Graph Theory for Dimensionality Reduction:

A Case Study to Prognosticate Parkinson's

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Presented at: the 11th Annual IEEE IEMCON 2020
Presented on: 4th to 7th November, 2020

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insidemaps

The Problem & Potential of Graphs, DSU, Spearman's *r*

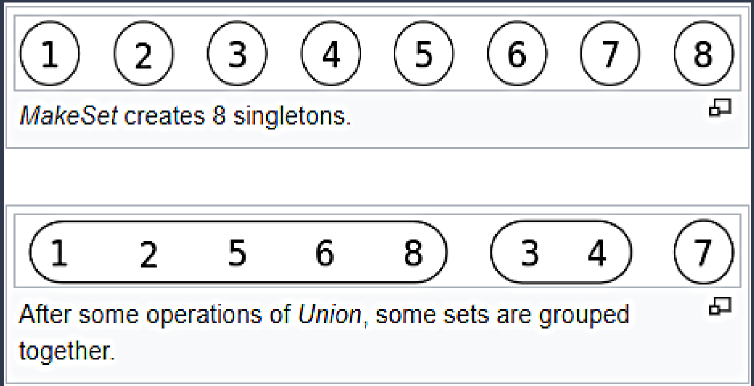

Fig. 1: a depiction of what Disjoint Set Union (DSU) practically does

- ***Parkinson's Disease (PD)*** is a neurodegenerative complication that affects the motor muscular system [1].
- PD, may cause a subject's speech to become mumbled, hoarse—endorsing speech as a potential detector [2].
- UCI garnered a dataset [4] on PD, having acoustic features and fewer tuples, inconvenient for ML algorithms.
- PCA renders obscure inside intel whereas Apriori rule mining is more popular for nominal itemsets.
- DSU may be used on graphs to track a set of features partitioned into a number of non-overlapping subsets.
- Spearman's *r* tells the magnitude and direction of a monotonic relationship, outputting Pearson's *r* more easily.

Literature Review in Two Paradigms

- Recent literature has explored structured, time-series and visual data.
- Some focused on preprocessing while the others, on advanced analytics.
- We review current literature with a focus on both:
  - Focus on Feature Selection
  - Focus on Predictive Modelling

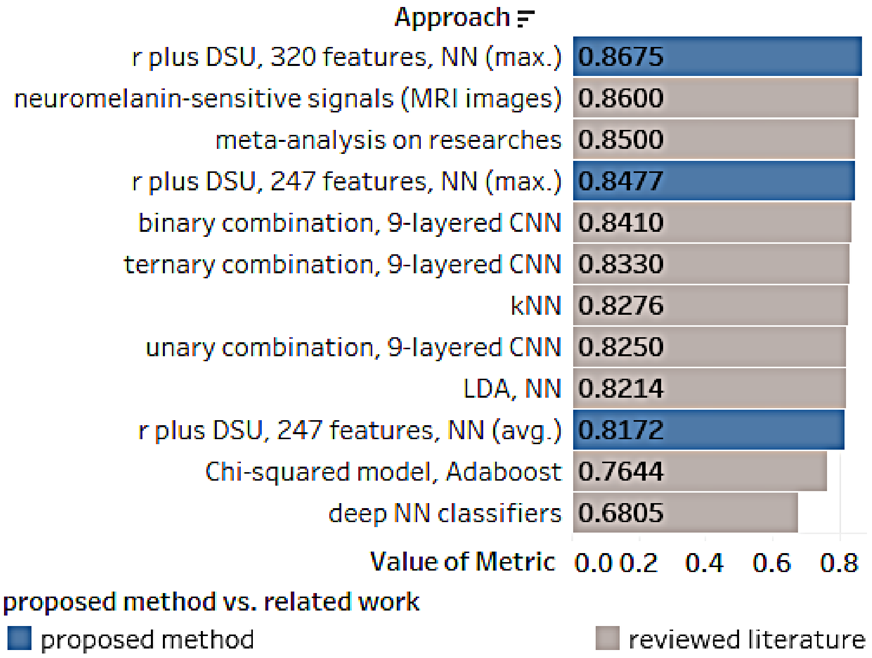

Fig. 2: a synopsis of the proposed method vs. related literature

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Proposed Method: Overview

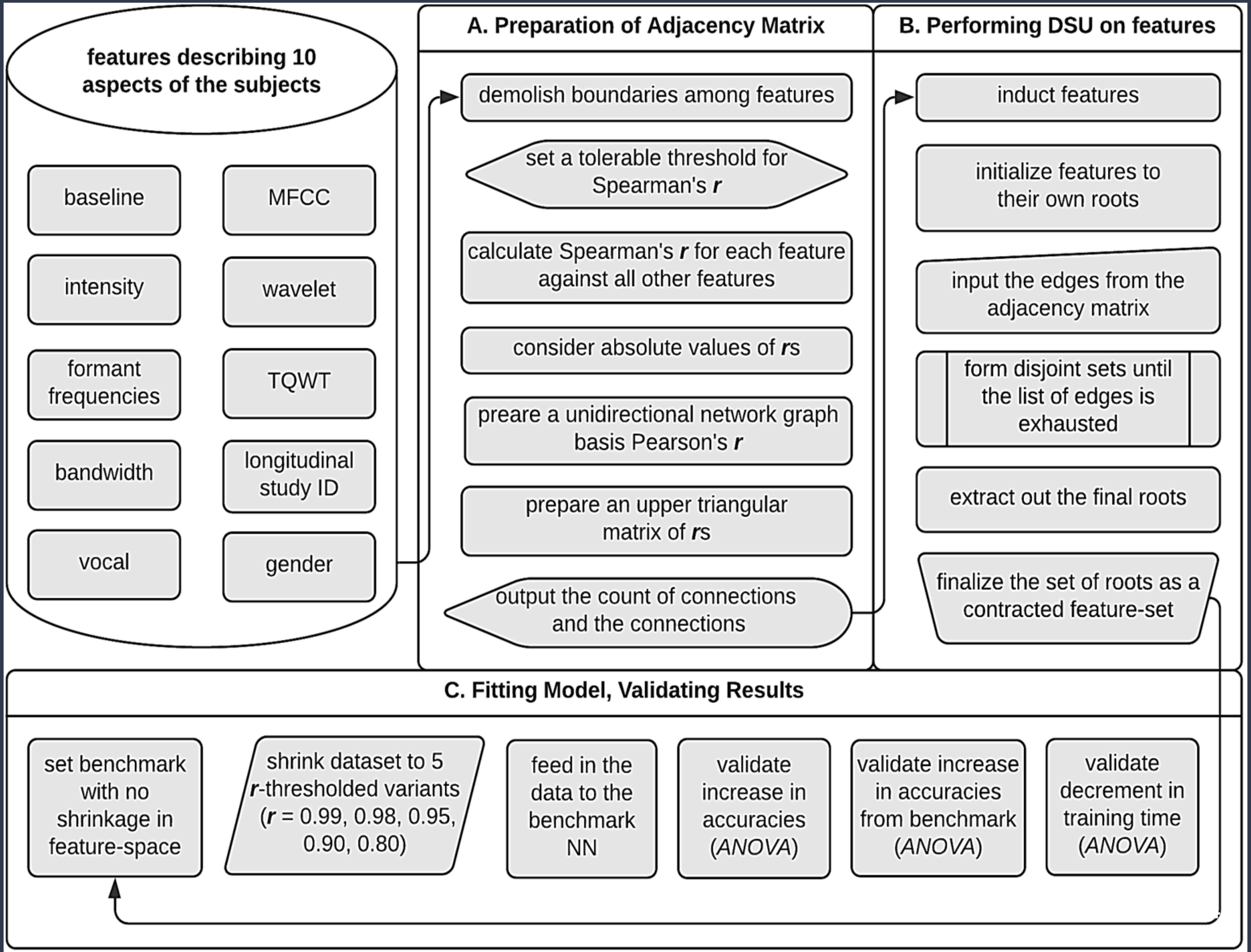

Fig. 3: a mindmap of the overall process followed for the proposed detection of *Parkinson's*

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Proposed Method:

Algorithm for Performing DSU on Features

```
Algorithm 1: Unification of Disjoint Feature-sets
  Input: binary tuples representing r-thresholded edges
  Output: roots after performing all unions

Function get_root(ftr):
    while true do
        if feature_root[ftr] = ftr then
            root ← ftr
            break
        else
            s.push(ftr)
            ftr ← feature_root[ftr]
    while !s.empty() do
        feature_root[s.top()] ← ftr
        s.pop()
    return root

Proc. unite_features(feature^1, feature^2):
    root_feature^1 ← get_root(feature^1)
    root_feature^2 ← get_root(feature^2)
    if root_feature^1 ≠ root_feature^2 then
        feature_root[root_feature^1] ← root_feature^2
        feature_size[root_feature^2] +=
          feature_size[root_feature^1]
        feature_root[root_feature^1] ← 0

Function new_feature(ftr):
    prev_size ← features.size()
    features.insert(ftr)
    present_size ← feature.size()
    if prev_size = present_size then
        return false
    return true

Function main:
    f ← count of feature
    for i = 0; i++; while i < f do
        input(feature)
        if new_feature(feature) then
            feature_root[feature] ← feature
            feature_size[feature] ← 1
    c ← count of correlations
    for i ← 0; i++; while i < c do
        input(feature^1, feature^2)
        unite_features(feature^1, feature^2)
    print out distinct elements of feature_root

    return control to system
```

Experimental Results & Discussion:

Training got Easier

Features / r-threshold

k	247 0.8	320 0.9	399 0.95	518 0.98	588 0.99	754 nil
1	176 0.06	524 0.15	5,228 0.39	25,119 0.91	53,202 3.39	34,260 0.44
2	566 0.05	497 0.14	5,676 0.25	14,457 0.09	17,777 0.09	34,518 13.67
3	380 0.07	508 0.14	4,444 0.09	12,710 0.14	39,231 1.01	41,125 0.19
4	672 0.05	734 0.17	6,062 0.02	11,541 0.65	32,671 0.10	17,070 0.09
5	89 0.05	490 0.15	4,177 0.02	16,639 0.16	8,298 0.80	25,376 0.58
6	399 0.06	519 0.23	5,473 0.07	38,187 0.12	22,298 0.13	19,180 0.18
7	282 0.07	150 0.17	5,256 0.09	64,138 2.31	34,482 10.91	31,873 0.07
8	383 0.08	206 0.16	9,365 0.07	32,280 0.26	16,993 0.17	34,142 0.10
9	482 0.08	204 0.16	4,665 0.06	29,248 0.08	36,109 0.35	11,838 0.32
10	640 0.06	364 0.14	6,195 0.01	20,666 0.08	24,750 0.46	30,054 0.17

initial/final training loss

0 64,138

Fig. 4: reduction in training loss with the reduction in *r*-threshold

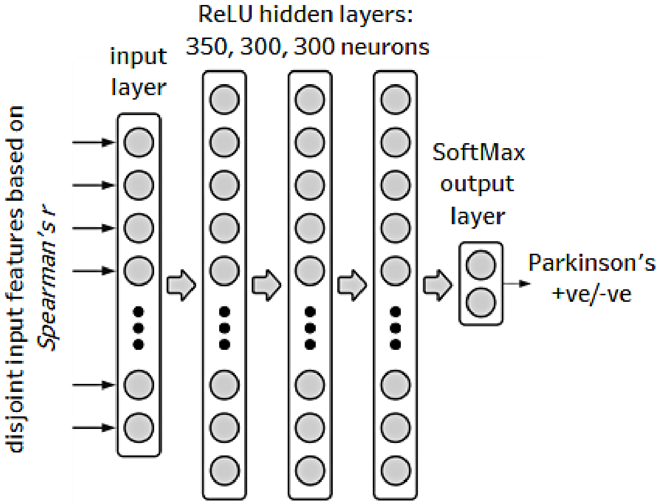


Fig. 5: the benchmark NN used in the proposed method

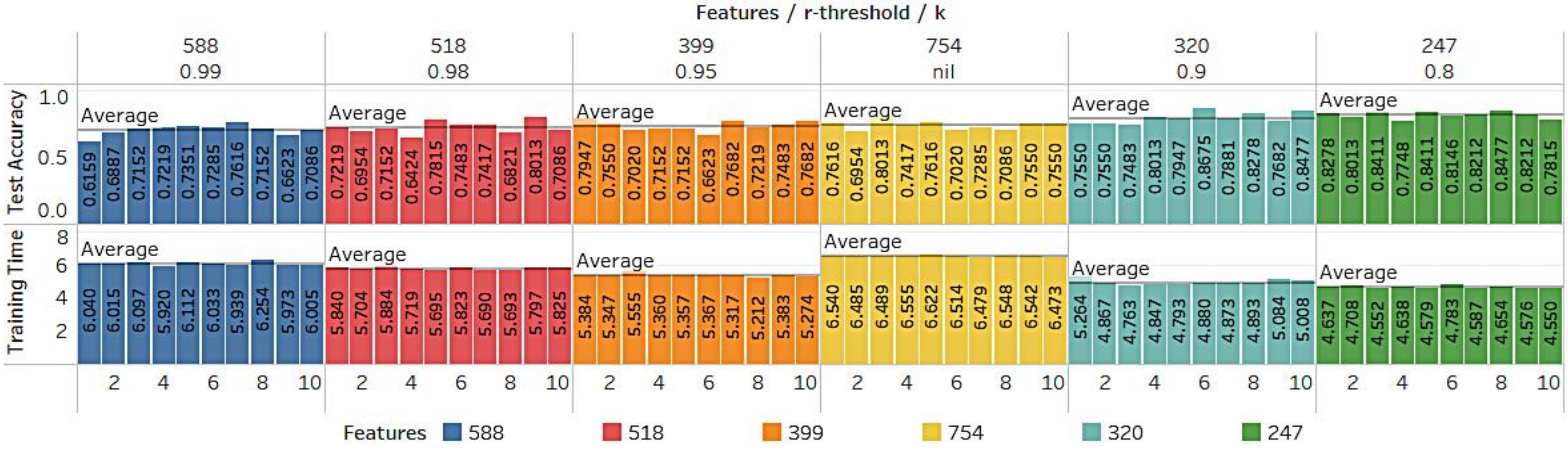
TABLE II: *ANOVA* (Analysis of Variance) results, verifying effective differences among training time and accuracy across 5 *r*-thresholds

ANOVA test metrics	values (for training time)	values (for test accuracy)
degrees of freedom	*ind*: 4, *residuals*: 45	*ind*: 4, *residuals*: 45
sum of squares	*ind*: 13.51, *residuals*: 0.46	*ind*: 0.09337, *residuals*: 0.06947
mean of squares	*ind*: 3.377, *residuals*: 0.01	*ind*: 0.023342, *residuals*: 0.001544
F-ratio	**330.2**	**15.12**
p-value, Pr(> F)	**<2e-16 *****	**6.59e-08 *****

Fig. 6: impact of *r*, influencing the count of DSU-roots (features), on average accuracy and training time

TABLE IV: t-test results, verifying incremental improvements in accuracy compared to the benchmark

Welch two sample *t-test* metrics	accuracy: using 320 features	accuracy: using 247 features
t-score	**3.2589**	**5.8542**
degrees of freedom	17.135	16.759
p-value	**0.004584**	**2.03e-05**
$H_0 : \mu_1 = \mu_2$	reject	reject
$H_a : \mu_1 \neq \mu_2$	retain	retain



Experimental Results & Discussion:

Features got Pruned

Conclusion & Future Scopes

- The work has introduced a novel feature-exclusion method based on the application of DSU.
- The research proposes construction of graphs using strong correlations, promoting Spearman's r.
- To optimize, the study makes the graphs unidirectional and reduces the matrices to upper triangular.
- The solution prunes a square dataset into a rectangular one, catering to the hunger of NNs for data.
- Contrary to PCA, DSU can reveal what features have been unified under a root till a timestamp.
- The solution has shown to improve performance through statistical inference.
- An r larger than the optimal will generate noise while a smaller one risks omitting patterns.
- Future researches may focus on nonlinear correlations.
- The research indicates ways to leverage traditional computing before diving into machine learning.

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