

Statistical Society of Canada

STAT 400/ DATA 500 Final Consulting Presentation
December 7th, 2017

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Background

- Every year there is a conference held by the Statistical Society of Canada (SSC) which has speakers within the field of statistics present their work.
 - Student Speakers
 - Invited Speakers
 - Contributed Speakers
- Pre-allocated timeframes are given to the invited speakers, and student speakers must present first
- The details of previous year SSC conferences are provided in LaTeX files

Problems

- At each table of speakers, there are speakers of unrelated areas present
 - Physics focused statisticians at a table composed primarily of biology statisticians
- Lots of manual work needs to be done to allocate presentation times and groups
- Parallel sessions topics are not as maximized for dissimilarity

Solution

- Extract author names, abstract titles, abstracts descriptions, and presentation times from the provided LaTeX files
- Process the abstract descriptions, feeding them into deep learning language models to determine similar abstracts, and perform cluster analysis to identify potential groups
- Provide a schedule for the abstracts based on the clusters given such that no talk with the same cluster would happen at the same time and the talks would be presented based on the priorities of speakers.

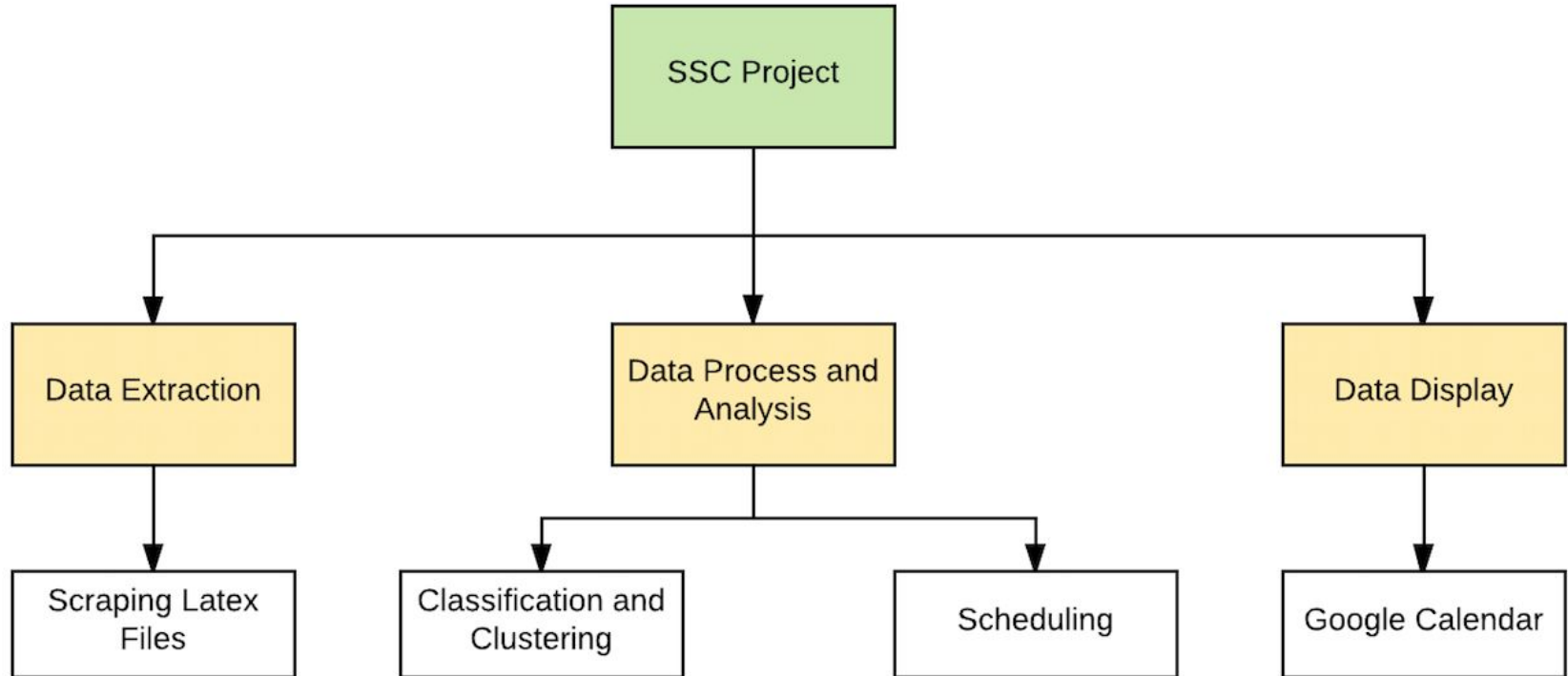
External Limitations

- Multi Platform
 - Work on all major operating systems (Linux, MacOS, Windows)
- Code must be written in the R or Python programming languages

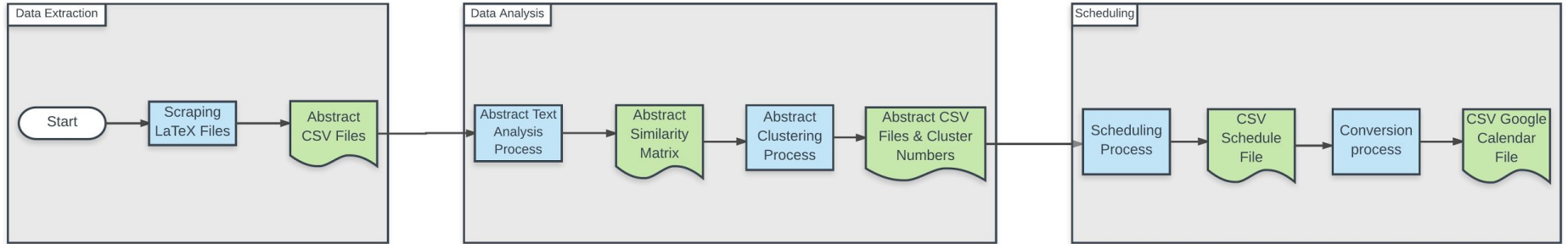
Internal Limitations

- Do not know who the keynote and student speakers are
 - Need to simulate these speakers to fulfill the project requirements
- Inconsistencies between the abstracts and program outline LaTeX files
 - Some entries are commented in one file and not the other

High-Level Architecture



System Box Diagram



Data Extraction

- Data written into two LaTeX files:
 - abstracts.tex: outlines an abstract title, abstract description, and who is presenting it
 - prog.tex: outlines who is an invited, contributed, or poster session speaker
- Data overlap between the abstracts and prog file
 - Which one is the correct file to use?
- Utilize Regular Expressions to handle a majority of the work
 - Allows for patterns to be extracted from text: `"\absTime{08:30:00}"` => `"08:30:00"`

Data Extraction: File Examples

abstracts

08:40-09:45

Don A. Dillman (Washington State University)

The Challenge of Creating Data Collection Methods that are Neither Too Far Ahead nor Behind our Survey Respondents / Le défi de construire une méthode de collecte de données qui n'est ni en avance, ni en retard pour les répondants



prog

08:40-09:45

Invited / Sur invitation

UC 210 (UC)

SSC Presidential Invited Address

Allocution de l'invité du président de la SSC

Organizer/Responsable: Jack Gambino

08:40-09:45

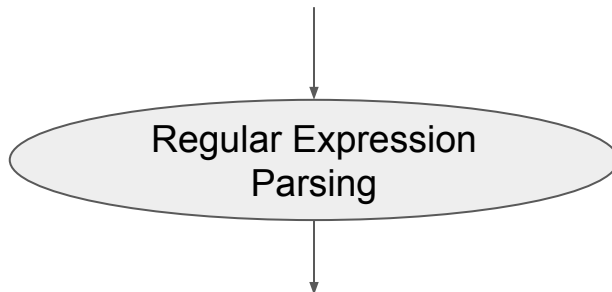
Don A. Dillman (Washington State University)

The Challenge of Creating Data Collection Methods that are Neither Too Far Ahead nor Behind our Survey Respondents / Le défi de construire une méthode de collecte de données qui n'est ni en avance, ni en retard pour les répondants



Data Extraction: Abstracts

```
{  
  absTime(Monday){10:50-11:20}  
  {  
    Author(Kelly M.)(Burkett)(University of Ottawa)  
  }  
  absTitle(An Ancestral Tree-Based Approach to Detect Rare and Common Variants)(Approche arborescente ancestrale pour détecter les  
  variants rares et communs)  
  absSideBySide(For detecting genetic variants associated with a disease or trait, it is useful to consider the ancestral trees that gave  
  rise to the sample's genetic variability. For both rare and common disease or trait influencing genetic variants, we expect to see  
  haplotypes from individuals with similar values of the disease or trait clustered together in the ancestral tree corresponding to the  
  genomic location of the variant. In this presentation, we describe how tree-based statistics can be used for detecting both rare and  
  common genetic variants associated with either continuous or dichotomous outcomes. We summarize the performance of these  
  statistics on simulated data having known and missing tree structures and we compare results to those obtained using conventional  
  approaches to detect genetic association. Finally, application of the tree-based method to real data is also discussed.)  
  Afin de détecter  
  les variants génétiques associés à une maladie ou à un caractère, il est utile de considérer les arbres ancestraux qui ont donné lieu à  
  la variabilité génétique des échantillons. Pour les variants génétiques rares et communs qui influencent les maladies ou certaines  
  caractéristiques, nous nous attendons à voir des haplotypes qui se regroupent chez des individus qui ont des valeurs de maladie ou de  
  caractéristique semblables, dans un arbre ancestral correspondant à la localisation génomique du variant. Dans cet exposé, nous  
  décrivons comment les statistiques arborescentes peuvent être utilisées pour détecter les variants génétiques rares et communs avec  
  des variables dépendantes soit continues ou dichotomiques. Nous montrons l'efficacité de ces statistiques avec des données simulées  
  qui ont des structures arborescentes connues et manquantes. Nous comparons les résultats à ceux qui ont été obtenus avec des  
  approches conventionnelles afin de détecter une association génétique. Enfin, nous présentons également l'application de la méthode  
  arborescente sur des données réelles.)  
}
```



Time: “Monday 10:50-11:20”

Author: “Kelly M. Burkett, University of Ottawa”

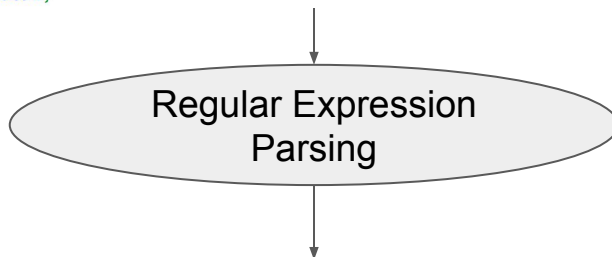
Abstract Title: “An Ancestral Tree-Based Approach ...”

Abstract Description: “For detecting genetic variants ...”

Data Extraction: Program

```
\grSciSession{10:20-11:50}{E3 270}{Analysis of Complex Traits in Families and Populations}{Analyse des caractères complexes dans les
familles et populations}{Invited}{Jinko Graham}{Jinko Graham}{Biostatistics Section / Groupe de biostatistique}{5425}

\grSchedTalk{10:20-10:50}
{
  \Author{J. Concepcion}{Loredo-Osti}{Memorial University of Newfoundland}
}
{The Analysis of Longitudinal Multivariate (Discrete or Continuous) Traits under Irregular Time Measurements}{Analyse longitudinale de traits
multivariés (discrets ou continus) avec des temps de mesure irréguliers}
{\bubbleE \enspace \screenE}
\grSchedTalk{10:50-11:20}
{
  \Author{Kelly M.}{Burkett}{University of Ottawa}
}
{An Ancestral Tree-Based Approach to Detect Rare and Common Variants}{Approche arborescente ancestrale pour détecter les variants rares et
communs}
{\bubbleE \enspace \screenE}
\grSchedTalk{11:20-11:50}
{
  \Author{Fabrice}{Lamibe}{Université du Québec à Montréal}
}
{Mapping Complex Traits, Rare Variants and Interaction via the Coalescent Process with Recombination}{Cartographie de traits complexes, de
variants rares et d'interaction par le processus de coalescence avec recombinaison}
{\bubbleE \enspace \screenE}
```



Abstract Title: “An Ancestral Tree-Based Approach ...”
Flag: “Invited”

Data Extraction: Mapping

- Identified which abstract is invited, contributed, or a poster session
 - How can it be related back to the original abstracts information?
- Requires a mapping from the data parsed from `abstracts.tex` and `prog.tex`
- Problem: there are some entries present within `abstracts.tex`, but no `prog.tex`
 - The curse of LaTeX commented text

Data Extraction: Mapping

Time: "Monday 10:50-11:20"

Author: "Kelly M. Burkett, University of Ottawa"

Abstract Title: "An Ancestral Tree-Based Approach ..."

Abstract Description: "For detecting genetic variants ..."

Abstract Title: "An Ancestral Tree-Based Approach ..."

Flag: "Invited"

Time: "Monday 10:50-11:20"

Author: "Kelly M. Burkett, University of Ottawa"

Abstract Title: "An Ancestral Tree-Based Approach ..."

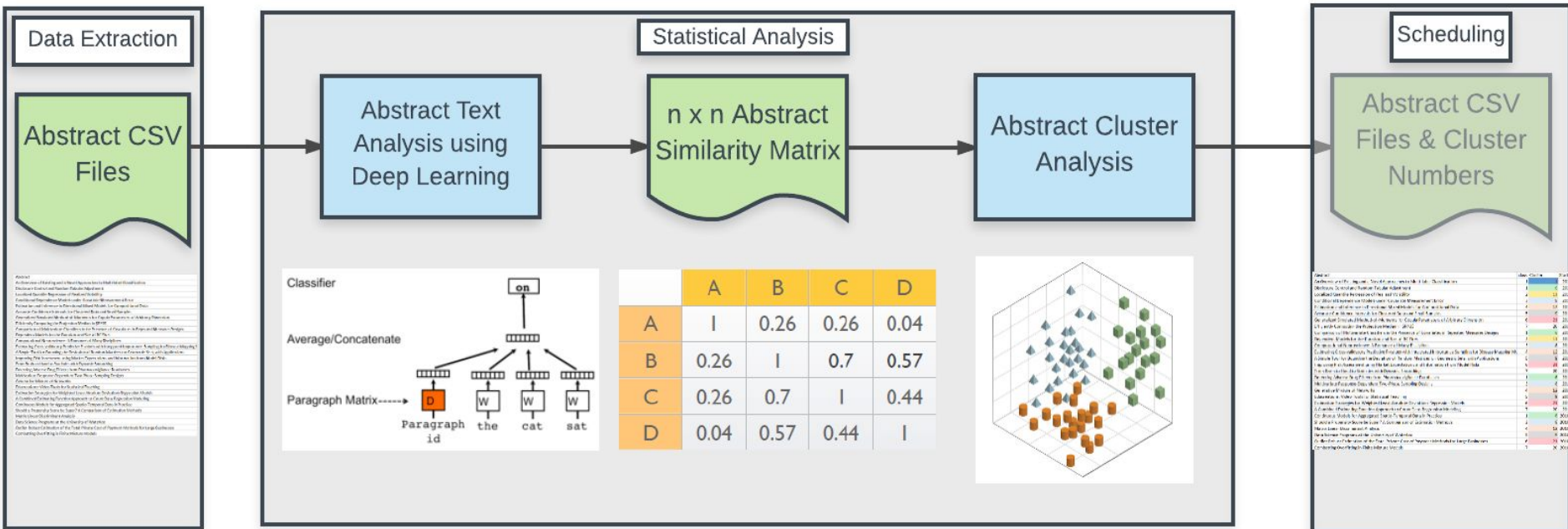
Abstract Description: "For detecting genetic variants ..."

Flag: "Invited"

Data Extraction: Random Labeling

- Due to the lack of student and keynote speaker labels, they needed to be randomly assigned
- Upon discussion with our client, the number of both categories were outlined
 - 3 Keynote speakers, 1 per day. Keynote speakers are invited talks
 - 30 student speakers. Student speakers are contributed talks
- Perform random sampling on the invited and contributed talks
 - 30 random entries with the flag of “Contributed” were assigned the flag of “Student”
 - 3 random entries with the flag of “Invited” were assigned the flag of “Keynote”

Statistical Analysis



Language Models

- Input: words
- Word Vector space
- Output: word cosine similarity

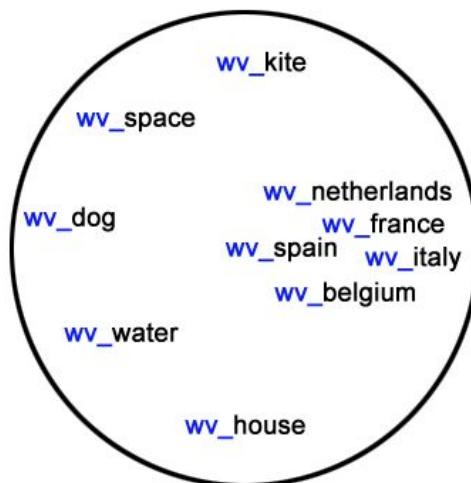
Input:
text

Lorem ipsum dolor
sit amet, conse-
tur eadipiscing elit,
sed diam nonumy
eirmod tempor
invidunt ut labore
et dolore magna
aliquyam erat, sed
diam voluptua. At
vero eos et

train for
each word
a word vector

word2vec

Model:



vector space:
consists of **word vectors**
for each word

most_similar('france'):

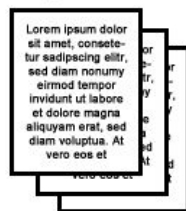
spain	0.678515
belgium	0.665923
netherlands	0.652428
italy	0.633130

highest cosine
distance values
in vector space
of the nearest
words

Language Models

- Input:
abstracts

Input:
many document



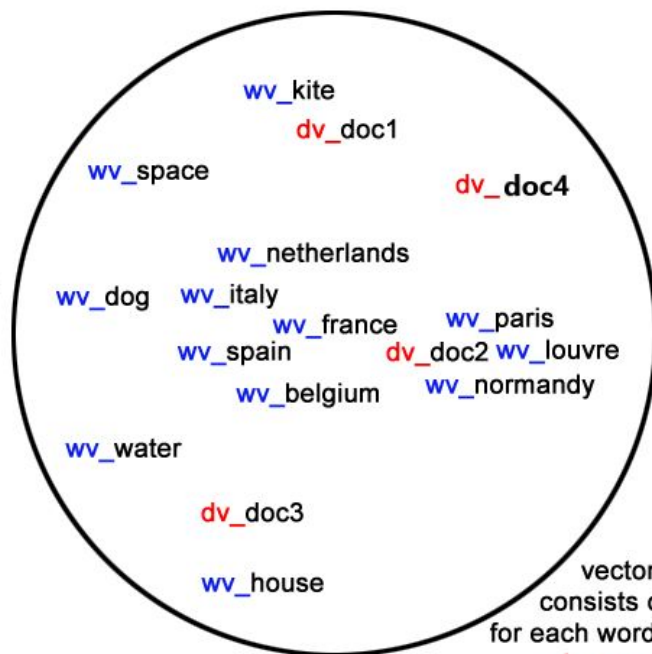
doc1,
doc2,
doc3 ...

- Document
Vector space

training a word
vector for each
word and each
document gets
an ID/tag with
a vector while
training

doc2vec

Model:



most_similar(' doc1 '):
doc4 0.876543
doc2 0.765432
doc3 0.654321
...

highest cosine
distance values
in vector space
with consideration
of the document
vectors

- Output:
Cosine
similarity
matrix

vector space:
consists of **word vectors**
for each word and additional
document vectors

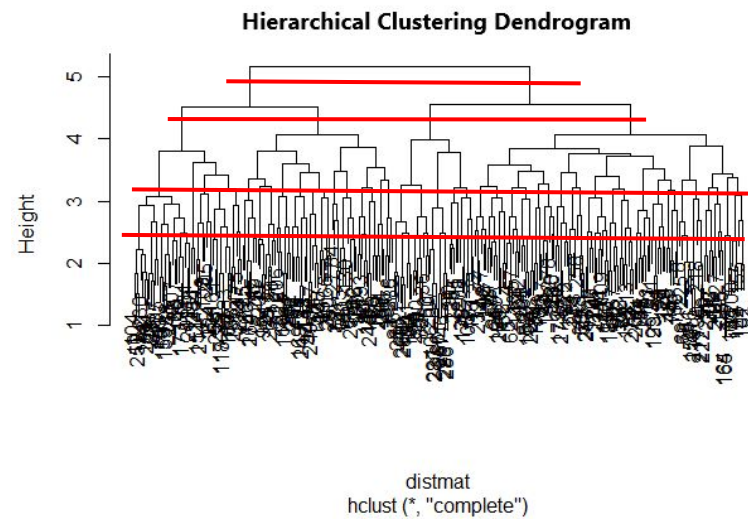
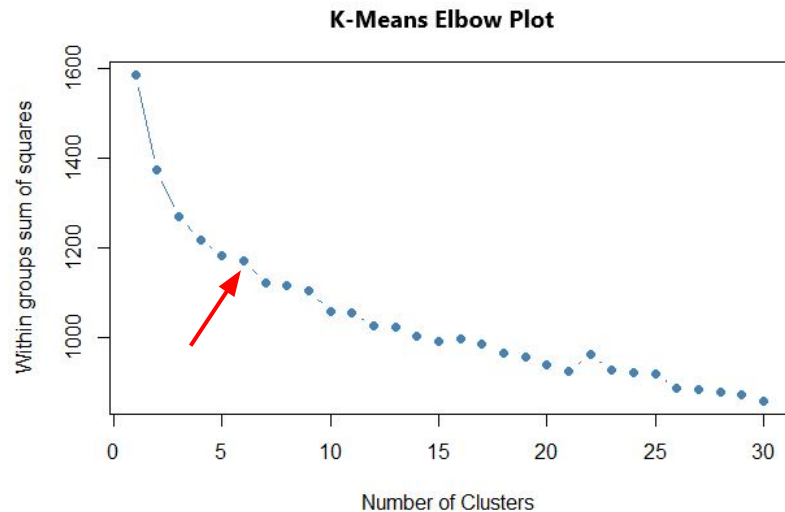
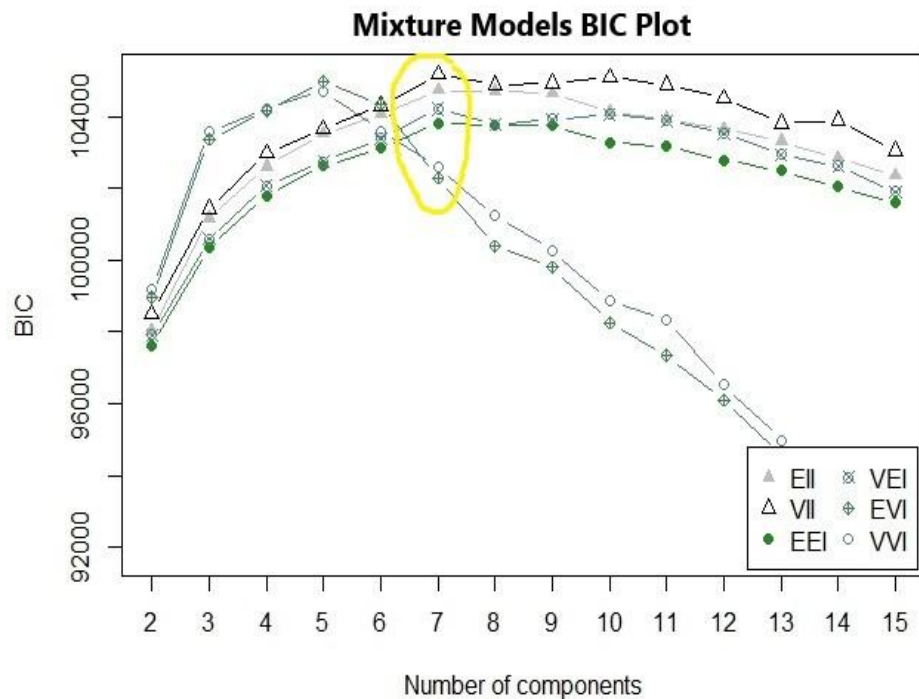
Abstract Similarity Cluster Analysis

- Input: Abstract Similarity Matrix

Output: Abstract Cluster Memberships

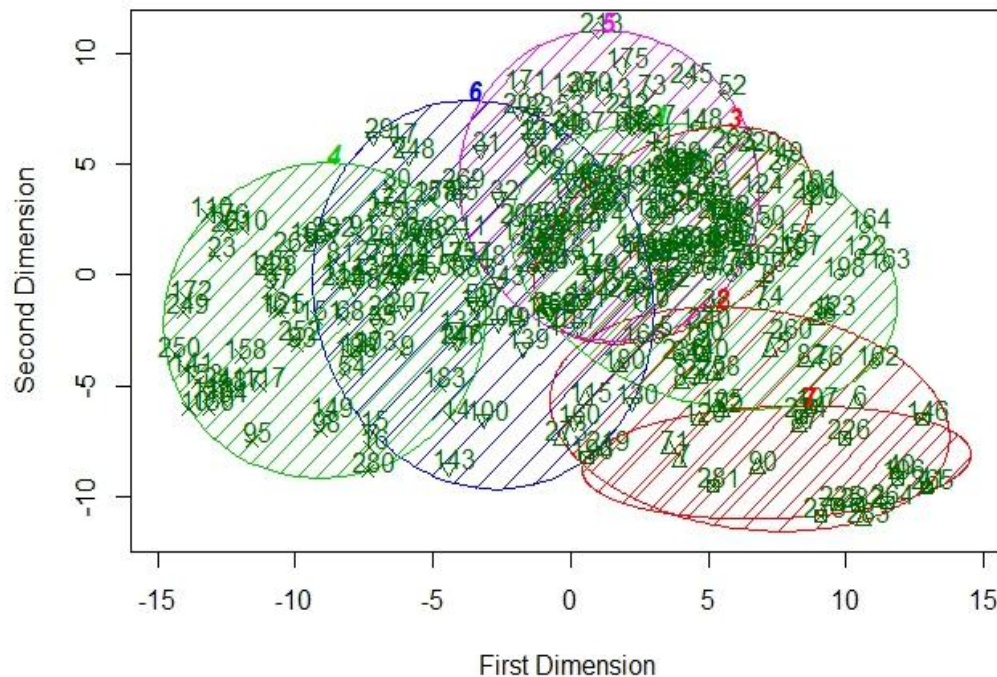
- First Task: Determine Number of Clusters (optimal cluster sizes ?)
- Second Task: Which Clustering algorithm(s) to use ?

Deciding on Number of Clusters



Abstract Cluster Visualization

Mixture Model Clustering Results on the Dissimilarity Matrix



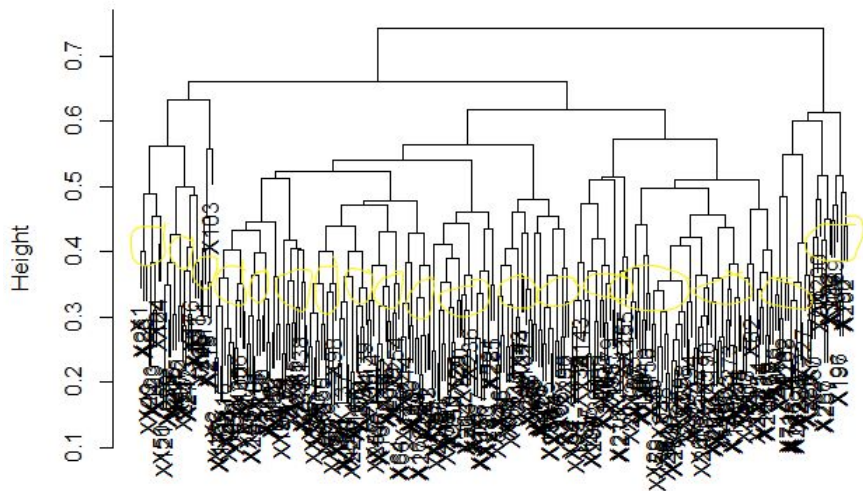
These two components explain 22.02 % of the point variability.

Classical Multidimensional Scaling Visualization of the Mixture Model Clustering Results



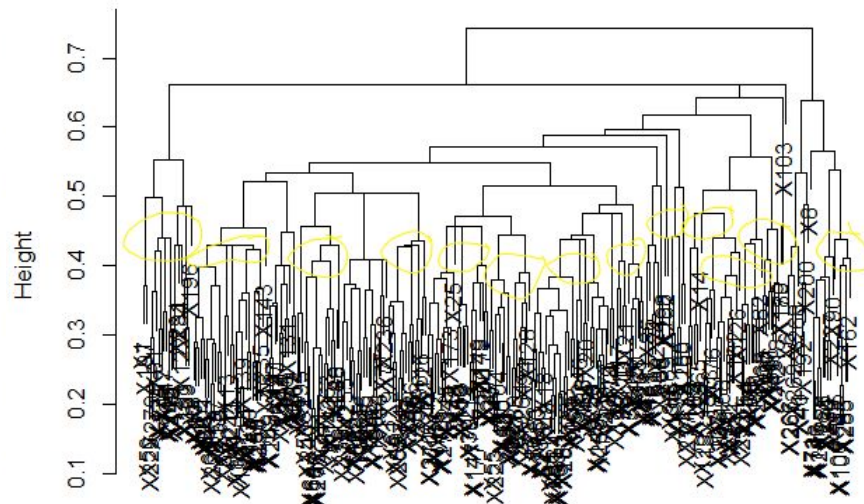
Exploring Subclusters

Dendrogram of `agnes(x = dissimilarityMat, diss = TRUE, method = "complete")`



dissimilarityMat
Agglomerative Coefficient = 0.61

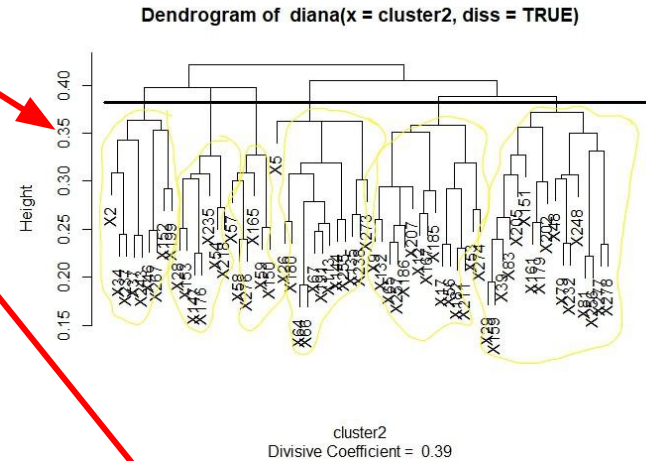
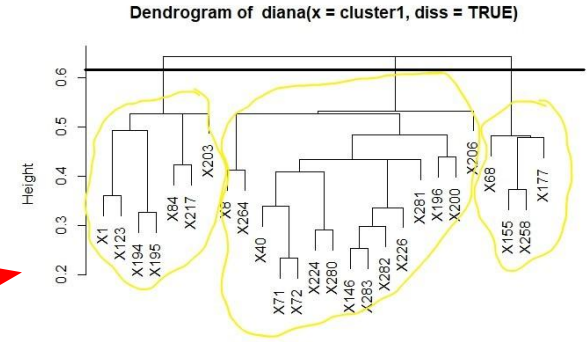
Dendrogram of `diana(x = dissimilarityMat, diss = TRUE)`



Divisive Coefficient = 0.59

Best Clustering Approach

1. Perform Mixture Model Clustering to obtain main clusters
2. Perform divisive clustering to obtain clusters within the main clusters (subclusters)



Statistical Analysis Results

- Used 6 different language models to get 6 different abstract similarity matrices:
 - Doc2Vec_300dim, Doc2Vec_apnews, Doc2Vec_Wiki, InferSent_GloVe, DocSim_LSI, WMD_GoogleNews300
- Applied the best clustering approach to each language model
 - Resulted in 6 different cluster analyses
- These 6 different analyses will result in 6 potential schedules
 - Which is the best ? Depends on evaluation criteria.

Scheduling Problem

- Can be viewed as an optimization problem
 - Hard constraints: the schedule must follow them to be feasible
 - Soft constraints: better schedule if follow them
- Requirements:
 - Code must be written in R
 - Scheduling the student talks
 - Satisfying the hard constraints
 - Exporting the schedule as a CSV file
- Wishes:
 - Scheduling invited, contributed, keynote speakers
 - Scheduling panel discussion
 - Scheduling poster sessions
 - Exporting as a CSV google calendar

Scheduling Problem

- The conference will be taken place in 3 consecutive days (Mon. to Wed.)
- Each day, three sessions except the last day (2 session)
- Each session can have up to n periods (n is dependent on the number of talks in each session and the period length)
- 286 talks to be scheduled
- We have up to 10 rooms
- We have four different types (flags) of speakers (listed in order):
 - Keynote
 - Student
 - Invited
 - Contributed
- Each talk has also a priority number

Hard Constraints [1]

H1: Talks with the same cluster should not happen at the same time.

H2: A talk must only appear once in the whole conference.

H3: A cluster c is to be assigned T_c talks in the whole conference.

H4: A talk cannot be assigned to more than one period.

H5: A room cannot be assigned to more than one talk at each time slot.

H6: The keynote talks should happen only once in each day of conference.

Feasible Schedule

A feasible schedule follows all hard constraints:

$$\sum_{i=1}^6 H_i = 0$$

Soft Constraints

S1: The bigger size of a cluster, the bigger size of a room should be assigned.

S2: The number of times that talks with the same cluster, session, day happen in different rooms.

S3: Talks with higher flag should be taken place first in each session.

S4: Keynote talks are preferred to happen in the first period of each day.

S5: Keynote talk are preferred to be in the largest rooms.

S6: No talk should be parallel with keynote talks. This penalty counts the number of talks that collides with the keynote talks.

S7: In each session, between two speakers with the same flag, the one with higher priority should go first.

Objective Function

The objective function is formulated as:

$$f = \sum_{i=1}^7 \theta_i S_i$$

Greedy Algorithm for Solving the Problem

Algorithm 1 A Greedy algorithm for solving the scheduling problem

Greedy (R, C, D, S, P, l)

Sort rooms in R based on their capacities

Sort clusters in C based on their sizes

Assign keynote speakers to the largest room and the first period of the first session of each day

Choose a cluster c in C with the largest size

For each r in R

 For each d in D

 For each s in S

 Set s_l as session length for s

 Set $n_p = s_l / l$

 For $p = 1$ to n_p

 If not the first p in the first s in d

 Choose a talk t in c with highest flag and priority, which has not been scheduled

 Assign t to our schedule X in day d , session s , period p .

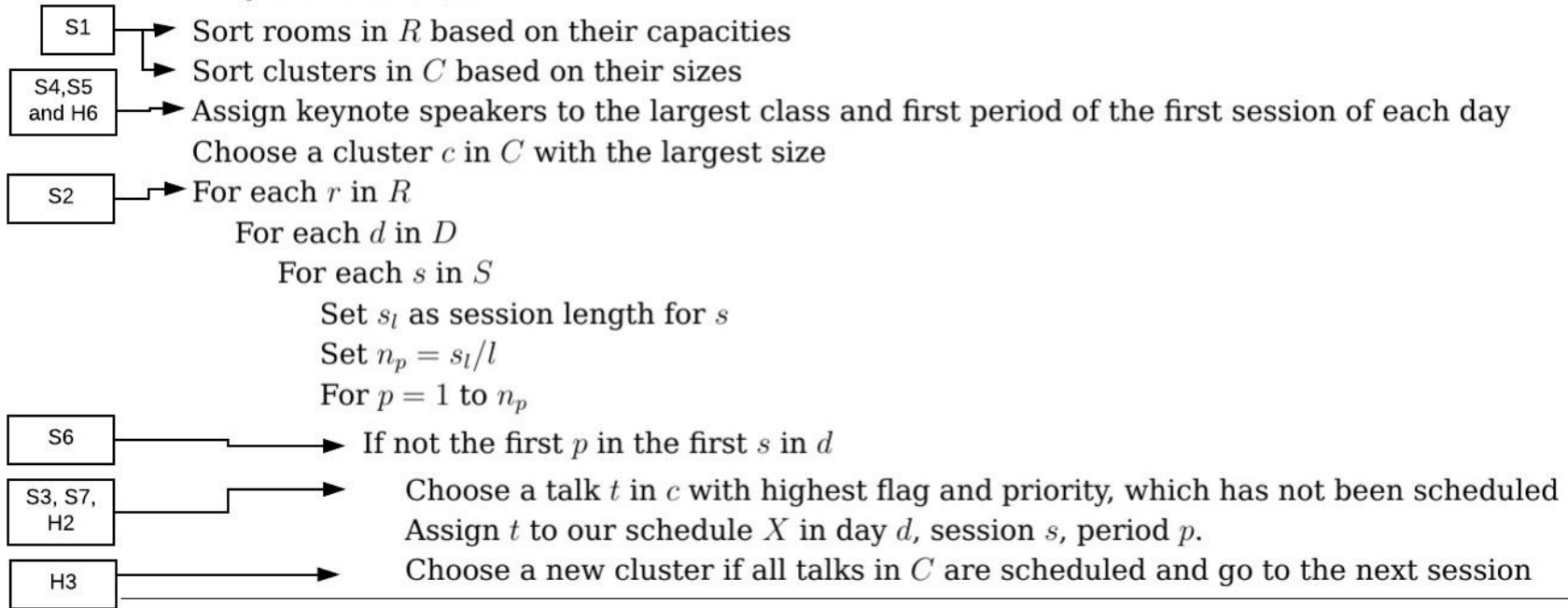
 Choose a new cluster if all talks in C are scheduled and go to the next session

Return X

Greedy Algorithm for Solving the Problem

Algorithm 1 A Greedy algorithm for solving the scheduling problem

Greedy (R, C, D, S, P, l)



Results for greedy algorithm

Clustering type	Computation Time (s)	Function Value (F)
Type 1	6.5	0
Type 2	7.2	0
Type 3	7.6	0
Type 4	6.5	0
Type 5	7.5	0
Type 6	7.3	0

Computation time for a function call: (20 s)

Why a Heuristic Algorithm is not a Good Idea?

- Objective function is computationally expensive (20 s)
- The greedy algorithm find the schedule in less than 8 seconds.
- Considering the soft constraints mentioned, the greedy algorithm gives us the best schedule.

Output Visualization (Clustering Method 1)

Monday											
Room	Start time	Cluster number	Flag	Start time	Cluster number	Flag	Priority	Start time	Cluster number	Flag	Priority
	2018-03-18 8:40			2018-03-18 9:01				2018-03-18 9:22			
Room 1	An Overview of Existing a	2	Keynote	Disclosure Control and Random Ta	6	Student	86	A Simple Tool for Boundi	6	Student	164
Room 2				Localized Quantile Regression of R	11	Contributed	233	Comparison of Multivaria	11	Contributed	281
Room 3				Conditional Dependence Models u	8	Contributed	179	Computational Neurosci	8	Contributed	189
Room 4				Estimation and Inference in Directi	12	Student	278	Dependent Models for th	12	Invited	12
Room 5				Accurate Confidence Intervals for	9	Student	100	Estimating Cross-validatc	9	Student	157
Room 6				Generalized Simulated Method-of-	21	Invited	112	From Brain to Hand to St	21	Invited	193
Room 7				Efficiently Computing the Projectic	20	Student	148	Improving Risk Assessme	20	Invited	11

Room Name	Room number	Room capacity
AMT 100	1	100
AMT 101	2	75
AMT 102	3	75
ASC 165	4	50
ASC 163	5	50
SCI 3333	6	50
SCI 124	7	30
EME 100	8	30

Output Google CSV Calendar

[Link](#)



Leadership

- Agile software development was utilized due to the alignment of its manifesto
 - Working software
 - Customer Collaboration
- Assign team members to components of the project based on domain knowledge
- Ten minute SCRUM weekly meeting on Thursdays to resolve any issues
 - Mahdi performed the role of SCRUM master

References

- [1] Zhang, D., Liu, Y., M'Hallah, R., & Leung, S. C. H. (2010). A simulated annealing with a new neighborhood structure based algorithm for high school timetabling problems. *European Journal of Operational Research*, 203(3), 550–558.

- [2] Kevin, L, Gordon, M. (2015, June 10). Graphic Representations of word2vec and doc2vec. Retrieved December 07, 2017, from <https://groups.google.com/forum/#!topic/gensim/EwK-6JgkWVI>

Thank You.