

Data Analyst : 김형준

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R

Statistics & Visualization

Statistics & Machine Learining

: GLM, GLMM, SEM, IRT, MLM(HLM), PCA, LSA, LDA MRFs, CRFs, SVM, Tree, RBF, MLP, Auto-Encoder, Deep-Learning

Visualization

: ggplot2, wordcloud, d3, shiny, map, spatial

1. A 대학 기숙사 컨설팅

Big-Data: Text & Query

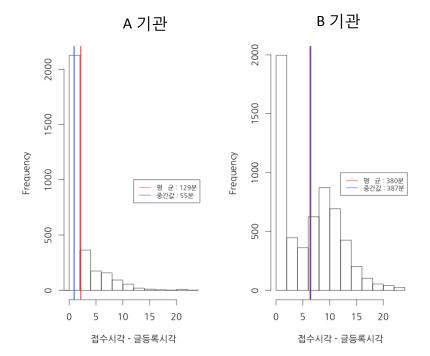
사생들의 건의 사항 분석 (2013)

Dormitory Issue





행정 서비스 비교 (2014)

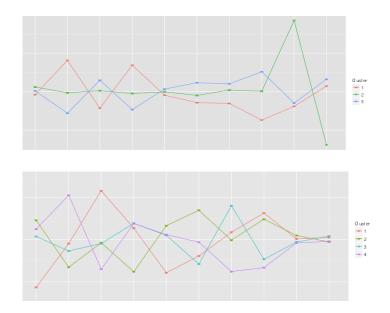


2. A 기업 인사 선발 개선 프로<u>젝트</u>

인적성 시험 응시자

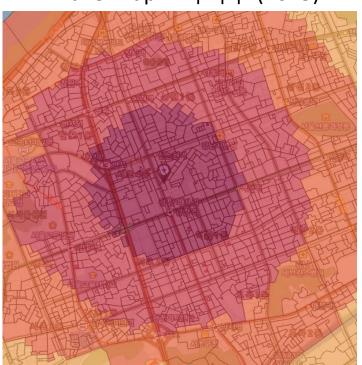
인사 선발 면접 프로세스 (2014)

 합격자 / 비합격자 프로파일링 (2014)

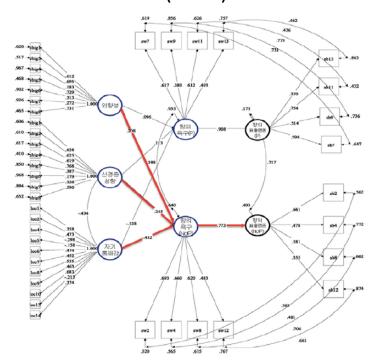


3. 공모전

Navermap + 지역구 (2015)



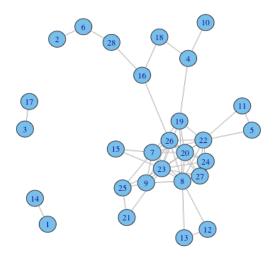
SEM (2012)



4. 논문 연구

LSA / LDA (2014) Topic proportions and **Topics Documents** assignments 0.02 Seeking Life's Bare (Genetic) Necessities genetic 0.01 COLD SPRING HARBOR, NEW YORK- "are not all that far apart," especially in How many genes does an organism need to comparison to the 75.000 genes survive: Last week at the genome meeting the survive of here," two genome researchers with radically Universi different approaches presented complementary views of the basic genes needed for life One research team, using computer analyevolve 0.01 ses to compare known genomes, concluded organism 0.01 that today sugarnisms can be sustained with just 250 genes, and that the earliest life forms any newly sequenced genome," explains required a mere 128 genes. The Arcady Mushegian, a computational moother researcher mapped genes lecular biologist at the National Center for Biotechnology Information (* CBI) in a simple parasite and estimated that for this organism. in Bethesda, Maryland. Comparin 800 genes are plenty to do the brain job-but that anything short 0.02 of 100 wouldn't be enough. nerve Although the numbers don't match precisely, those predictions * Genome Mapping and Sequencing, Cold Spring Harbor, New York, Stripping down. Computer analysis yields an estimate of the minimum modern and ancient genomes. SCIENCE • VOL. 272 • 24 MAY 1996 0.02 computer 0.01

Link Prediction (2014)



4. 논문 연구

0.0

0.2

0.4

False positive rate

0.6

0.8

1.0

