.1
Residue ASP- A0052_ pKa/Em=3.152
=====
Terms           pH      meV      Kcal
-----
vdw0            -0.01   -0.85   -0.02
vdw1             0.00    0.23    0.01
tors            -0.10   -5.86   -0.14
ebkb            -1.27  -73.44  -1.73
dsol             1.99  115.38   2.71
offset          -0.62  -36.17  -0.85
pH&pK0           1.60   92.75   2.18
Eh&Em0           0.00    0.00    0.00
- TS            0.00    0.00    0.00
residues        -1.36  -79.01  -1.86
*****
TOTAL           0.22   13.04    0.31  sum_crg
*****
ASNA0044_       -0.46  -26.92   -0.63    0.00
ARGA0045_       -0.11   -6.36   -0.15    1.00
ASNA0046_       -0.19  -11.09   -0.26    0.00
ASPA0048_        0.50   28.96    0.68   -0.96
SERA0050_        0.13    7.28    0.17    0.00
GLNA0057_        0.22   12.78    0.30    0.00
ASNA0059_       -0.99  -57.18   -1.34    0.00
ARGA0061_       -0.26  -15.37   -0.36    1.00
ASPA0066_        0.27   15.72    0.37   -0.94
ARGA0112_       -0.19  -11.11   -0.26    1.00
ARGA0114_       -0.10   -5.86   -0.14    1.00
=====
```

You can do mfe calculation at pH other than mid-point.

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