```
Python 3.7.8 (default, Jun 24 2020, 07:20:10)
[GCC 4.8.5 20150623 (Red Hat 4.8.5-44)] on linux2
Type "help", "copyright", "credits" or "license" for more information.
IPython 7.2.0 -- An enhanced Interactive Python.

In [1]: runfile('/home/c/josephkarolyuks/Hunger By Programmer Dog', wdir='/home/c/josephkarolyuks')
/home/c/josephkarolyuks/lib/python3/bin/pytohon
Using TensorFlow backend.

Class 0: 12
Class 1: 2
Class 2: 2182
Class 3: 5248
Class 4: 1248
Class 5: 2148
Class 6: 1248
Class 7: 1223
Class 8: 1223

Fit KS22
SMOTE SS200
Fit SMOTE
Fit KS22
Fit SMOTE

Kfold Stats 47/007

Mm: Stats 5/10

Mg_p: Stats 5/210
Mg_n: Stats 2/1000
Mg_p: Stats 2/1000
Mg_n: Stats 2/1000

SMOTE_p: Stats 2000/0
SMOTE_n: Stats 2000/0
SMOTE_p: Stats 2000/0
SMOTE_n: Stats 2000/0

Mg_p: Stats 5/0010
Mg_n: Stats 2/0000
Mg_p: Stats 2/0000
Mg_n: Stats 2/0000

Mg_p: Stats 5/210
Mg_n: Stats 2/1000
Mg_p: Stats 2/1000
Mg_n: Stats 2/1000

Mg_p: Stats 5/2200
Mg_n: Stats 2/1000
Mg_p: Stats 2/1000
Mg_n: Stats 2/1000

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length: 64
subsamples: 1
num_genes: 1002

cu_pcs: 8361
mean_sequence: 1007
length: 64
subsamples: 1
num_genes: 5129

Mm: 17614
mean_sequence: 1076
length: 1002
subsamples: 1
num_genes: 5129

Mm: 3661
mean_sequence: 1062
length: 64
subsamples: 1
num_genes: 1500

Mm_dset: 7/0
mean_sequence: 1
length: 64
subsamples: 1
num_genes: 1411

Mm_ultimat: 7/0
mean_sequence: 1000
length: 64
subsamples: 1
num_genes: 1411

Mm: 3661
mean_sequence: 1130
length: 64
subsamples: 1
num_genes: 1500

Mm: 3661
mean_sequence: 1062
length: 64
subsamples: 1
num_genes: 1500

Mm_dset: 7/0
mean_sequence: 1
length: 64
subsamples: 1
num_genes: 1411

Mm_ultimat: 7/0
mean_sequence: 1000
length: 64
subsamples: 1
num_genes: 1411

Mm: 3661
mean_sequence: 1130
length: 64
subsamples: 1
num_genes: 1500

Kfold: 8011
mean_sequence: 1044
length: 64
subsamples: 27
num_genes: 1146

mmsm: 10015
mean_sequence: 1000
length: 64
subsamples: 1
num_genes: 1146

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length: 64
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num_genes: 1

mm_clust: 203
mean_sequence: 75
length: 64
subsamples: 1
num_genes: 111

cluster_pc: 5/0
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length: 64
subsamples: 1
num_genes: 6170

cluster_pc: 2/0
mean_sequence: 1000
length: 64
subsamples: 1
num_genes: 5/0

cluster_pc: 5/0
mean_sequence: 1000
length: 64
subsamples: 1
num_genes: 5/0

cluster_pc: 2/0
mean_sequence: 1000
length: 64
subsamples: 1
num_genes: 5/0

clusters_pc: 5/0
mean_sequence: 1000
length: 64
subsamples: 1
num_genes: 5/0

clusters_pc: 2/0
mean_sequence: 1000
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subsamples: 1
num_genes: 5/0

clusters_pc: 8/0
mean_sequence: 1000
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subsamples: 1
num_genes: 5/0

cluster_pc: 1/0
mean_sequence: 1000
length: 64
subsamples: 1
num_genes: 5/0

mmgc/kmeb: 7/0
mean_sequence: 1017
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subsamples: 1
num_genes: 6/0

mc: 1/0
mean_sequence: 1
length: 64
subsamples: 1
num_genes: 1/0

mc_clust: 2/0
mean_sequence: 1
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num_genes: 1/0

Mg_dset: 204
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length: 1
subsamples: 1
num_genes: 1/0

Mm_dset: 1/0/2
mean_sequence: 1013
length: 1/0/1
subsamples: 1
num_genes: 6/0/4

Mg_dset: 1/0/
mean_sequence: 1/0/3
length: 1/0/1
subsamples: 1
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mean_sequence: 1/0/3
length: 1/0/1
subsamples: 1
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Mm
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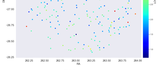

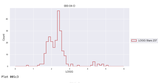

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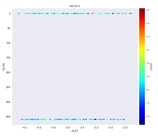

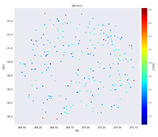

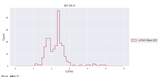

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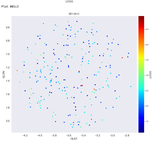

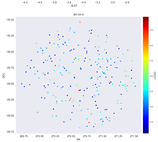

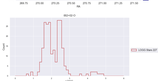

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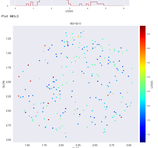

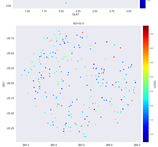

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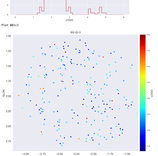

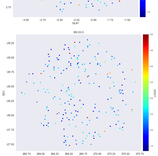

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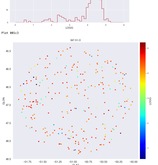

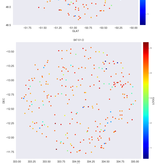

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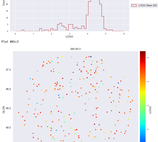

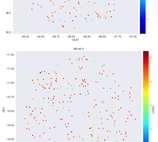

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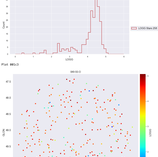

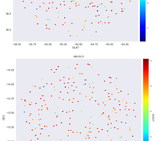

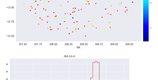

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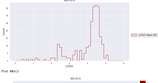
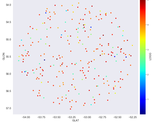
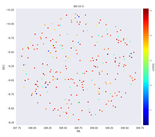
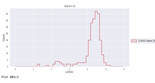
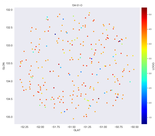


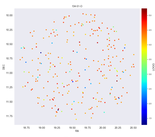


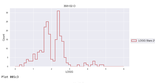




Plot MBL0







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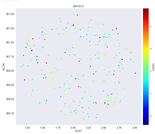

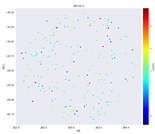

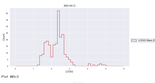

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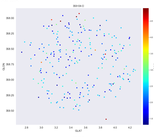
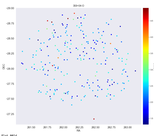
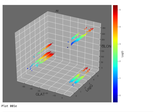




Plot MB4



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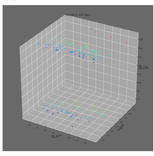
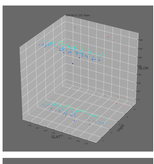
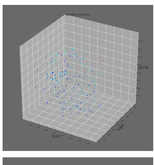
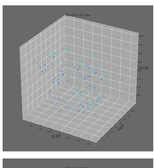
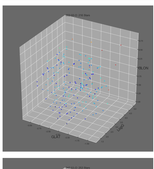
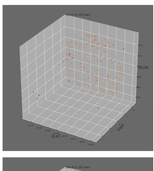


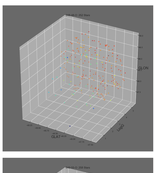


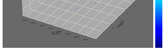


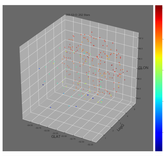


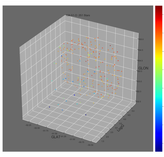


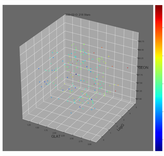


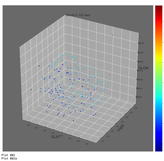




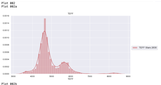






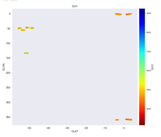


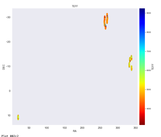
Plot 002
Plot 003



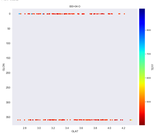
Plot 004

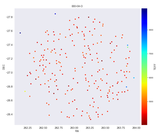
Plot 005

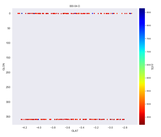


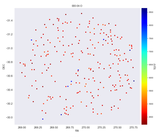


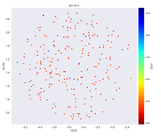
Plot 006

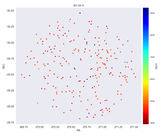


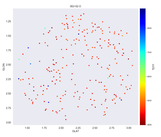


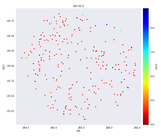


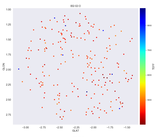


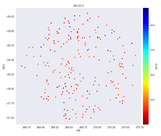


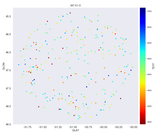


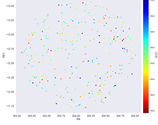


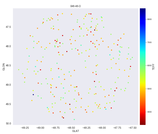


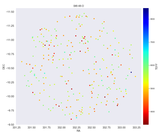


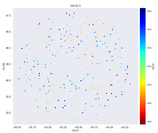


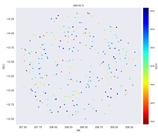


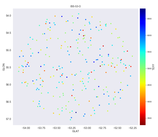


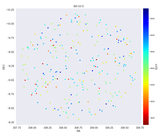


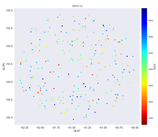


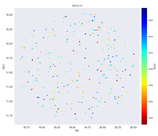


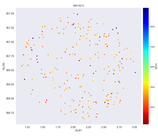


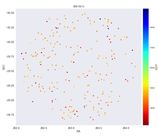


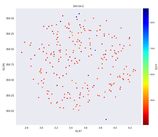


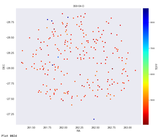


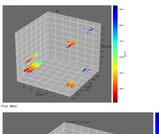




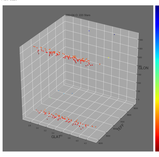




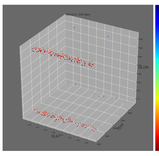


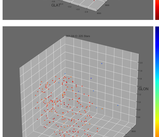


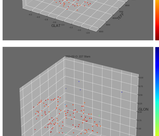
Plot Mbin

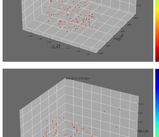


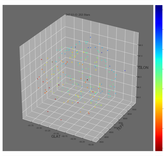
Plot Mbin







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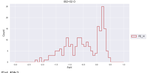

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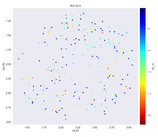

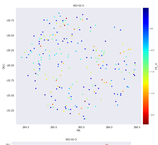

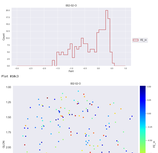

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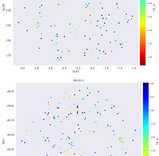

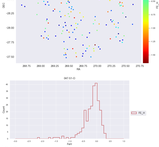

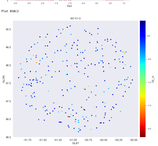

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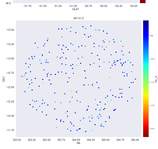

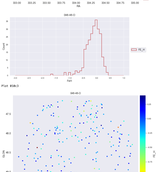

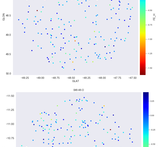

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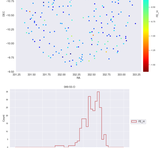

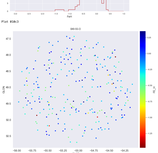

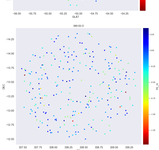

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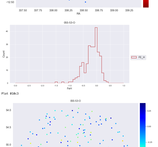

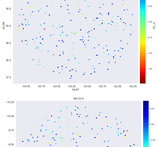

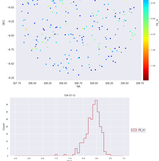

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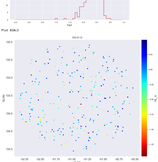

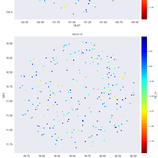

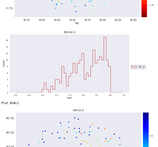

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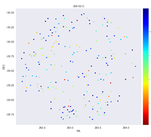

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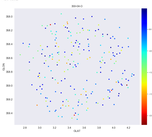
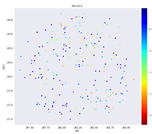
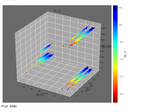




Plot 2024



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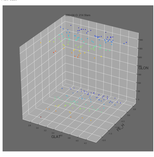

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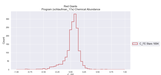
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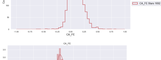
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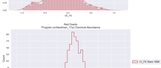
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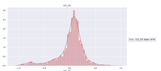
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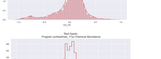
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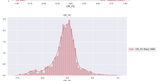
Value
MN_FE Data 5002


Count
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MN_FE Data 5002

Stat Charts
Program: JackpotMax_7 Fix Chemical Resistance
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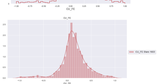
Value
N_FE Data 5070

Count
Value
N_FE Data 5070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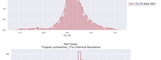
NA_FE Data 5070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Stat Charts
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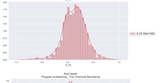
NI_FE Data 5106

Count
Value
NI_FE Data 5106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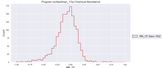
Program: JackpotMax_7 Fix Chemical Resistance
Count
Value
O_FE Data 5004


Count
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Stat Charts
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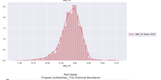
Count
Value
P_FE Data 5005


Count
Value
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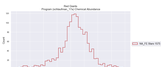
Stat Charts
Program: JackpotMax_7 Fix Chemical Resistance
Count
Value
S_FE Data 5005

Count
Value
S_FE Data 5005

Stat Charts
Program: JackpotMax_7 Fix Chemical Resistance
Count
Value
TI_FE Data 5004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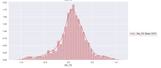
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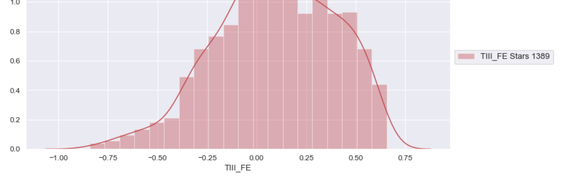

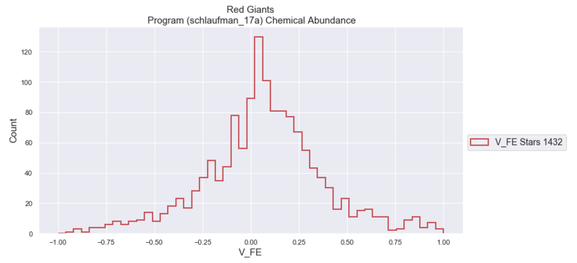

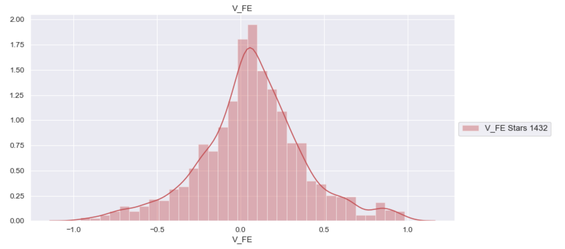

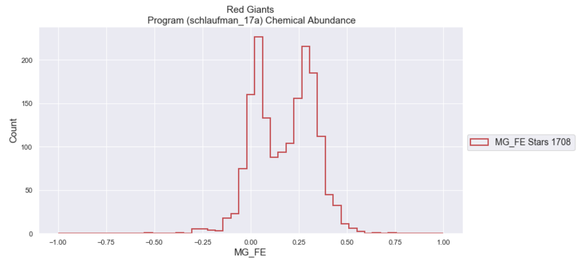

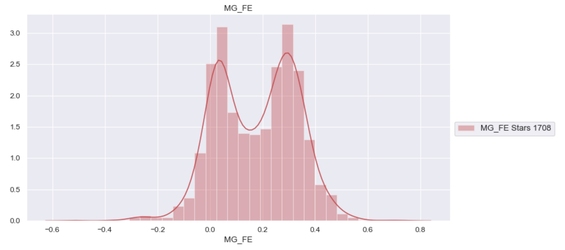

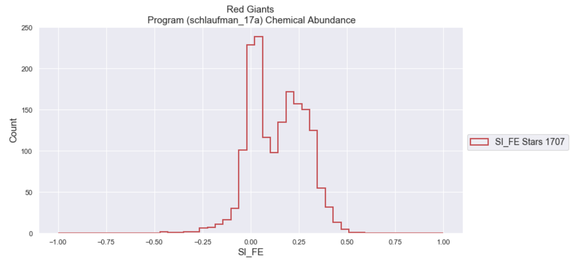

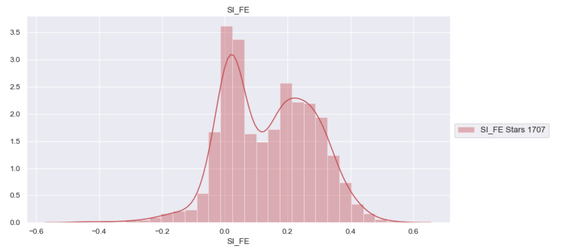


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Class O: 0
Class B: 0
Class A: 138
Class F: 115
Class G: 486
Class K: 626
Class M: 1305
Class L: 1
Class T: 0

Fd: 178
GKd: 700
GKg: 1767
Md: 91
Mg: 48

All: Stars 2846

BA: Stars 62

Fd_a: Stars 79
Fd_b: Stars 49
Fd_c: Stars 34
Fd_d: Stars 16

GKd_a: Stars 363
GKd_b: Stars 157
GKd_c: Stars 115
GKd_d: Stars 65

GKg_a: Stars 873
GKg_b: Stars 332
GKg_c: Stars 385
GKg_d: Stars 177

Md_a: Stars 43
Md_b: Stars 18
Md_c: Stars 14
Md_d: Stars 16

Mg_a: Stars 20
Mg_b: Stars 10
Mg_c: Stars 12
Mg_d: Stars 6

Fields: ['000+04-0' '000-04-0' '001-04-0' '002+02-0' '002-02-0' '047-51-0'
 '048-48-0' '049-55-0' '055-53-0' '134-51-0' '358+02-0' '359+04-0']

Program: schlaufman_17a


schlaufman_17a: 3157
The oldest stars in the Milky Way are thought to be very metal-poor stars (i.e., [Fe/H] < -2.0) in the inner Galaxy.
However, extreme reddening, extinction, and crowding in the inner bulge have made finding metal-poor stars there
impossible with traditional techniques. In Schlaufman & Casey (2014), we published an efficient
 metal-poor star selection that uses only infrared photometry, thereby overcoming all barriers to the identification
 of metal-poor stars in the inner Galaxy. We have applied this selection to dereddened 2MASS and
 Spitzer/IRAC photometry in the inner bulge to identify a sample of 9,208 candidates metal-poor K giants
 with H <= 12.5 mag. We expect APOGEE-2S observations of that sample to discover and characterize more
 than 1,000 K giants with [Fe/H] < -2.0 dex.

Done!
```

In [2]: