clytia_tutorial

February 16, 2026

1 Single-Cell Differential Expression with edgePython: *Clytia hemisphaerica*

This notebook demonstrates **single-cell differential expression analysis** using edgePython's NEBULA-LN negative binomial mixed model with empirical Bayes dispersion shrinkage.

1.1 Dataset

Single-cell RNA-seq of the jellyfish *Clytia hemisphaerica* from Chari et al. (2021). The experiment compares **fed** vs **starved** animals across 10 organisms (5 per condition). We focus on 2,564 gastrodigestive cells.

Data obtained from CaltechDATA (accession mm6y6-g4569).

1.2 Analysis

The NEBULA-LN mixed model accounts for both biological variation between organisms (random effect) and the fed/starved condition (fixed effect). Empirical Bayes shrinkage stabilizes per-gene dispersion estimates, which is especially important in single-cell data where per-gene sample sizes are small.

This notebook reproduces the panels of Figure 2 from the edgePython paper.

[1]:
```
import sys, subprocess

IN_COLAB = 'google.colab' in sys.modules

try:
    import edgepython as ep
except ImportError:
    subprocess.check_call([sys.executable, '-m', 'pip', 'install', '-q',␣
 ↪'edgepython'])
    import edgepython as ep

import os, tempfile, gzip, urllib.request
import numpy as np
import pandas as pd
import h5py
import scipy.sparse as sp
```

```
import matplotlib.pyplot as plt
import matplotlib.patches as mpatches
from matplotlib.lines import Line2D

%matplotlib inline

# Download data from CaltechDATA
DATA_URL = 'https://data.caltech.edu/records/mm6y6-g4569/files/
 ↪fedStarved_withUMAPPaga.h5ad.gz?download=1'
data_dir = tempfile.mkdtemp()
gz_path = os.path.join(data_dir, 'data.h5ad.gz')
h5ad_path = os.path.join(data_dir, 'fedStarved_withUMAPPaga.h5ad')

print('Downloading Clytia scRNA-seq data (491 MB)...', flush=True)
urllib.request.urlretrieve(DATA_URL, gz_path)
print('Decompressing...', flush=True)
with gzip.open(gz_path, 'rb') as f_in:
    with open(h5ad_path, 'wb') as f_out:
        while True:
            chunk = f_in.read(1 << 20)
            if not chunk:
                break
            f_out.write(chunk)
os.remove(gz_path)
print('Download complete.')

# Load via h5py
h5 = h5py.File(h5ad_path, 'r')
raw_data = np.round(np.expm1(h5['raw']['X']['data'][:])).astype(np.float64)
raw_indices = h5['raw']['X']['indices'][:]
raw_indptr = h5['raw']['X']['indptr'][:]
n_obs = len(raw_indptr) - 1
raw_gene_names = np.array([g.decode() for g in h5['raw']['var']['index'][:]])
n_var_raw = len(raw_gene_names)
X_raw = sp.csr_matrix((raw_data, raw_indices, raw_indptr), shape=(n_obs,␣
 ↪n_var_raw))

annosSub_cats = [c.decode() for c in h5['obs']['__categories']['annosSub'][:]]
annosSub_codes = h5['obs']['annosSub'][:]
fed_cats = [c.decode() for c in h5['obs']['__categories']['fed'][:]]
fed_codes = h5['obs']['fed'][:]
orgID_cats = [c.decode() for c in h5['obs']['__categories']['orgID'][:]]
orgID_codes = h5['obs']['orgID'][:]
h5.close()

print(f'Full dataset: {n_obs:,} cells x {n_var_raw:,} genes')
```

```
Using local data file.
Full dataset: 13,673 cells x 28,514 genes
```

[2]:
```
plt.rcParams.update({
    'figure.dpi': 120, 'font.size': 11, 'axes.titlesize': 13,
    'axes.labelsize': 12, 'xtick.labelsize': 10, 'ytick.labelsize': 10,
    'legend.fontsize': 10, 'figure.figsize': (8, 5),
    'axes.spines.top': False, 'axes.spines.right': False,
})

BLUE = '#4878cf'
ORANGE = '#e8823a'
RED = '#c44e52'
GREY = '#aaaaaa'
```

1.3 1. Explore the Dataset

We subset to **gastrodigestive** cells, which are involved in nutrient processing and are expected to show strong fed vs starved transcriptional differences.

[3]:
```
# Subset to GastroDigestive cells
gastro_idx = [i for i, c in enumerate(annosSub_cats) if c.
 ↪startswith('GastroDigestive')]
cell_mask = np.isin(annosSub_codes, gastro_idx)
counts_gastro = X_raw[cell_mask, :]
fed_gastro = np.array([fed_cats[c] for c in fed_codes[cell_mask]])
org_gastro = np.array([orgID_cats[c] for c in orgID_codes[cell_mask]])
subtype_gastro = np.array([annosSub_cats[c] for c in annosSub_codes[cell_mask]])
n_gastro = cell_mask.sum()

print(f'GastroDigestive cells: {n_gastro:,}')
print(f'  Fed: {(fed_gastro == "True").sum():,}')
print(f'  Starved: {(fed_gastro == "False").sum():,}')
print(f'  Organisms: {len(np.unique(org_gastro))}')
print()
print('Cell subtypes:')
for st in sorted(set(subtype_gastro)):
    print(f'  {st}: {(subtype_gastro == st).sum()} cells')
```

```
GastroDigestive cells: 2,564
  Fed: 1,316
  Starved: 1,248
  Organisms: 10

Cell subtypes:
  GastroDigestive-A: 850 cells
  GastroDigestive-B: 632 cells
  GastroDigestive-C: 321 cells
```

```
  GastroDigestive-D: 304 cells
  GastroDigestive-E: 257 cells
  GastroDigestive-F: 200 cells
```

1.4 2. Design Matrix

We model a simple intercept + fed effect. The `sample` argument to `glm_sc_fit` specifies the organism ID as the random effect grouping variable.

[4]:
```
fed_binary = (fed_gastro == 'True').astype(float)
design = pd.DataFrame({
    'Intercept': np.ones(n_gastro),
    'fed': fed_binary,
}, columns=['Intercept', 'fed'])

# glm_sc_fit expects genes x cells
counts_T = counts_gastro.T.toarray().astype(np.float64)

print(f'Design matrix: {design.shape[0]} cells x {design.shape[1]}␣
 ↪coefficients')
print(f'Count matrix: {counts_T.shape[0]:,} genes x {counts_T.shape[1]:,}␣
 ↪cells')
print()
print('Design:')
print(design.head())
```

```
Design matrix: 2564 cells x 2 coefficients
Count matrix: 28,514 genes x 2,564 cells

Design:
   Intercept  fed
0        1.0  1.0
1        1.0  0.0
2        1.0  0.0
3        1.0  1.0
4        1.0  1.0
```

1.5 3. Fit NEBULA-LN Mixed Model

The NEBULA-LN model fits a negative binomial generalized linear mixed model per gene, with organism as a random effect. After fitting, we apply **empirical Bayes shrinkage** to stabilize the per-gene dispersion estimates by borrowing information across genes.

[5]:
```
import time

print('Fitting NEBULA-LN model...', flush=True)
t0 = time.perf_counter()
fit = ep.glm_sc_fit(counts_T, design=design, sample=org_gastro,
                    norm_method='TMM', verbose=False)
```

```
t_fit = time.perf_counter() - t0
print(f'Model fitting: {t_fit:.1f}s')

print('\nApplying empirical Bayes shrinkage...')
fit = ep.shrink_sc_disp(fit, robust=True)

n_converged = (fit['convergence'] == 1).sum()
n_total = len(fit['convergence'])
print(f'\nGenes tested: {n_total:,}')
print(f'Converged: {n_converged:,} / {n_total:,} ({100*n_converged/n_total:.
  ↪1f}%)')
```

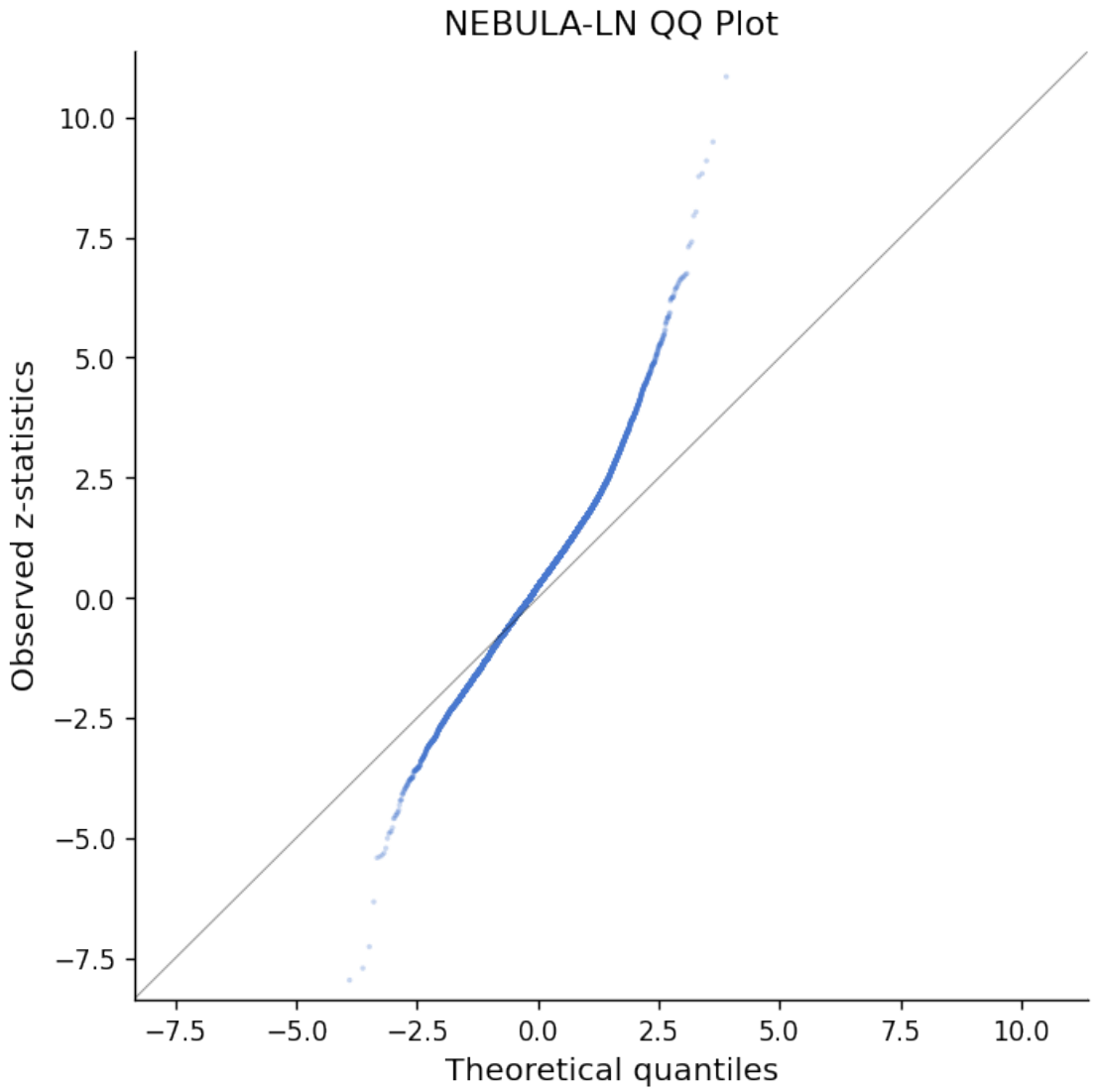
```
Fitting NEBULA-LN model…
Model fitting: 44.7s

Applying empirical Bayes shrinkage…

Genes tested: 10,377
Converged: 10,285 / 10,377 (99.1%)
```

1.6 4. QQ Plot of Z-Statistics

Under the null hypothesis, the Wald z-statistics should follow a standard normal distribution. This QQ plot verifies the calibration of the NEBULA-LN model.

[6]:
```
from scipy.stats import norm

conv = fit['convergence'] == 1
z_vals = fit['coefficients'][conv, 1] / fit['se'][conv, 1]
z_vals = z_vals[np.isfinite(z_vals)]

n_z = len(z_vals)
theoretical = norm.ppf((np.arange(1, n_z + 1) - 0.5) / n_z)
observed = np.sort(z_vals)

fig, ax = plt.subplots(figsize=(6, 6))
ax.scatter(theoretical, observed, c=BLUE, s=4, alpha=0.3, edgecolors='none',
           rasterized=True)
lims = [min(theoretical.min(), observed.min()) * 1.05,
        max(theoretical.max(), observed.max()) * 1.05]
ax.plot(lims, lims, 'k-', lw=0.5, alpha=0.5)
ax.set_xlim(lims); ax.set_ylim(lims)
ax.set_xlabel('Theoretical quantiles')
ax.set_ylabel('Observed z-statistics')
ax.set_title('NEBULA-LN QQ Plot')
plt.tight_layout()
plt.show()
```

```
print(f'Number of z-statistics: {n_z:,}')
```



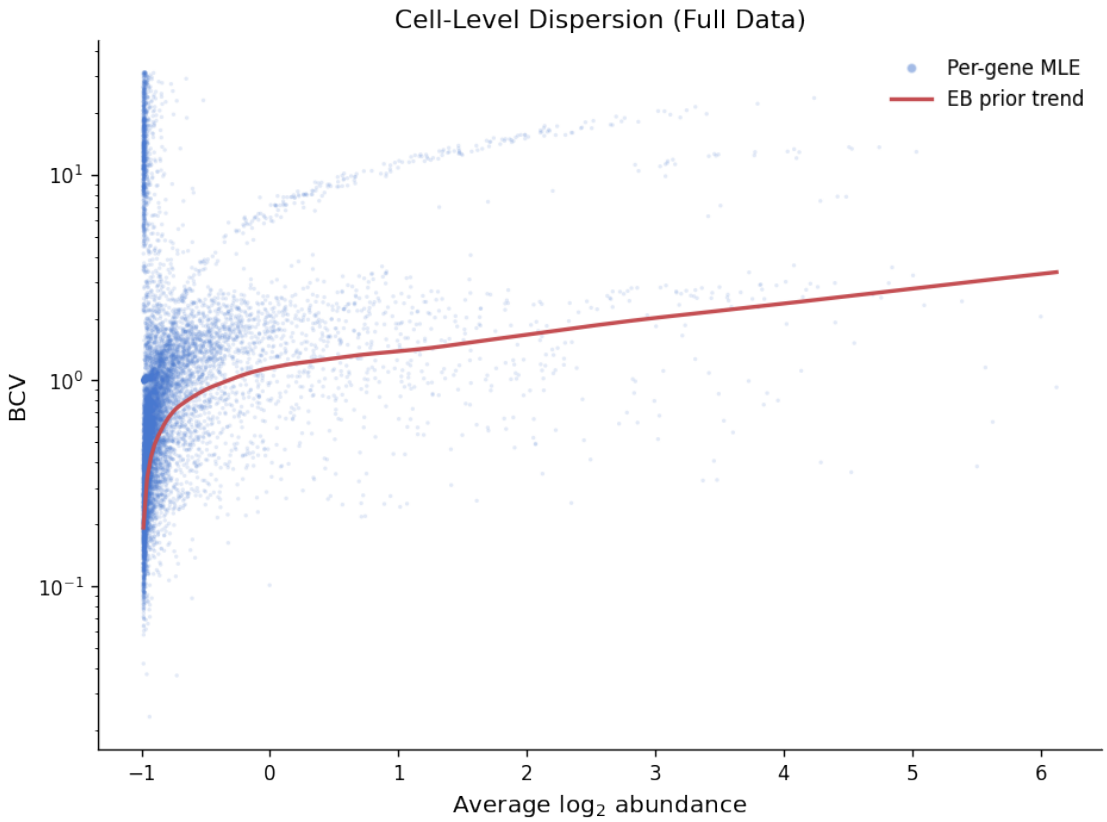

```
Number of z-statistics: 10,285
```

1.7 5. Cell-Level BCV Plot

The biological coefficient of variation (BCV) is the square root of the dispersion parameter. This plot shows the per-gene maximum likelihood dispersion estimates and the empirical Bayes prior trend as a function of gene abundance.

[7]:
```
phi_raw = fit['phi_raw']
abund = fit['ave_log_abundance']
ok = conv & np.isfinite(phi_raw) & (phi_raw > 0) & (phi_raw < 999)
```

```
abund_ok = abund[ok]
bcv_raw = np.sqrt(phi_raw[ok])

fig, ax = plt.subplots(figsize=(8, 6))
ax.scatter(abund_ok, bcv_raw, c=BLUE, s=4, alpha=0.15, edgecolors='none',
           rasterized=True)

phi_prior = fit['phi_prior'][ok]
order = np.argsort(abund_ok)
ax.plot(abund_ok[order], np.sqrt(phi_prior[order]), color=RED,
        lw=2.0, label='EB prior trend', zorder=5)

ax.set_yscale('log')
ax.set_xlabel('Average log$_2$ abundance')
ax.set_ylabel('BCV')
ax.set_title('Cell-Level Dispersion (Full Data)')
legend_elements = [
    Line2D([0], [0], marker='o', color='w', markerfacecolor=BLUE,
           markersize=5, alpha=0.5, label='Per-gene MLE'),
    Line2D([0], [0], color=RED, lw=2.0, label='EB prior trend'),
]
ax.legend(handles=legend_elements, frameon=False)
plt.tight_layout()
plt.show()

print(f'Genes plotted: {ok.sum():,}')
```




```
Genes plotted: 10,222
```

1.8 6. Differential Expression: Fed vs Starved

We test the `fed` coefficient using the Wald test via `top_tags`.

[8]:
```
# Attach gene names
gene_mask = fit['gene_mask']
if fit['genes'] is None:
    fit['genes'] = pd.DataFrame({'gene': raw_gene_names[gene_mask]})

n_genes = fit['coefficients'].shape[0]
tt = ep.top_tags(fit, n=n_genes, coef='fed')
table = tt['table']

n_sig = (table['FDR'] < 0.05).sum()
n_up = ((table['FDR'] < 0.05) & (table['logFC'] > 0)).sum()
n_down = ((table['FDR'] < 0.05) & (table['logFC'] < 0)).sum()
print(f'Genes tested: {len(table):,}')
print(f'DE at FDR < 0.05: {n_sig} ({n_up} up in fed, {n_down} down in fed)')
print()
```

```
print('Top 20 DE genes:')
table.head(20)
```

```
Genes tested: 10,377
DE at FDR < 0.05: 689 (524 up in fed, 165 down in fed)

Top 20 DE genes:
```

[8]:

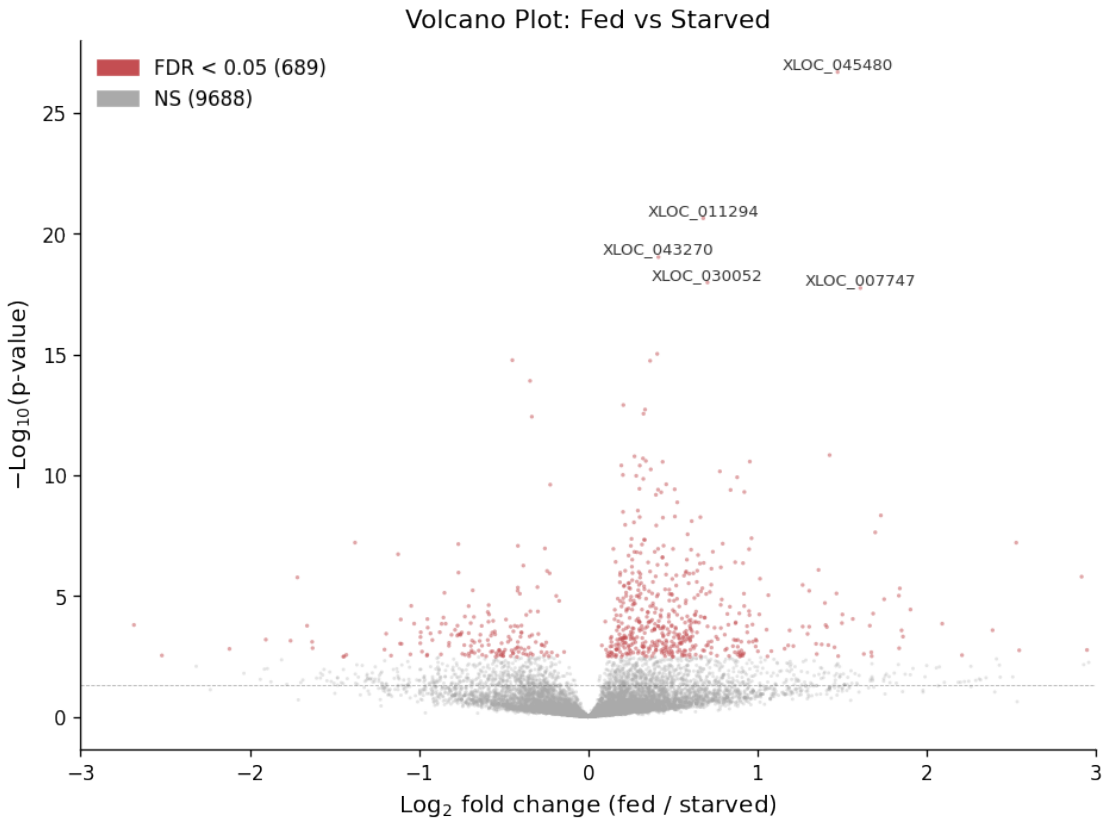
	gene	logFC	SE	z	PValue	FDR
10287	XLOC_045480	1.473719	0.135827	10.849991	1.994451e-27	2.069641e-23
3388	XLOC_011294	0.679634	0.071599	9.492252	2.260961e-21	1.173100e-17
9661	XLOC_043270	0.414579	0.045566	9.098383	9.168643e-20	3.171434e-16
6193	XLOC_030052	0.704744	0.079799	8.831439	1.033373e-18	2.680829e-15
2368	XLOC_007747	1.608403	0.183355	8.772073	1.754062e-18	3.640379e-15
7697	XLOC_035885	0.407564	0.050724	8.035018	9.356523e-16	1.618211e-12
3278	XLOC_010859	-0.448499	0.056338	-7.960911	1.707778e-15	2.347707e-12
112	XLOC_000300	0.365625	0.045969	7.953720	1.809931e-15	2.347707e-12
8924	XLOC_040487	-0.343887	0.044586	-7.712943	1.229494e-14	1.417606e-11
7410	XLOC_034593	0.207443	0.027982	7.413358	1.231411e-13	1.277836e-10
6489	XLOC_031118	0.335983	0.045675	7.355960	1.895593e-13	1.788234e-10
10305	XLOC_045581	0.326579	0.044721	7.302583	2.822945e-13	2.441142e-10
8926	TRINITY_DN8304_c0_g1_i1.mrna1	-0.333396	0.045893	-7.264598	3.741490e-13	2.986572e-10
10237	XLOC_045278	1.426430	0.211271	6.751678	1.461449e-11	1.083247e-08
2611	TRINITY_DN5042_c0_g1_i2.mrna1	0.273250	0.040573	6.734697	1.642719e-11	1.136433e-08
2104	XLOC_006862	0.323407	0.048227	6.705914	2.001499e-11	1.298098e-08
5773	TRINITY_DN66803_c0_g1_i1.mrna1	0.340465	0.051039	6.670676		
507	XLOC_001549	0.954878	0.143337	6.661772		
9802	XLOC_043777	0.439648	0.066032	6.658133		
8324	XLOC_038107	0.195603	0.029603	6.607461		

```
5773   2.546273e-11  1.514644e-08
507    2.705461e-11  1.514644e-08
9802   2.773271e-11  1.514644e-08
8324   3.909673e-11  1.952527e-08
```

1.9 7. Volcano Plot

Log-fold-change vs significance, with genes significant at FDR < 0.05 highlighted in red.

[9]:
```
logfc = table['logFC'].values
logp = -np.log10(table['PValue'].values + 1e-300)
fdr = table['FDR'].values
sig = fdr < 0.05

fc_lim = max(np.percentile(np.abs(logfc), 99.5), 3.0)
fc_lim = min(fc_lim, 5.0)

fig, ax = plt.subplots(figsize=(8, 6))
ax.scatter(logfc[~sig], logp[~sig], c=GREY, s=3, alpha=0.3,
           edgecolors='none', rasterized=True)
ax.scatter(logfc[sig], logp[sig], c=RED, s=4, alpha=0.5,
           edgecolors='none', rasterized=True)

# Label top 5 genes
for idx in table.head(5).index:
    row = table.loc[idx]
    gene = row.get('gene', str(idx))
    if len(gene) > 15:
        gene = gene[:12] + '...'
    fc_val = row['logFC']
    pval = -np.log10(row['PValue'] + 1e-300)
    fc_plot = np.clip(fc_val, -fc_lim * 0.95, fc_lim * 0.95)
    ax.annotate(gene, (fc_plot, pval), fontsize=8, alpha=0.8,
                ha='center', va='bottom')

ax.set_xlim(-fc_lim, fc_lim)
ax.set_xlabel('Log$_2$ fold change (fed / starved)')
ax.set_ylabel('$-$Log$_{10}$(p-value)')
ax.set_title('Volcano Plot: Fed vs Starved')
ax.axhline(-np.log10(0.05), color='k', ls='--', lw=0.5, alpha=0.3)

handles = [mpatches.Patch(color=RED, label=f'FDR < 0.05 ({n_sig})'),
           mpatches.Patch(color=GREY, label=f'NS ({len(table) - n_sig})')]
ax.legend(handles=handles, frameon=False)
plt.tight_layout()
plt.show()
```



1.10 8. Empirical Bayes Shrinkage Effect

To illustrate the effect of shrinkage, we subsample 30 cells and refit the model. With so few cells, the per-gene MLE dispersions are very noisy. Empirical Bayes shrinkage pulls these estimates toward an abundance-dependent prior trend, producing more stable posterior estimates.

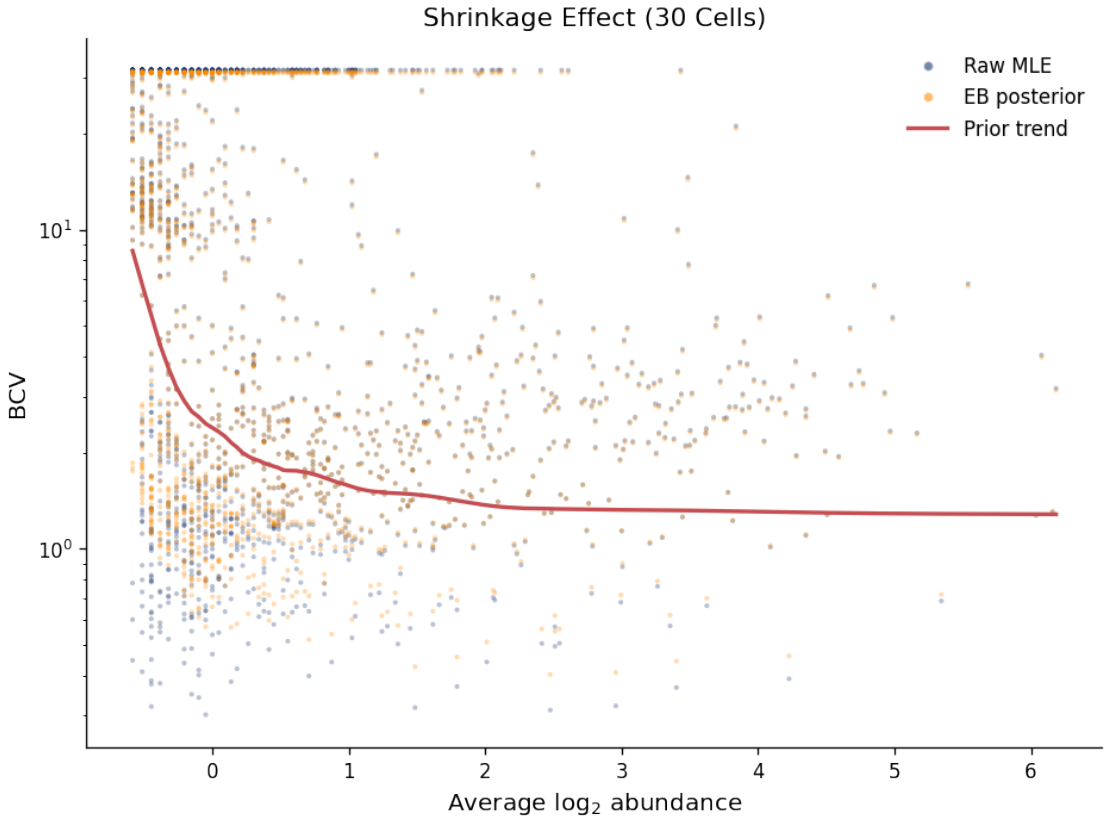
[10]:
```
n_sub = 30
rng = np.random.RandomState(42)
idx_sub = rng.choice(n_gastro, size=n_sub, replace=False)
idx_sub.sort()

counts_sub = counts_T[:, idx_sub]
design_sub = design.iloc[idx_sub].reset_index(drop=True)
org_sub = org_gastro[idx_sub]

print(f'Fitting subsampled model ({n_sub} cells)...', flush=True)
t0 = time.perf_counter()
fit_sub = ep.glm_sc_fit(counts_sub, design=design_sub, sample=org_sub,
                        norm_method='TMM', verbose=False)
print(f'Fit in {time.perf_counter()-t0:.1f}s')
fit_sub = ep.shrink_sc_disp(fit_sub, robust=True)
```

```
n_conv_sub = (fit_sub['convergence'] == 1).sum()
n_total_sub = len(fit_sub['convergence'])
print(f'Genes: {n_total_sub:,}, converged: {n_conv_sub:,}')
```

```
Fitting subsampled model (30 cells)…

/Users/lpachter/Dropbox/claude/projects/edgestar/upload/edgepython/normalization
.py:181: UserWarning: One or more quantiles are zero
  warnings.warn("One or more quantiles are zero")

Fit in 1.1s
Genes: 1,605, converged: 1,602
```

[11]:
```
conv_s = fit_sub['convergence'] == 1
phi_raw_s = fit_sub['phi_raw']
phi_post_s = fit_sub['phi_post']
abund_s = fit_sub['ave_log_abundance']
ok_s = conv_s & np.isfinite(phi_raw_s) & (phi_raw_s > 0)
ok_s = ok_s & np.isfinite(phi_post_s) & (phi_post_s > 0)
abund_s_ok = abund_s[ok_s]

BLUE_DARK = '#1a3670'
ORANGE_BRIGHT = '#ff8c00'

fig, ax = plt.subplots(figsize=(8, 6))
ax.scatter(abund_s_ok, np.sqrt(phi_raw_s[ok_s]), c=BLUE_DARK, s=6, alpha=0.3,
           edgecolors='none', rasterized=True, zorder=2)
ax.scatter(abund_s_ok, np.sqrt(phi_post_s[ok_s]), c=ORANGE_BRIGHT, s=6, alpha=0.
 ↪3,
           edgecolors='none', rasterized=True, zorder=3)

phi_prior_s = fit_sub['phi_prior'][ok_s]
order_s = np.argsort(abund_s_ok)
ax.plot(abund_s_ok[order_s], np.sqrt(phi_prior_s[order_s]), color=RED,
        lw=2.0, zorder=5)

ax.set_yscale('log')
ax.set_xlabel('Average log$_2$ abundance')
ax.set_ylabel('BCV')
ax.set_title(f'Shrinkage Effect ({n_sub} Cells)')
legend_elements = [
    Line2D([0], [0], marker='o', color='w', markerfacecolor=BLUE_DARK,
           markersize=5, alpha=0.6, label='Raw MLE'),
    Line2D([0], [0], marker='o', color='w', markerfacecolor=ORANGE_BRIGHT,
           markersize=5, alpha=0.6, label='EB posterior'),
    Line2D([0], [0], color=RED, lw=2.0, label='Prior trend'),
]
```

```
ax.legend(handles=legend_elements, frameon=False)
plt.tight_layout()
plt.show()

print(f'Genes plotted: {ok_s.sum():,}')
```



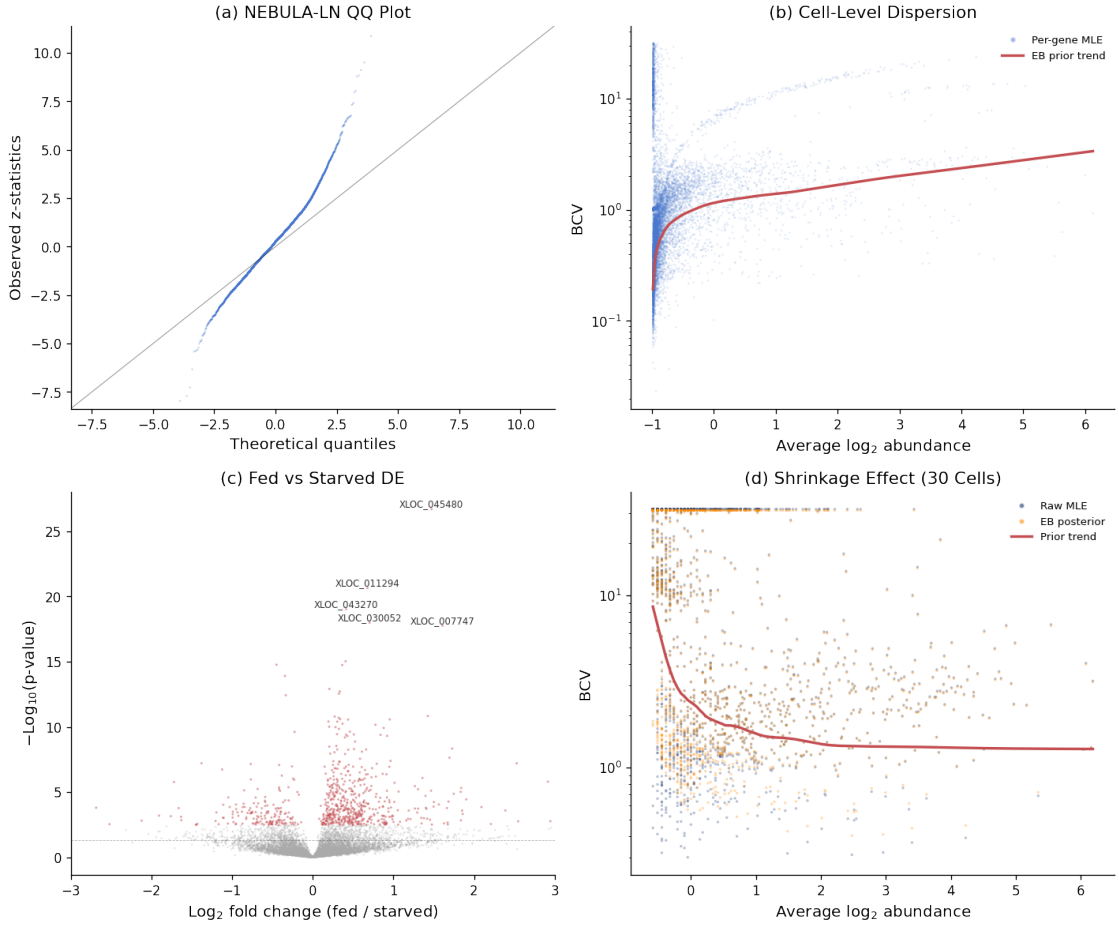

```
Genes plotted: 1,602
```

1.11 9. Combined Figure

[12]:
```
fig, axes = plt.subplots(2, 2, figsize=(12, 10))

# (a) QQ plot
ax = axes[0, 0]
ax.scatter(theoretical, observed, c=BLUE, s=2, alpha=0.3, edgecolors='none',
           rasterized=True)
ax.plot(lims, lims, 'k-', lw=0.5, alpha=0.5)
ax.set_xlim(lims); ax.set_ylim(lims)
ax.set_xlabel('Theoretical quantiles')
ax.set_ylabel('Observed z-statistics')
ax.set_title('(a) NEBULA-LN QQ Plot')
```

```
# (b) BCV plot
ax = axes[0, 1]
ax.scatter(abund_ok, bcv_raw, c=BLUE, s=2, alpha=0.15, edgecolors='none',
           rasterized=True)
ax.plot(abund_ok[order], np.sqrt(phi_prior[order]), color=RED,
        lw=2.0, zorder=5)
ax.set_yscale('log')
ax.set_xlabel('Average log$_2$ abundance')
ax.set_ylabel('BCV')
ax.set_title('(b) Cell-Level Dispersion')
legend_b = [
    Line2D([0], [0], marker='o', color='w', markerfacecolor=BLUE,
           markersize=4, alpha=0.5, label='Per-gene MLE'),
    Line2D([0], [0], color=RED, lw=2.0, label='EB prior trend'),
]
ax.legend(handles=legend_b, fontsize=8, frameon=False)

# (c) Volcano plot
ax = axes[1, 0]
ax.scatter(logfc[~sig], logp[~sig], c=GREY, s=2, alpha=0.3,
           edgecolors='none', rasterized=True)
ax.scatter(logfc[sig], logp[sig], c=RED, s=3, alpha=0.5,
           edgecolors='none', rasterized=True)
for idx in table.head(5).index:
    row = table.loc[idx]
    gene = row.get('gene', str(idx))
    if len(gene) > 15:
        gene = gene[:12] + '...'
    fc_val = row['logFC']
    pval = -np.log10(row['PValue'] + 1e-300)
    fc_plot = np.clip(fc_val, -fc_lim * 0.95, fc_lim * 0.95)
    ax.annotate(gene, (fc_plot, pval), fontsize=7, alpha=0.8,
                ha='center', va='bottom')
ax.set_xlim(-fc_lim, fc_lim)
ax.set_xlabel('Log$_2$ fold change (fed / starved)')
ax.set_ylabel('$-$Log$_{10}$(p-value)')
ax.set_title('(c) Fed vs Starved DE')
ax.axhline(-np.log10(0.05), color='k', ls='--', lw=0.5, alpha=0.3)

# (d) Shrinkage
ax = axes[1, 1]
ax.scatter(abund_s_ok, np.sqrt(phi_raw_s[ok_s]), c=BLUE_DARK, s=4, alpha=0.3,
           edgecolors='none', rasterized=True, zorder=2)
ax.scatter(abund_s_ok, np.sqrt(phi_post_s[ok_s]), c=ORANGE_BRIGHT, s=4, alpha=0.
 ↪3,
           edgecolors='none', rasterized=True, zorder=3)
```

```
ax.plot(abund_s_ok[order_s], np.sqrt(phi_prior_s[order_s]), color=RED,
        lw=2.0, zorder=5)
ax.set_yscale('log')
ax.set_xlabel('Average log$_2$ abundance')
ax.set_ylabel('BCV')
ax.set_title(f'(d) Shrinkage Effect ({n_sub} Cells)')
legend_d = [
    Line2D([0], [0], marker='o', color='w', markerfacecolor=BLUE_DARK,
           markersize=4, alpha=0.6, label='Raw MLE'),
    Line2D([0], [0], marker='o', color='w', markerfacecolor=ORANGE_BRIGHT,
           markersize=4, alpha=0.6, label='EB posterior'),
    Line2D([0], [0], color=RED, lw=2.0, label='Prior trend'),
]
ax.legend(handles=legend_d, fontsize=8, frameon=False)

plt.tight_layout()
plt.show()
```



1.12 10. Summary

[13]:
```
summary = pd.DataFrame({
    'Statistic': [
        'Full dataset (cells x genes)',
        'GastroDigestive cells',
        'Organisms',
        'Genes tested (after filtering)',
        'Converged genes',
        'DE genes (FDR < 0.05)',
        'Up in fed',
        'Down in fed',
        'Model fitting time',
    ],
    'Value': [
        f'{n_obs:,} x {n_var_raw:,}',
        f'{n_gastro:,}',
        f'{len(np.unique(org_gastro))}',
        f'{n_total:,}',
        f'{n_converged:,}',
        f'{n_sig}',
        f'{n_up}',
        f'{n_down}',
        f'{t_fit:.1f}s',
    ]
})
summary
```

[13]:

	Statistic	Value
0	Full dataset (cells x genes)	13,673 x 28,514
1	GastroDigestive cells	2,564
2	Organisms	10
3	Genes tested (after filtering)	10,377
4	Converged genes	10,285
5	DE genes (FDR < 0.05)	689
6	Up in fed	524
7	Down in fed	165
8	Model fitting time	44.7s