Identification of Anomalous Data Entries in Repeated Surveys

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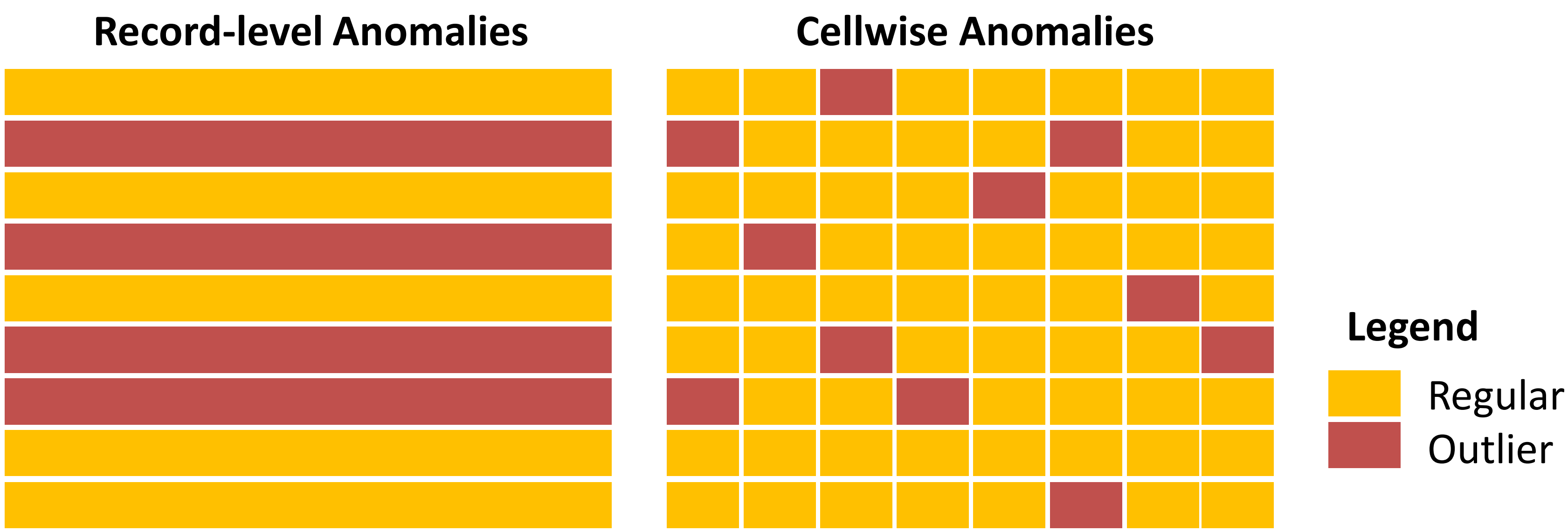
Government Advances in Statistical Programming 2023

NASS Editing System

- The USDA’s NASS conducts hundreds of surveys every year and prepares reports covering virtually every aspect of U.S. agriculture
- Data are acquired through repeated surveys
- Reviewing and vetting processes are time consuming
- **A semi-automated system** for editing
- The automation is **based on traditional** anomaly detection algorithms (**univariate outliers, edit limit thresholds**)
- There is a need for improved algorithms

A More Informative Approach

- Identifying anomalous data entries (**cells**) of a record (**row**)



Existing Approaches for Cellwise Outliers

- An R package (Raymaekers et al., 2022) that implements Agostinelli et al. (2015) and Rousseeuw et al. (2018)
- Not suitable for
  - Sparse datasets
  - Usage of previously reported data
  - Non-gaussian distributions
  - Stratified samples

Types of cellwise anomalies

- Four types of cellwise anomalies are identified cellwise anomalies
    1. Format anomalies
    2. Historical anomalies
    3. Tail anomalies
    4. Relational anomalies
- Score values are statistics obtained through transformations of the original data

A Distribution-free Approach

- Anomaly scores are based on Chebyshev-like inequalities proposed by Chepulis and Shevlyakov (2020)

$$\Pr(|X - \mu_\delta| \geq |\varepsilon|) \leq \min\left\{1, \frac{\sigma^\delta}{|\varepsilon|^\delta}\right\}$$

where X is a random variable, ε denotes the residuals, and

	$\delta = 1$	$\delta = 2$
μ_δ	Median	Mean
σ^δ	Mean absolute error	Variance

Combining Scores via Fuzzy Logic

- The scores are computed using
$$S_t = \min\left\{1, \frac{\sigma^\delta}{|\varepsilon|^\delta}\right\}$$
for any $t = 1,2,3,4$ type of anomaly
- The product t-norm (or triangular norm; Gupta 1991) defined as
$$S^* = \prod_t S_t$$
is used to identify anomalous entries
- These are detected when S^* is lower than the $100\tau\%$ quantile, where τ is predetermined by the user

Implementation & Testing

- FUZZY HRT was tested also with other datasets of varying sizes and different complexities
  - 5 to 50 variables of interest
  - 218 to 21,154 records
  - varying from higher to lower incidence of anomalies
- To improve calculation time, algorithm was developed based on SIMD instructions and the OpenMP library in C
- C code was interfaced in R to run the algorithm, using the `.C()` function (R Core Team, 2023)

Code for Format Anomalies

```
/**
 * @brief Checking format inconsistencies in the data vector
 * @param zScore pointer to an empty vector (for the output)
 * @param x pointer to the vector of data
 * @param n pointer to the size of the data vector
 */
void format_check(double *zScore, double *x, int *n) {
    int i;
    #pragma omp parallel for simd
    for (i = 0; i < *n; i++) {
        zScore[i] = (double) (x[i] > 0.0);
    }
}
```

Code for Historical Anomalies

```
...
vr = 0.0; nn = 0;
#pragma omp parallel for simd reduction(+ : vr, nn)
for (i = 0; i < *n; i++) {
    hdta[i] = log(current_data[i] / previous_data[i]);
    hdta[i] = isfinite(hdta[i]) ? fabs(hdta[i]) : 0.0;
    vr += hdta[i]; nn += (int) (hdta[i] > 0.0);
}
vr /= (double) nn;
#pragma omp parallel for simd private(tmp)
for (i = 0; i < *n; i++) {
    tmp = vr / hdta[i];
    hScore[i] = tmp < 1.0 ? tmp : 1.0;
} ...
```

Code for Tail Anomalies

```
/**
 * @brief Checking distribution tails of each columns by group
 * @param dta Pointer to the input dataset
 * @param dim Pointer to the size of the input dataset
 * @param gr  Pointer to the integer vector with group IDs
 * @param ng  Pointer to total number of groups
 * @param tScore Pointer to the scoring vector for tail outliers
 */
void tail_check(double *dta, int *dim, int *gr, int *ng, double *tScore) {
    int i, g;
    #pragma omp parallel for default(shared) private(i, g) collapse(2)
    for (i = 0; i < dim[1]; i++) {
        for (g = 1; g <= *ng; g++) {
            group_tail(&tScore[*dim * i], &dta[*dim * i], dim, gr, g);
        }
    } ...
```

Further Details on Tail Anomalies

```
...
m = median(preprocess_data, n_valid_samples);
for (i = 0; i < n_valid_samples; i++) {
    preprocess_data [i] -= m;
    preprocess_data [i] = fabs(preprocess_data[i]);
}
v = median(preprocess_data, n_valid_samples);
v = (double) (v <= 0.0) + (double) (v > 0.0) * v;
v = 1.0 / v;
for (i = 0; i < nn; i++) {
    res[i] += (double) (gr[i] == g) * (data[i] - m) * v;
}
...
```

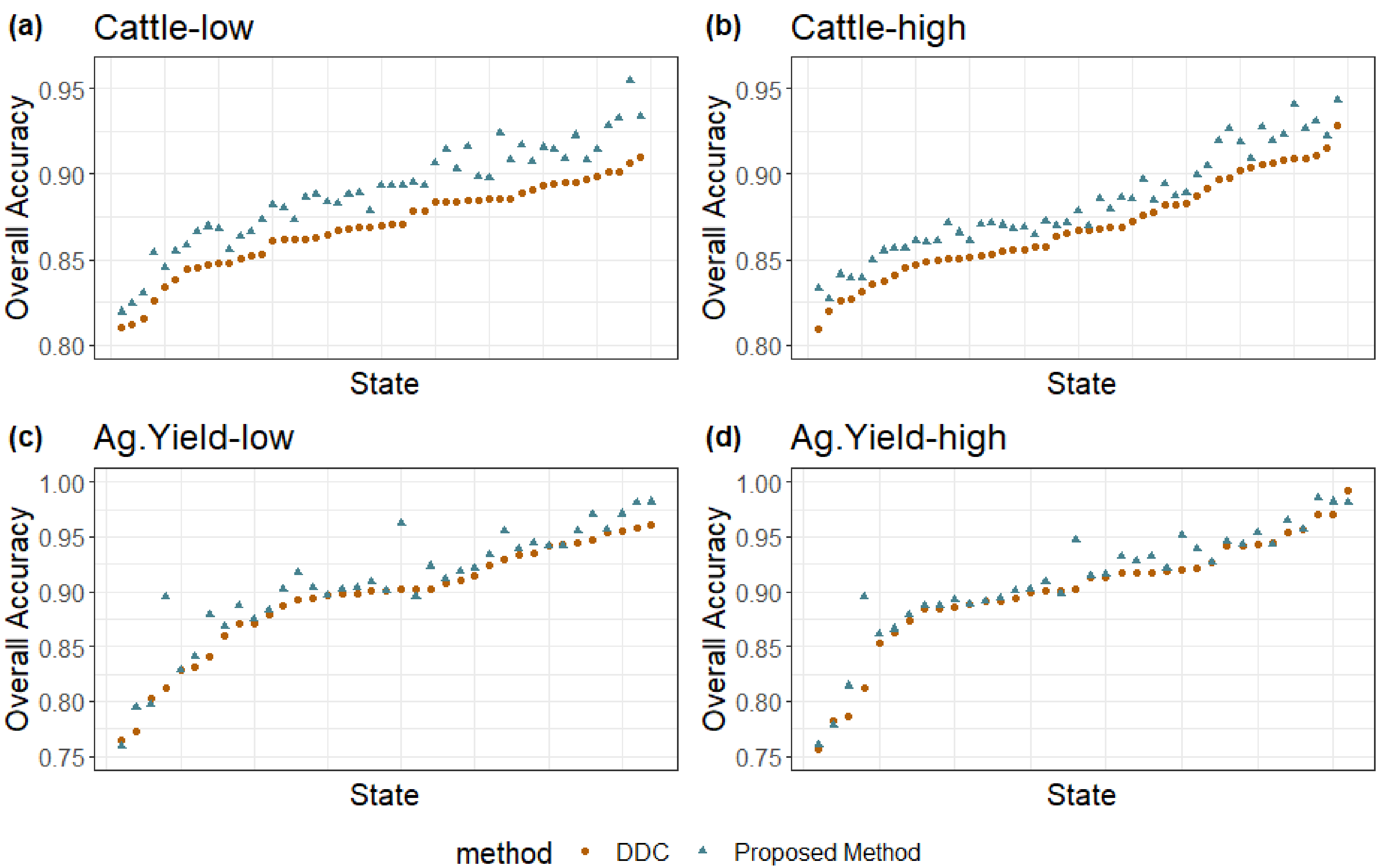
Code for Relational Anomalies

```
...
    * @param A   Pointer to input data matrix
    * @param dim Pointer to size of input matrix
...
void relat_check(double *A, int *dim) {
    int i; double tmp, v, *Q, *E, *qty; ...
    E = (double *) malloc(dim[0] * dim[1] * sizeof(double));
    ...
    #pragma omp parallel for default(shared) private(i)
    for (i = 0; i < dim[1]; i++) col_check(E, A, dim, i);
    #pragma omp parallel for simd
    for (i = 0; i < dim[0] * dim[1]; i++) A[i] = E[i];
    ...
```

Further Details on Relational Anomalies

```
... /** @param s skipping index */ ...
void col_check(double *E, double *A, int *dim, int s) {
    int i, j, k; double tmp, v, *Q, *qty;
    Q = (double *) malloc(dim[0] * (dim[1] - 1) * \
                              sizeof(double));
    qty = (double *) malloc((dim[1] - 1) * sizeof(double));
    if (Q && qty) {
    /* Compute only the matrix Q of the QR-decomposition */...
    /* Computing Q^t y */...
    /* Computing the residuals (i.e., y - Q(Q^t y)) */...
    }
    free(Q); free(qty);
}
```

Application and Results



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Conclusions

- Modern editing systems must identify cellwise outliers not just anomalous records
- Our algorithm has been more effective than existing approaches when detecting cellwise outliers
- High-performance computing in R can be achieved via using SIMD instructions and the OpenMP library in C
- More research is needed for generalizing our approach to discrete distributions

References

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Thank you!

Questions?

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