Last time. . .

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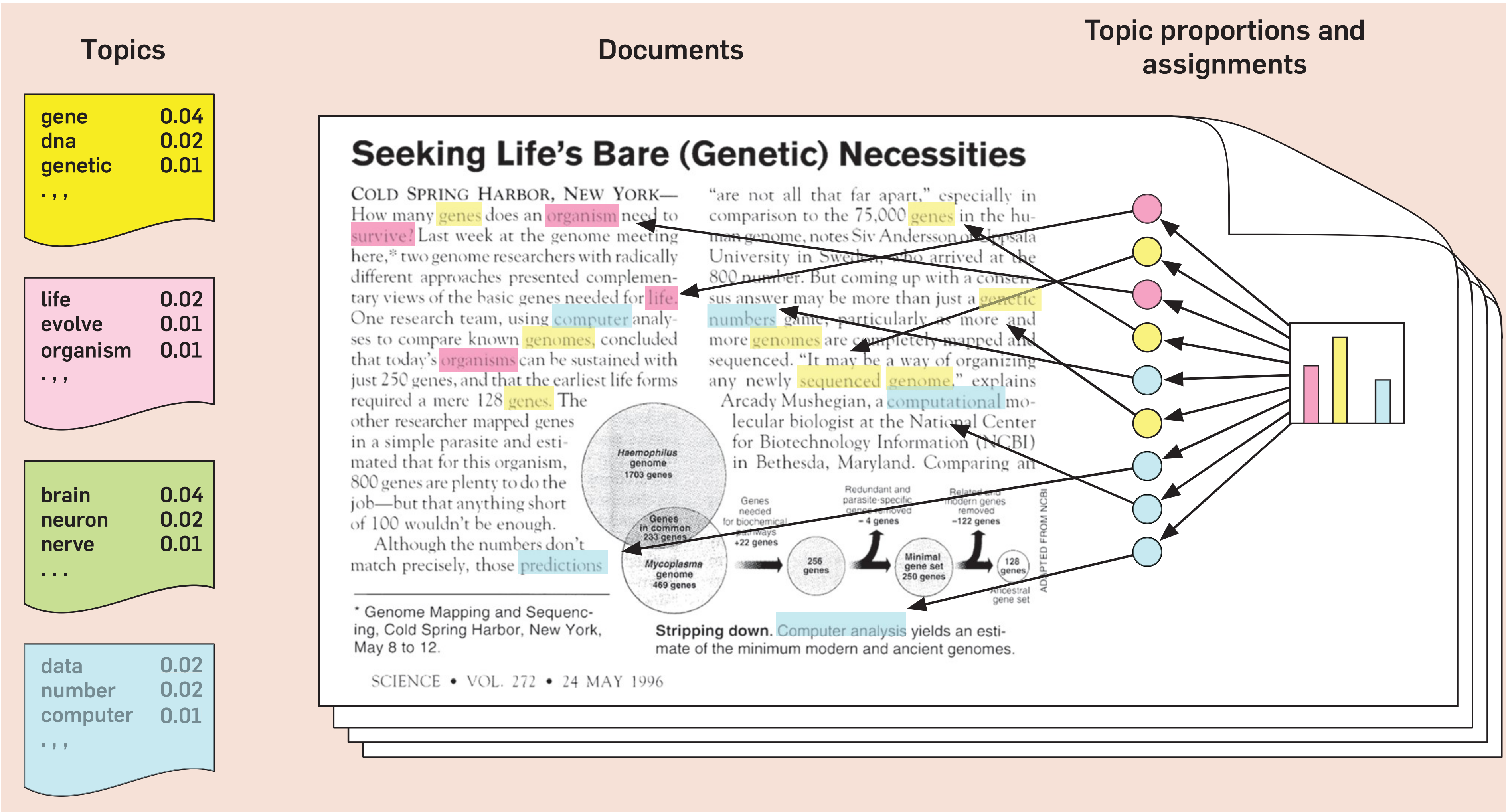

Topics
Documents
Topic proportions and assignments
gene 0.04
dna 0.02
genetic 0.01
. , ,
life 0.02
evolve 0.01
organism 0.01
. , ,
brain 0.04
neuron 0.02
nerve 0.01
. . .
data 0.02
number 0.02
computer 0.01
. , ,
Seeking Life's Bare (Genetic) Necessities
COLD SPRING HARBOR, NEW YORK— How many genes does an organism need to survive? Last week at the genome meeting here,* two genome researchers with radically different approaches presented complementary views of the basic genes needed for life. One research team, using computer analyses to compare known genomes, concluded that today's organisms can be sustained with just 250 genes, and that the earliest life forms required a mere 128 genes. The other researcher mapped genes in a simple parasite and estimated that for this organism, 800 genes are plenty to do the job—but that anything short of 100 wouldn't be enough.
Although the numbers don't match precisely, those predictions
* Genome Mapping and Sequencing, Cold Spring Harbor, New York, May 8 to 12.
"are not all that far apart," especially in comparison to the 75,000 genes in the human genome, notes Siv Andersson of Uppsala University in Sweden, who arrived at the 800 number. But coming up with a consensus answer may be more than just a genetic numbers game, particularly as more and more genomes are completely mapped and sequenced. "It may be a way of organizing any newly sequenced genome," explains Arcady Mushegian, a computational molecular biologist at the National Center for Biotechnology Information (NCBI) in Bethesda, Maryland. Comparing an
Haemophilus genome 1703 genes
Genes in common 233 genes
Mycoplasma genome 469 genes
Genes needed for biochemical pathways +22 genes
256 genes
Redundant and parasite-specific genes removed −4 genes
Minimal gene set 250 genes
Related and modern genes removed −122 genes
128 genes
Ancestral gene set
ADAPTED FROM NCBI
Stripping down. Computer analysis yields an estimate of the minimum modern and ancient genomes.
SCIENCE • VOL. 272 • 24 MAY 1996

Extensions and Special Cases

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Assn no covariates
But topic prevalence and topic content are $f(X)$ [STM]

Lots of other ideas!

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hierarchical LDA, pachinko allocation, nonparametric pachinko allocation,factorial LDA, gamma-poisson factorization, shared component topic models, dirichlet multinomial regression topic models, nested hierarchical dirichlet process topic model, focused topic model, inverse regression topic model, ideal point topic model, discrete innite logistic normal topic model multilingual topic model, markov topic model, relational topic model, syntactic topic model, supervised latent dirichlet allocation

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Senators from same states have similar agendas

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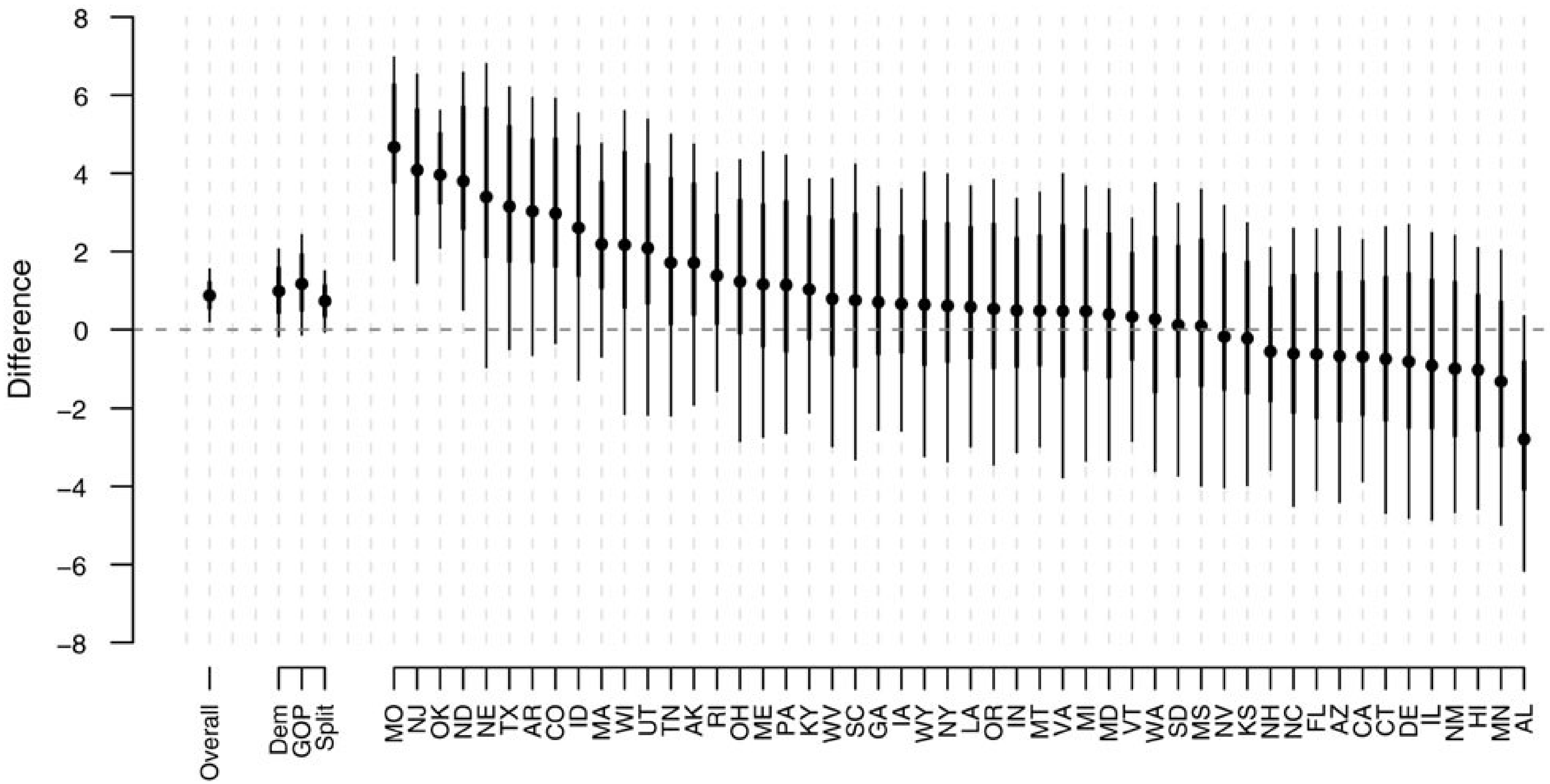

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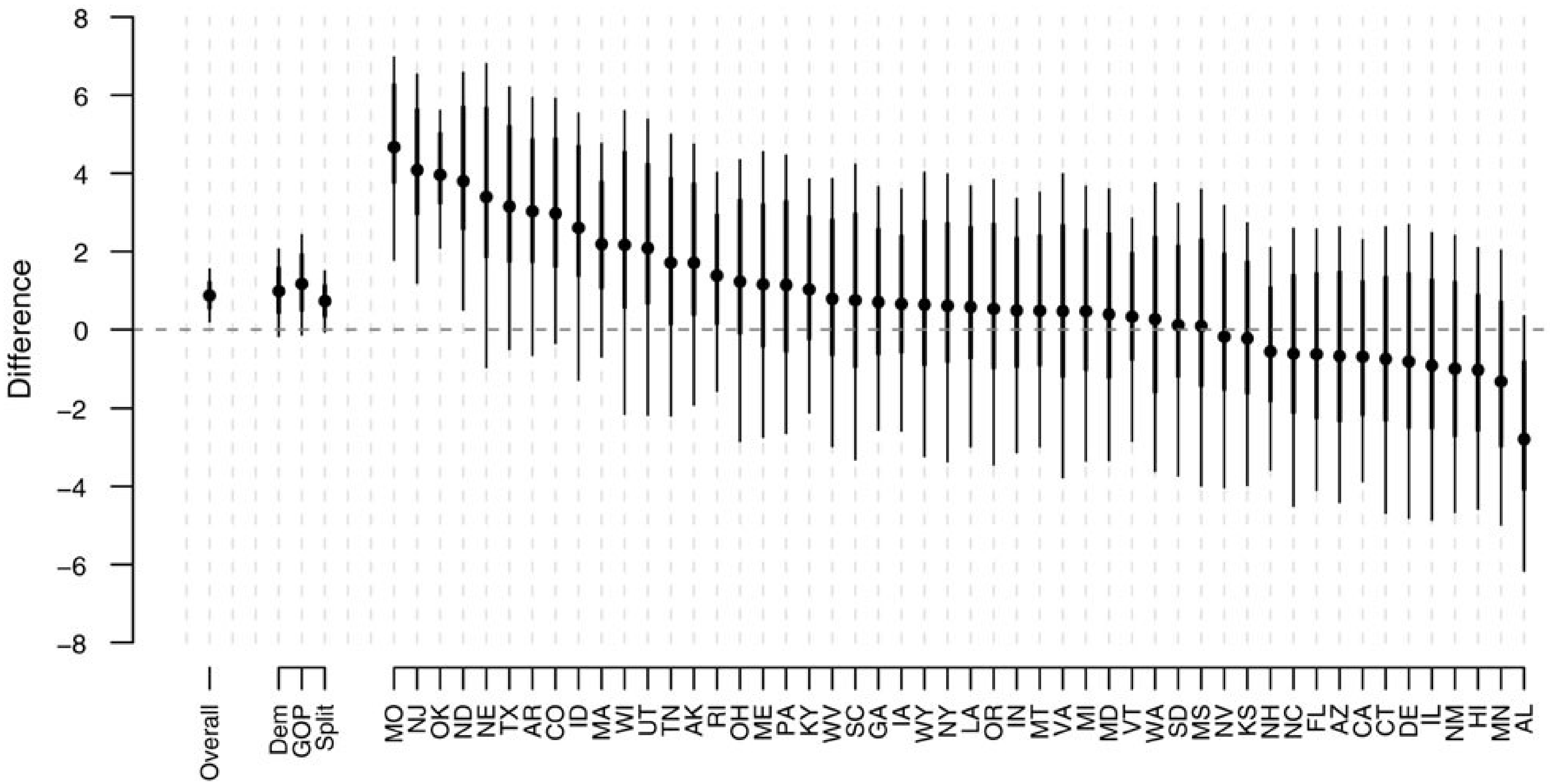

Senators from same states talk about more similar things than Senators from different states (generally).

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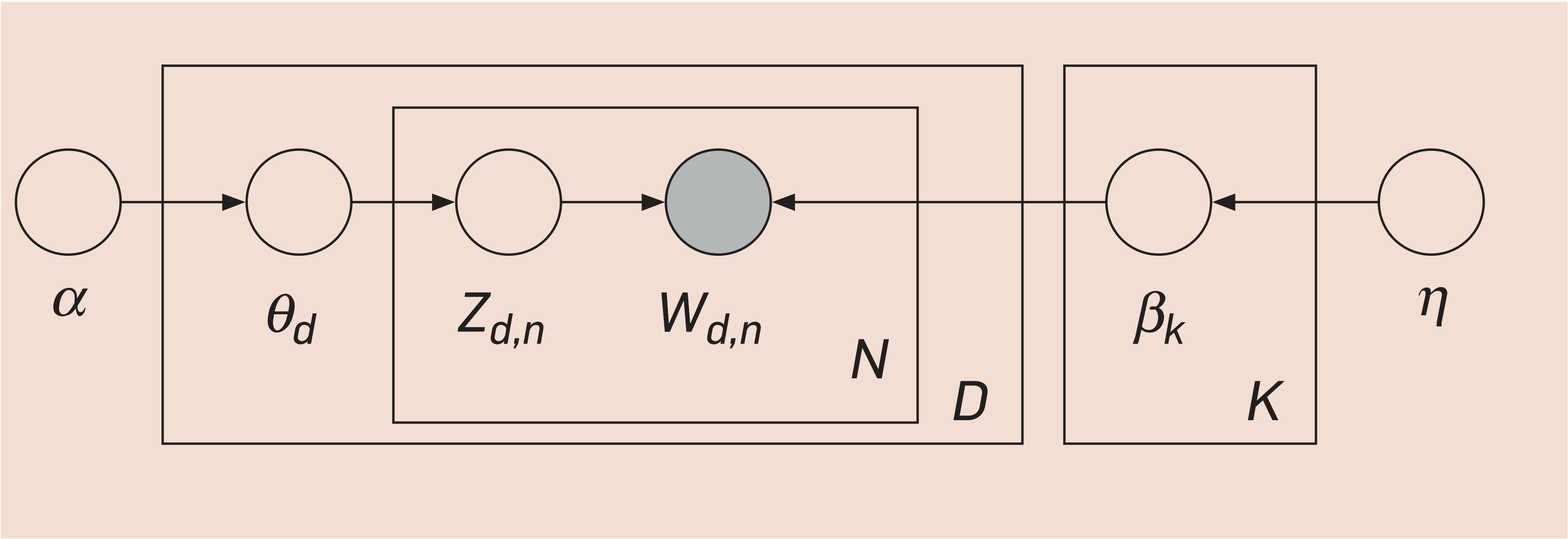
Recall LDA...



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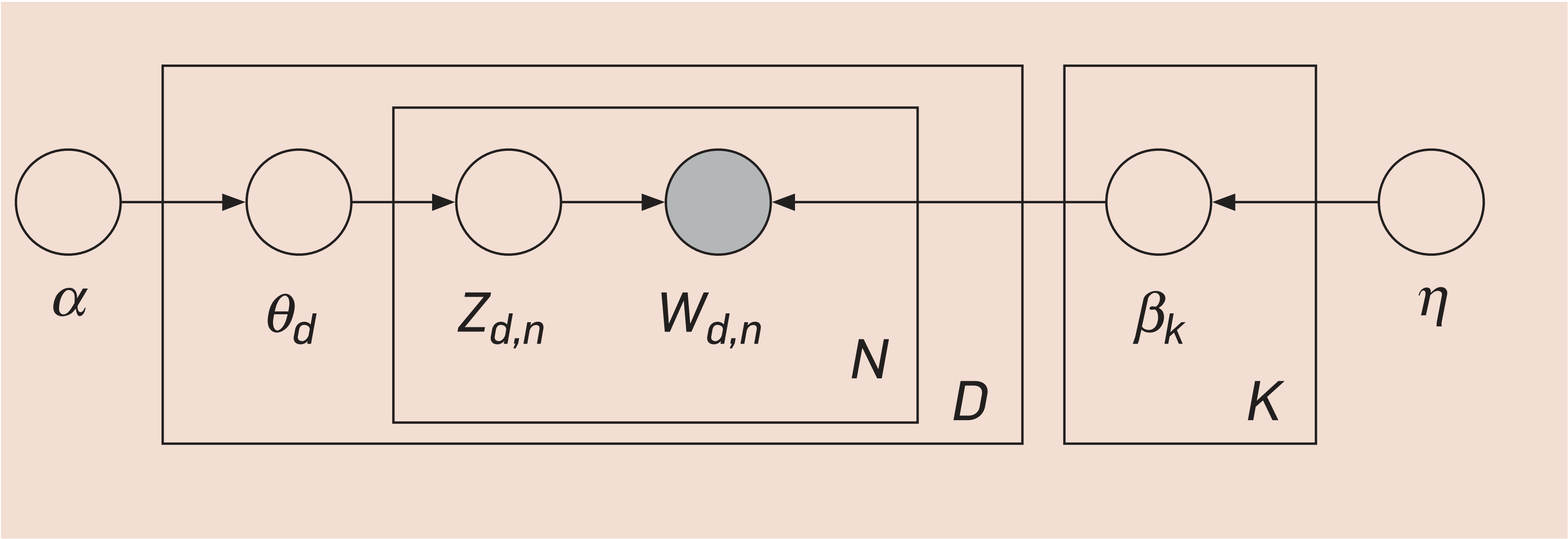

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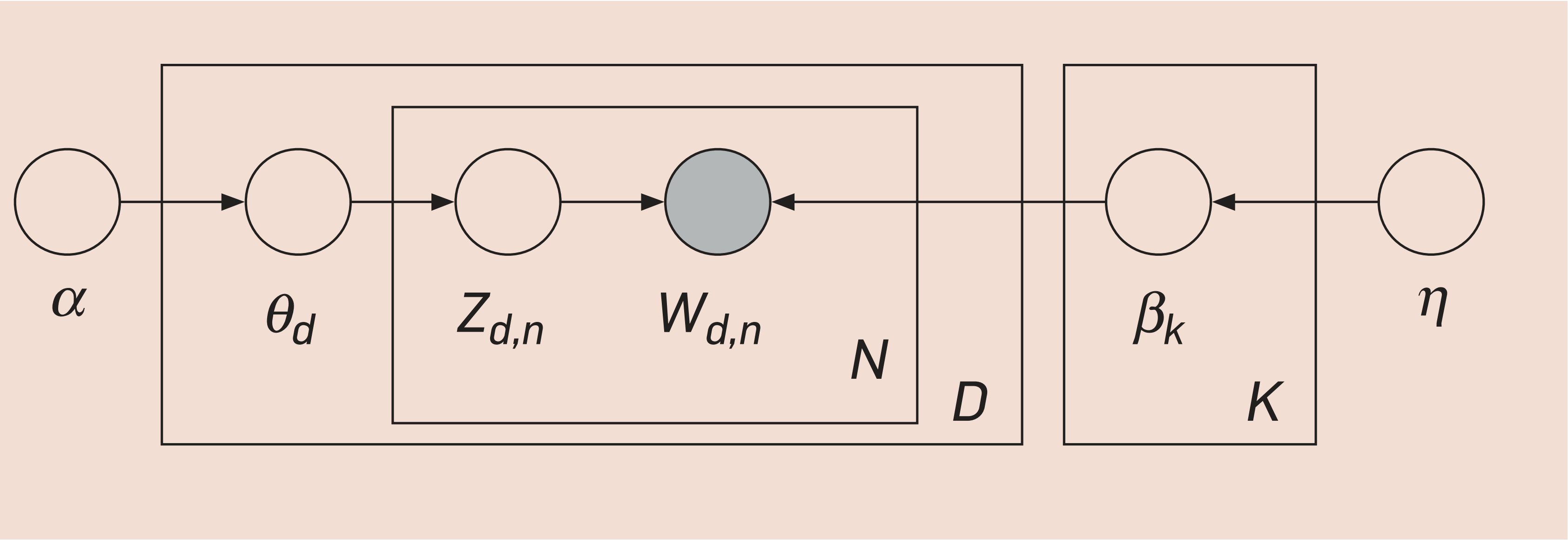

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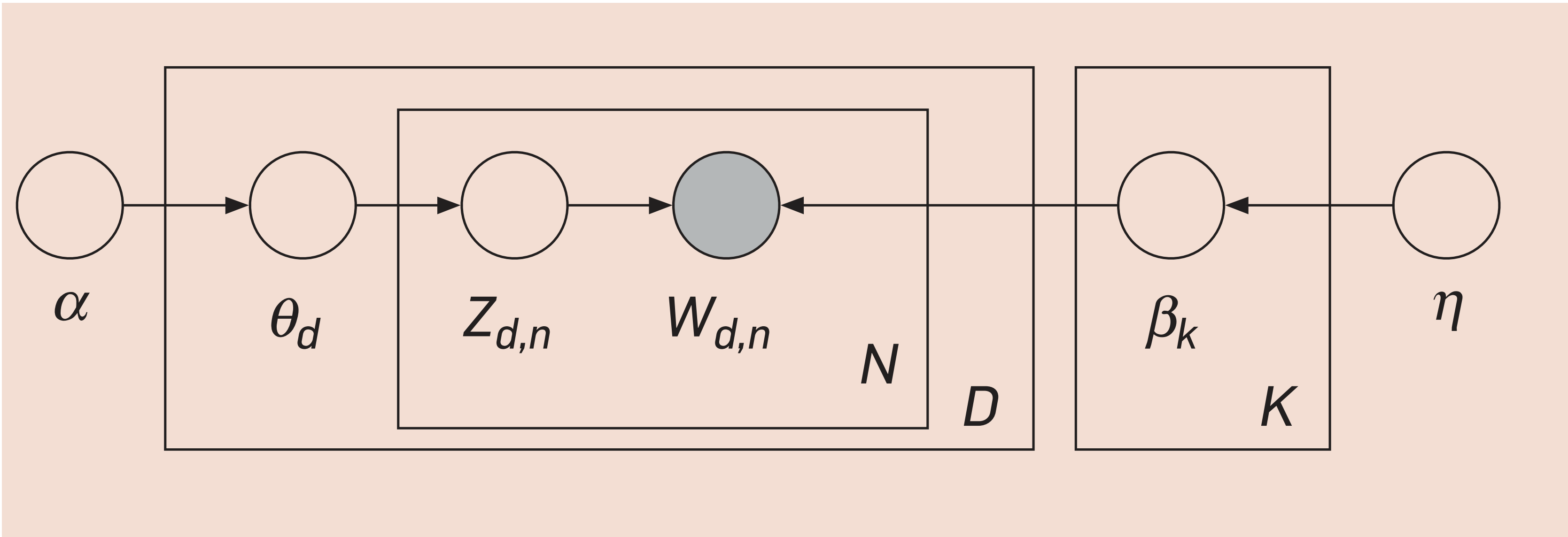

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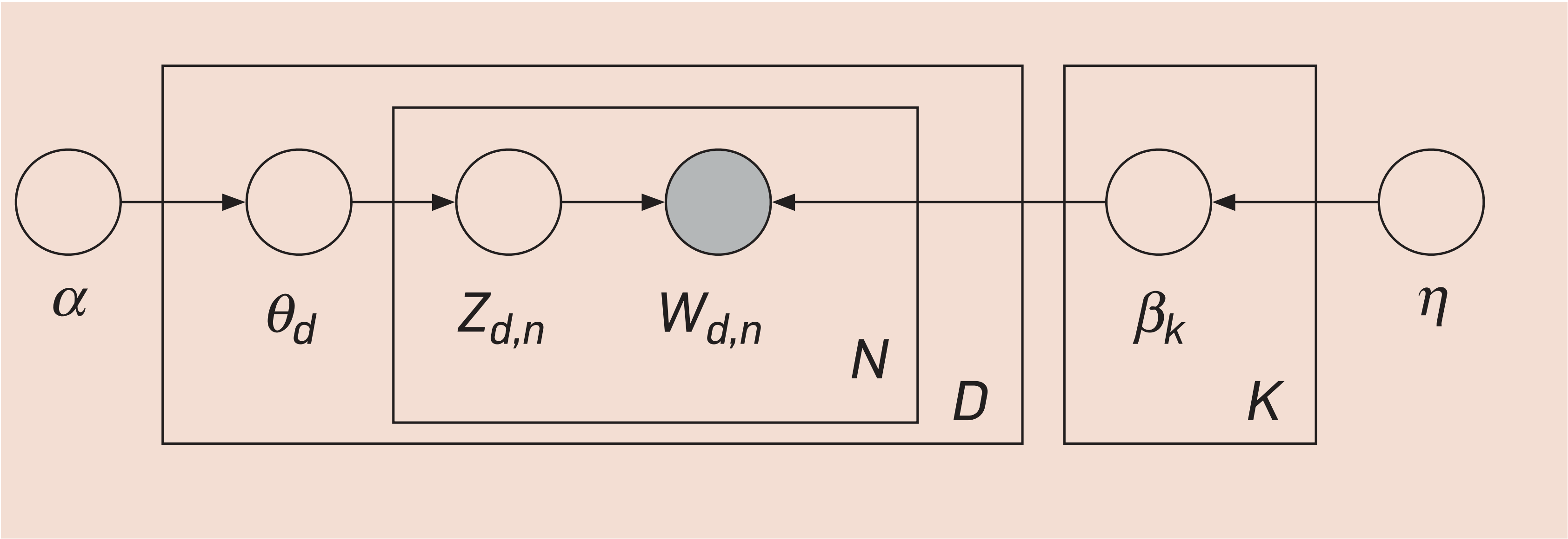

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Dynamic Topic Model has a different model for each time period, with topics allowed to evolve over time. . .

So. . .

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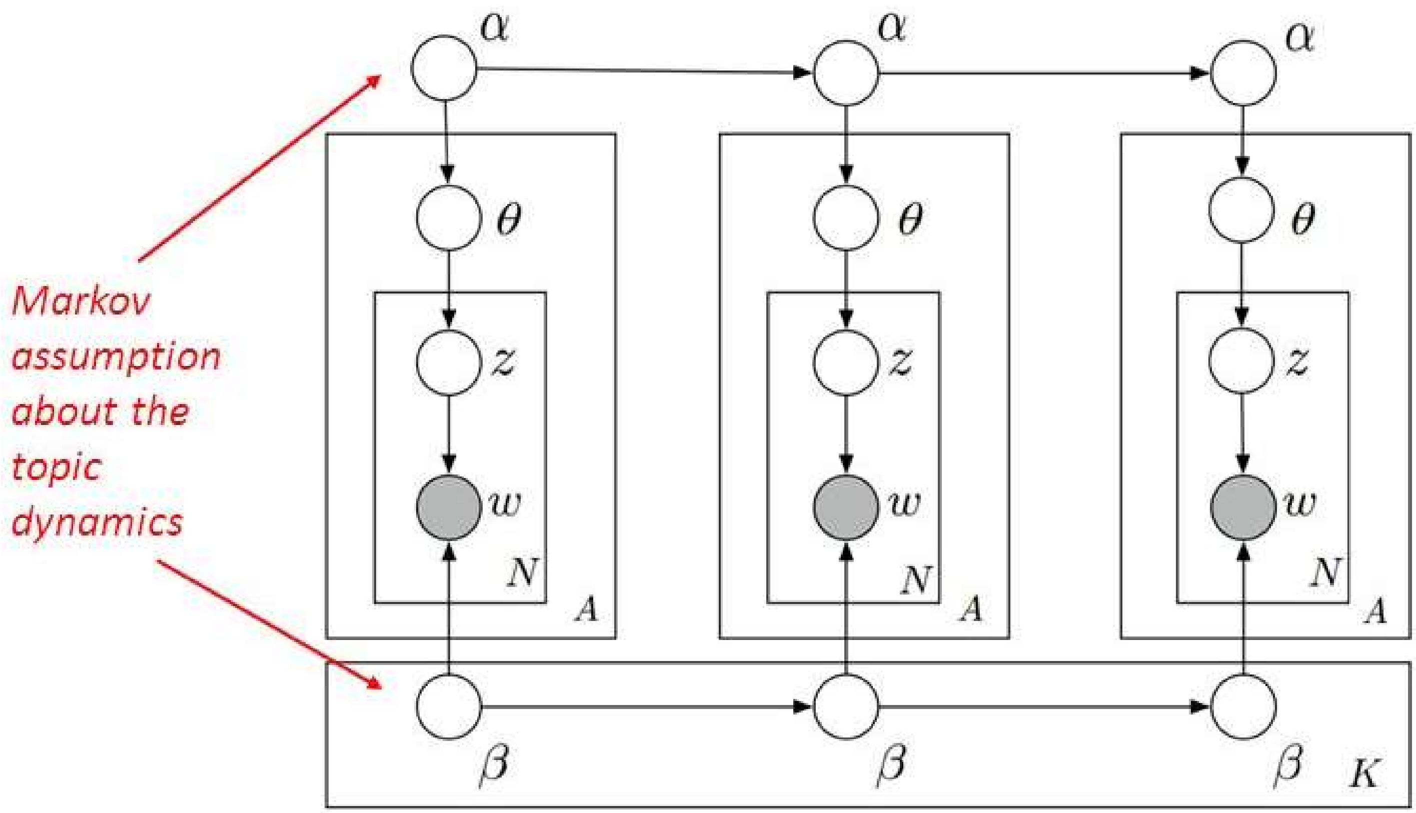

Markov
assumption
about the
topic
dynamics
α
α
α
θ
θ
θ
z
z
z
w
w
w
N
N
N
A
A
A
β
β
β
K

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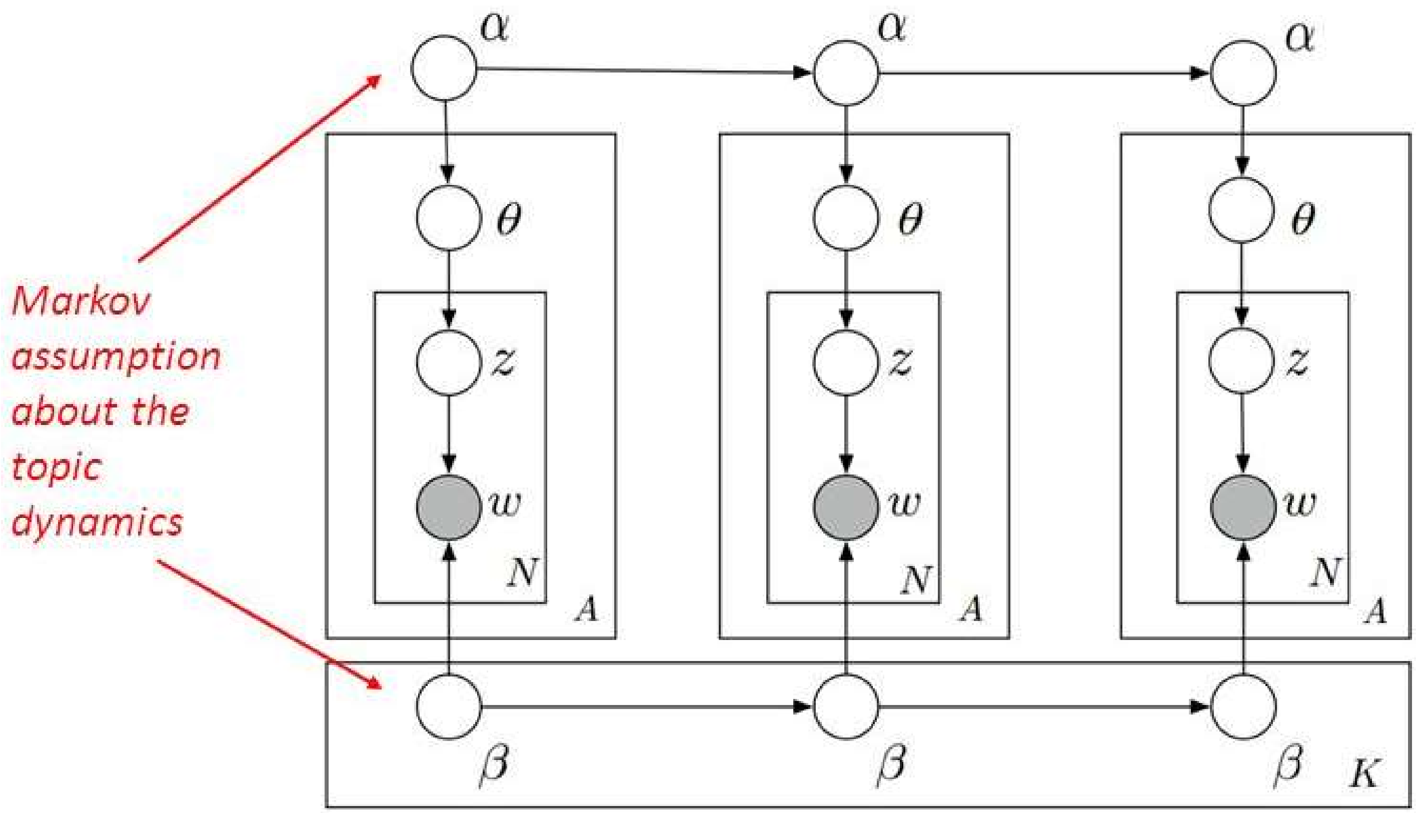

Now, mean parameters for the topic proportions (αs) and the what's in the topics (in terms of words, βs) are connected over time via a simple evolutionary process (West & Harrison, 1997).

How to Analyze Political Attention with Minimal Assumptions and Costs (Quinn et al, 2010)

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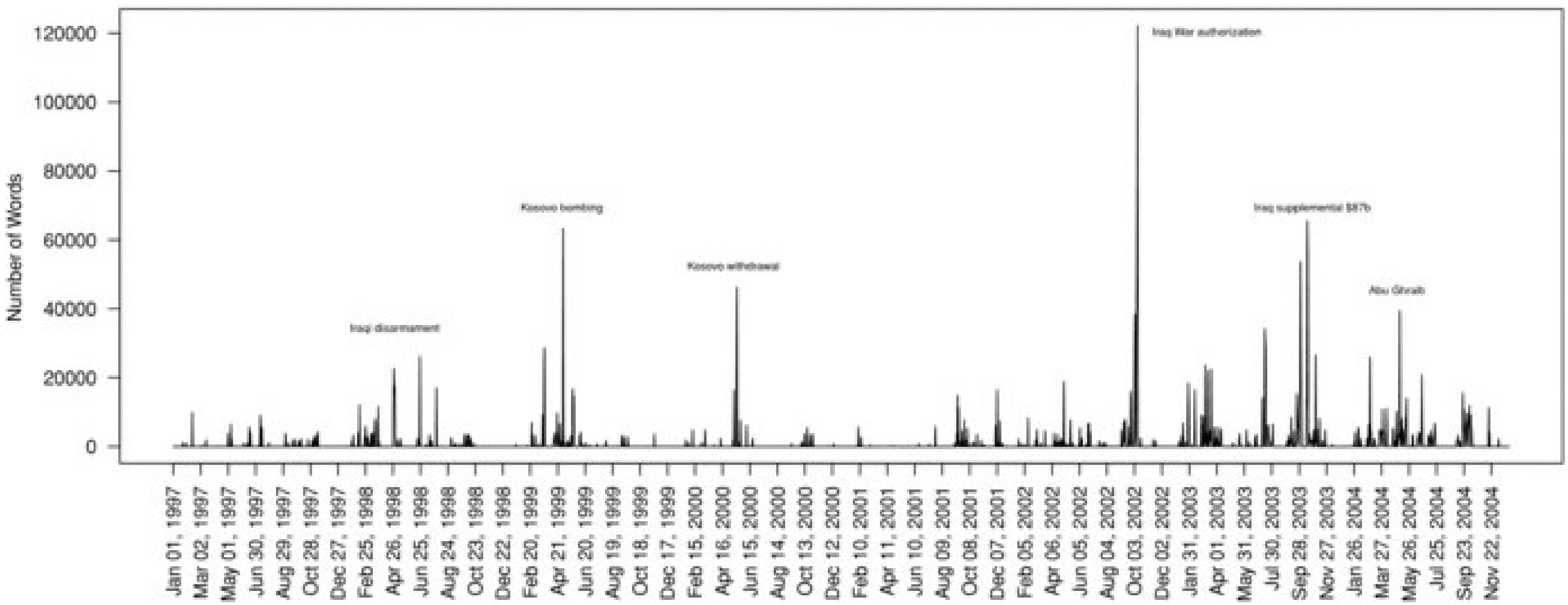
BTW, paper has a lot of validation!

Attention to Defense [Use of Force]



(b) *The Number of Words on the 'Defense [Use of Force]' Topic Per Day*

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Including covariates allows for (a) more accurate estimation and (b) better interpretatability.

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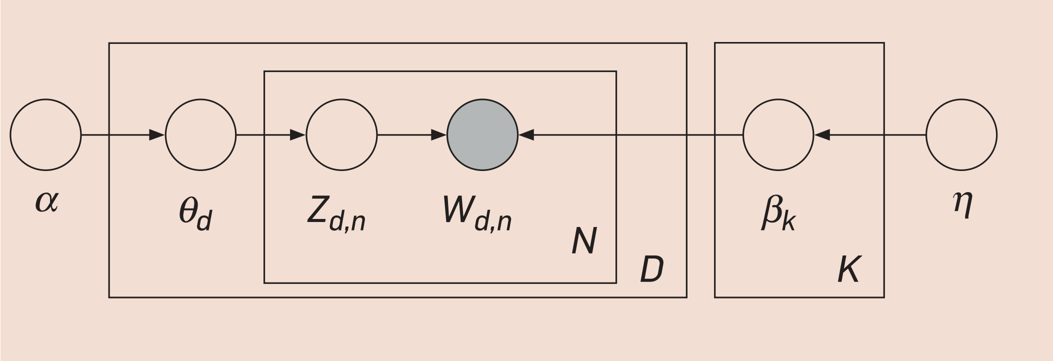

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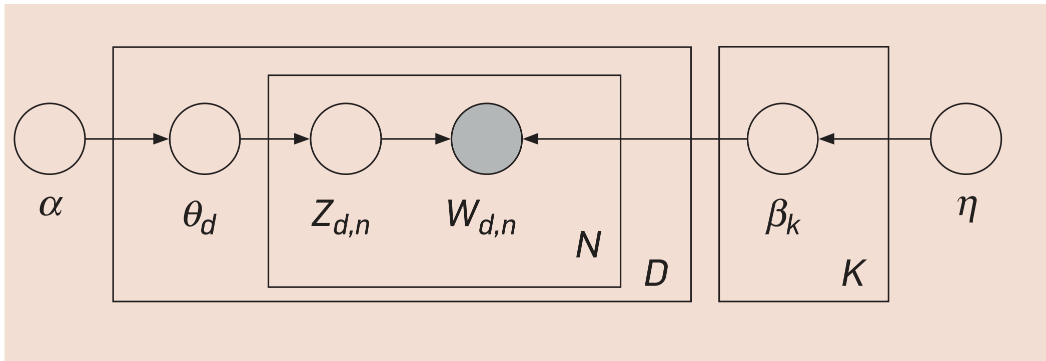

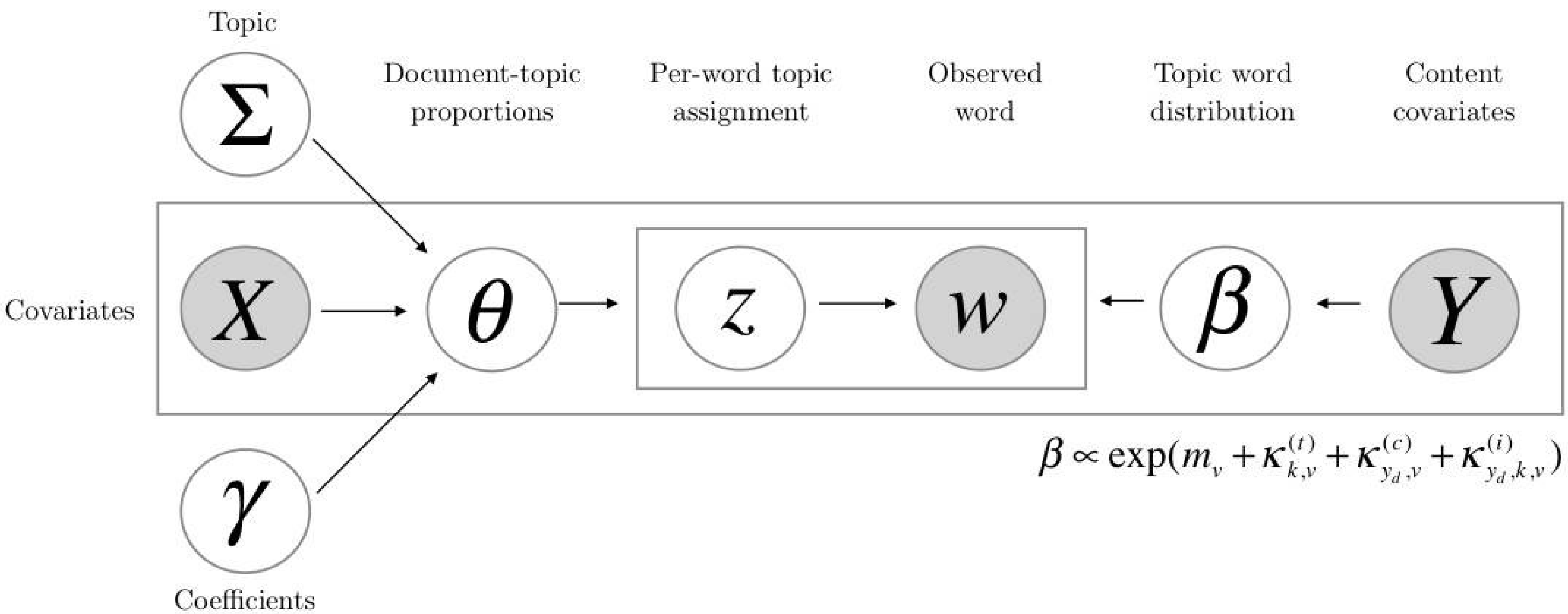

$$\beta \propto \exp(m_v + \kappa^{(t)}_{k,v} + \kappa^{(c)}_{y_d,v} + \kappa^{(i)}_{y_d,k,v})$$

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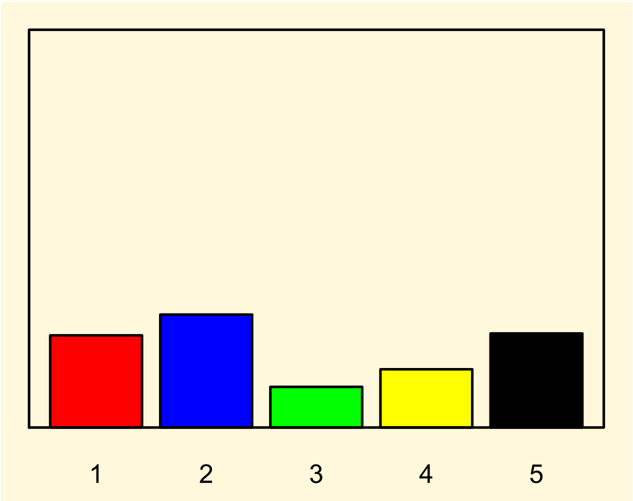

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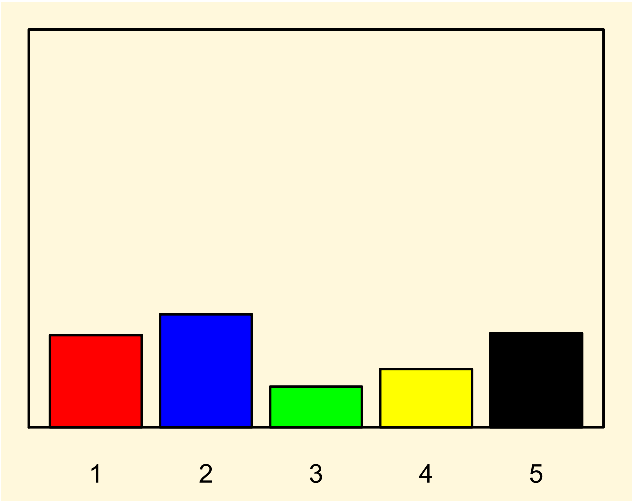

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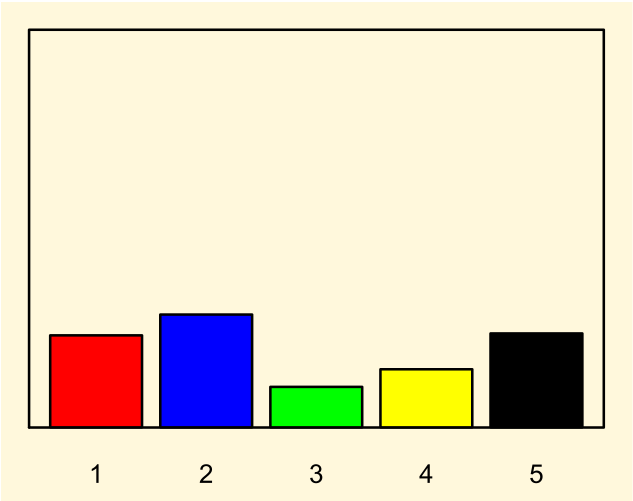

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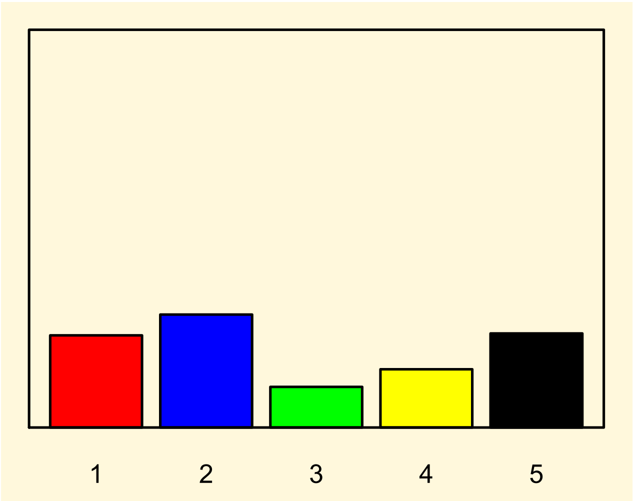

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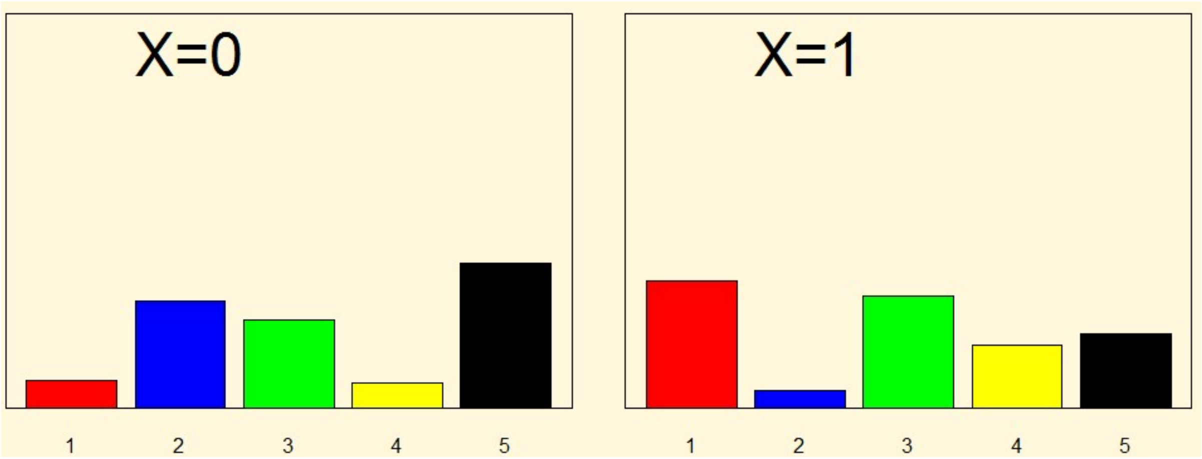

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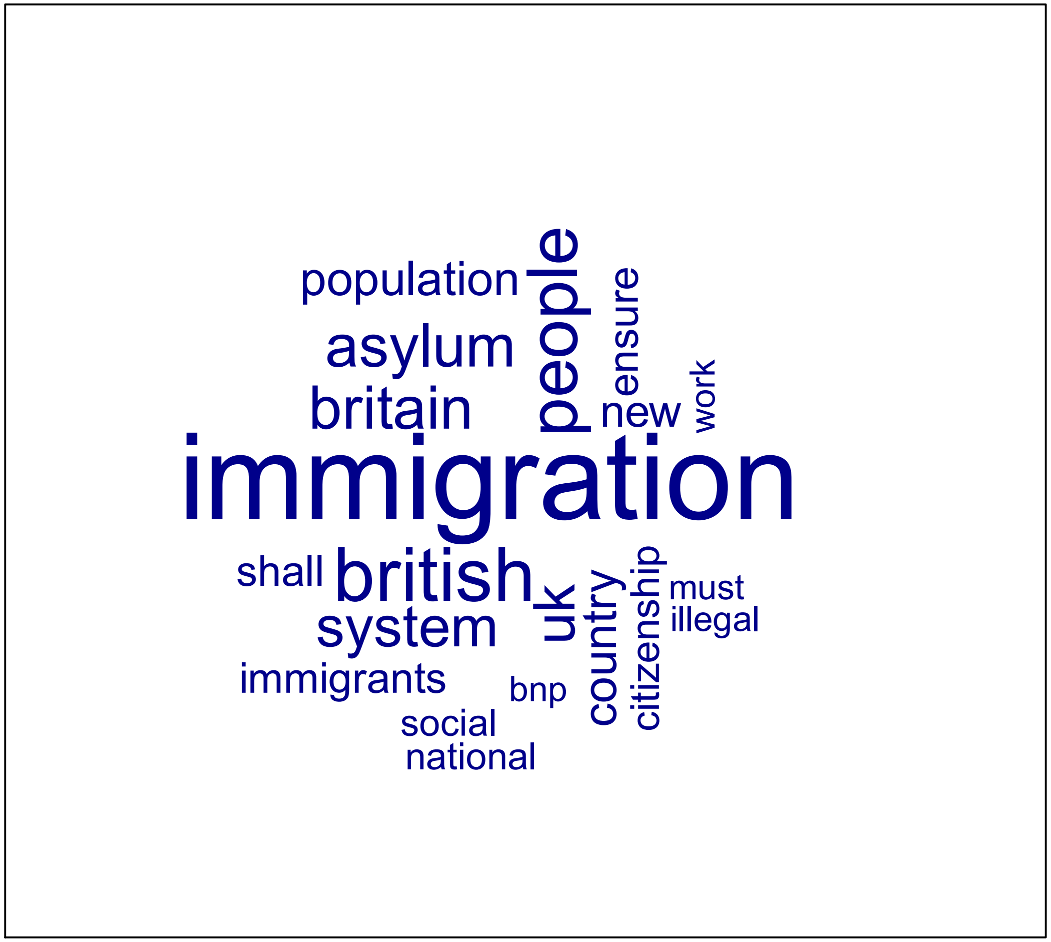

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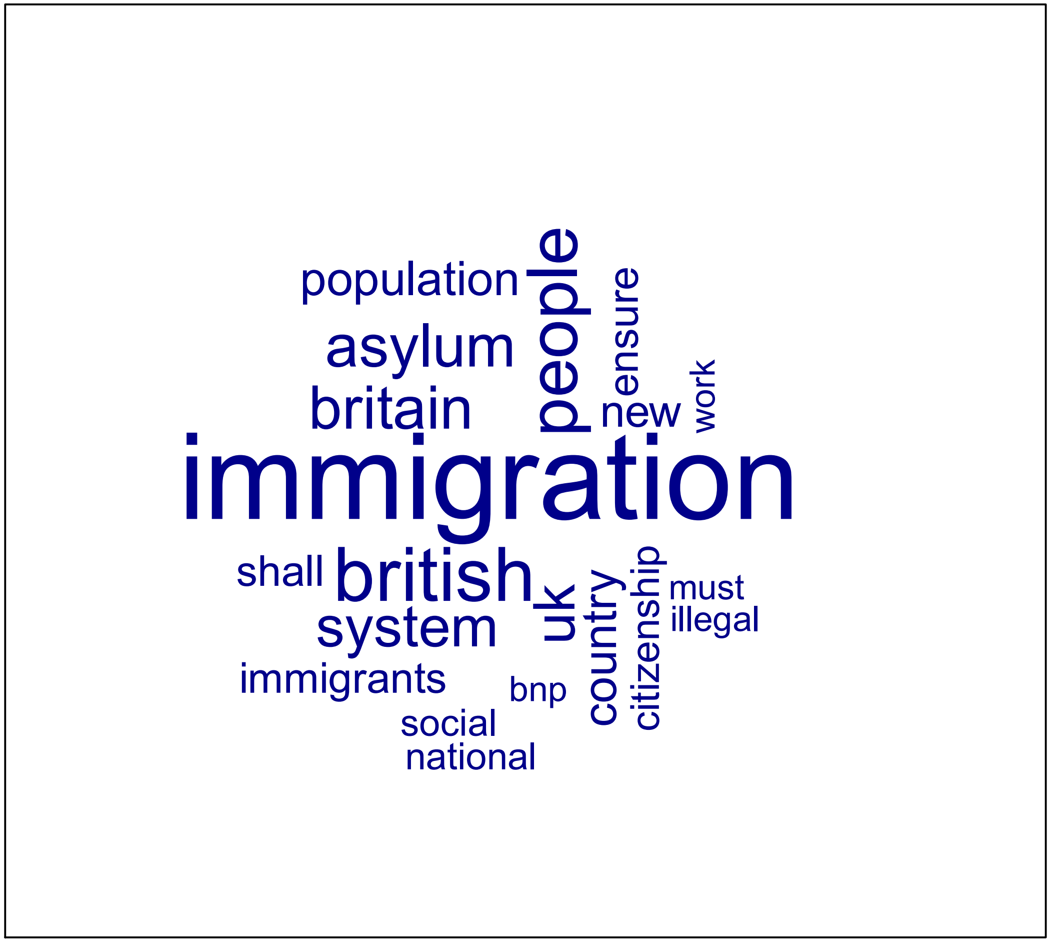

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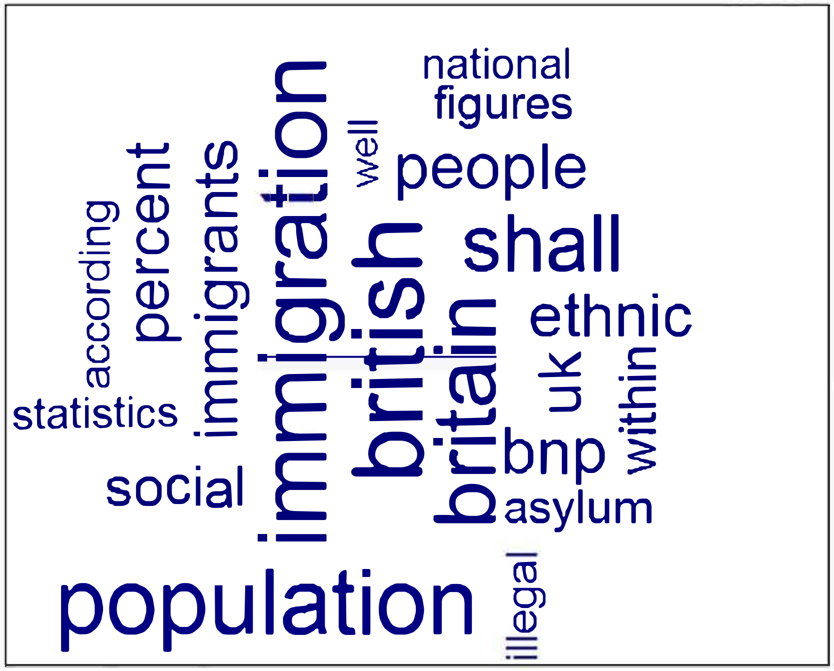
Y=0



Y=1