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- ▶ \$ Abstract
- ▶ \$ Background
- ▶ \$ Results and discussion
- ▶ \$ Conclusions
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 - Positions of two vulture...
 - Demographic history of...
- ▼ Figures by Section
- ▼ \$ Comparative evolutiona...

The first whole genome and transcriptome of the Old World vulture reveals adaptation in the gastric and immune defense systems and possible convergent evolution with the Old and New World vultures

Oksung Chung¹, Seondeok Jin², Yun Sung Cho^{1,3}, Jeongheui Lim⁴, Hyunho Kim³, Hak-Min Kim³, JeHoon Jun¹, HyeJin Lee¹, Alvin Chon³, Junsu Ko⁵, Jeremy Edwards⁶, David J. Weber⁷, Kyudong Han^{8,9}, Stephen J. O'Brien^{10,11,12}, Andrea Manica¹³, Jong Bhal Paek⁴

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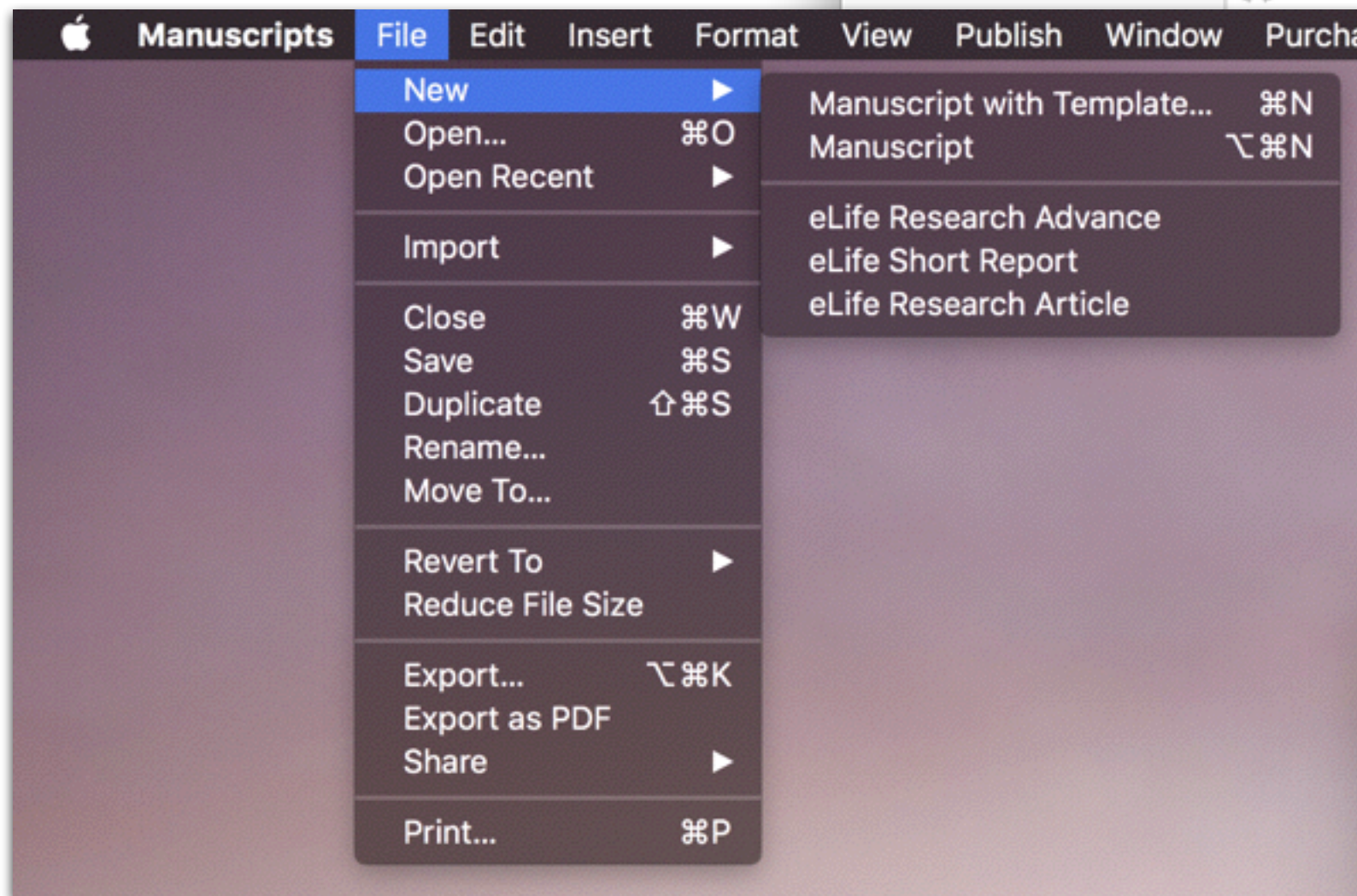
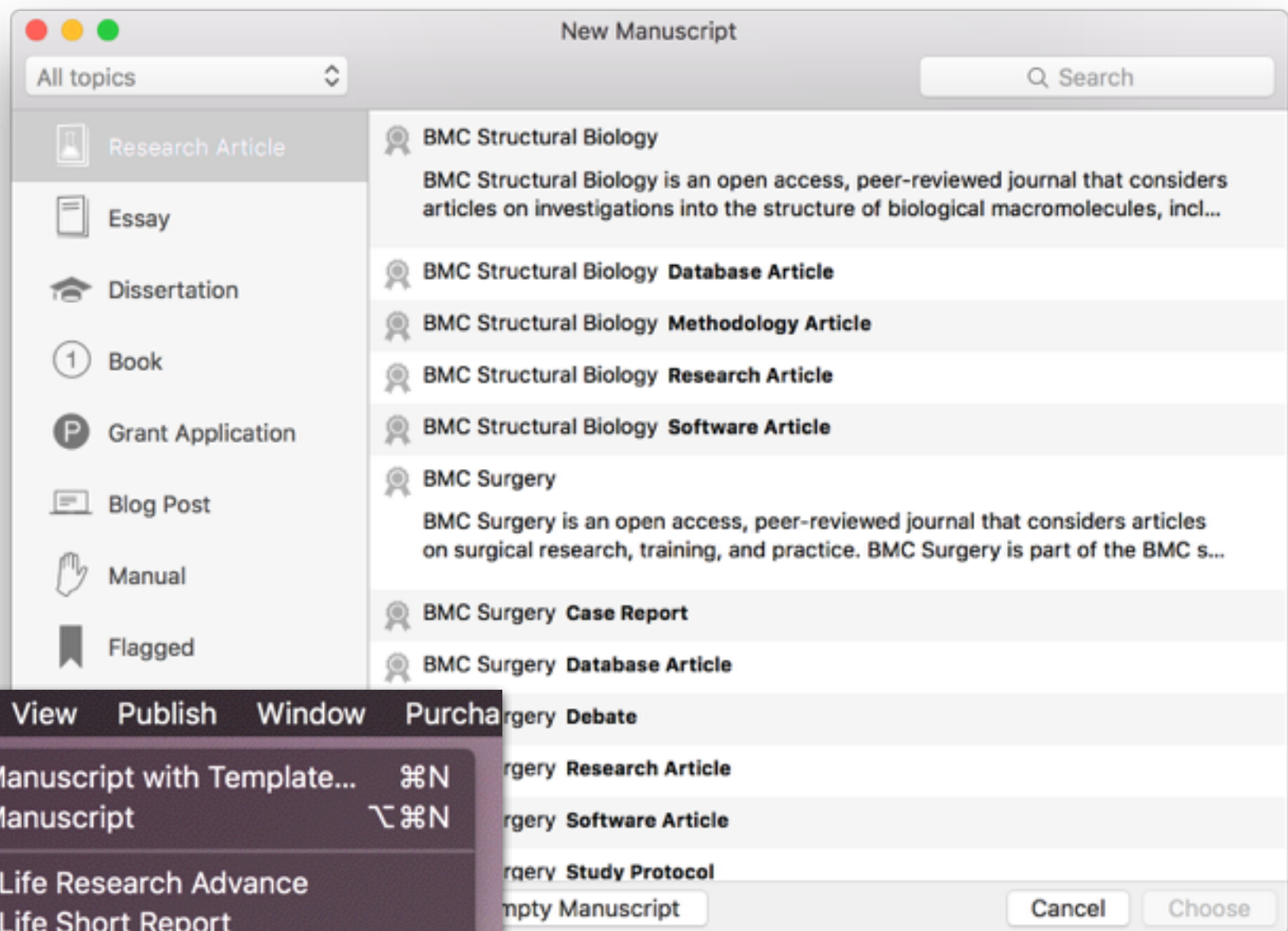
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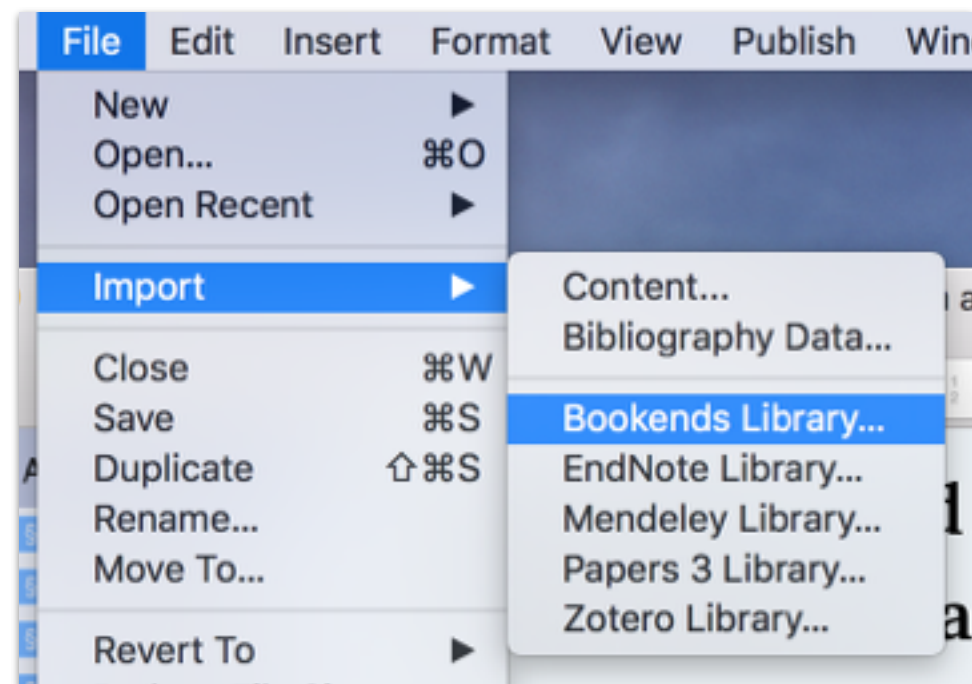
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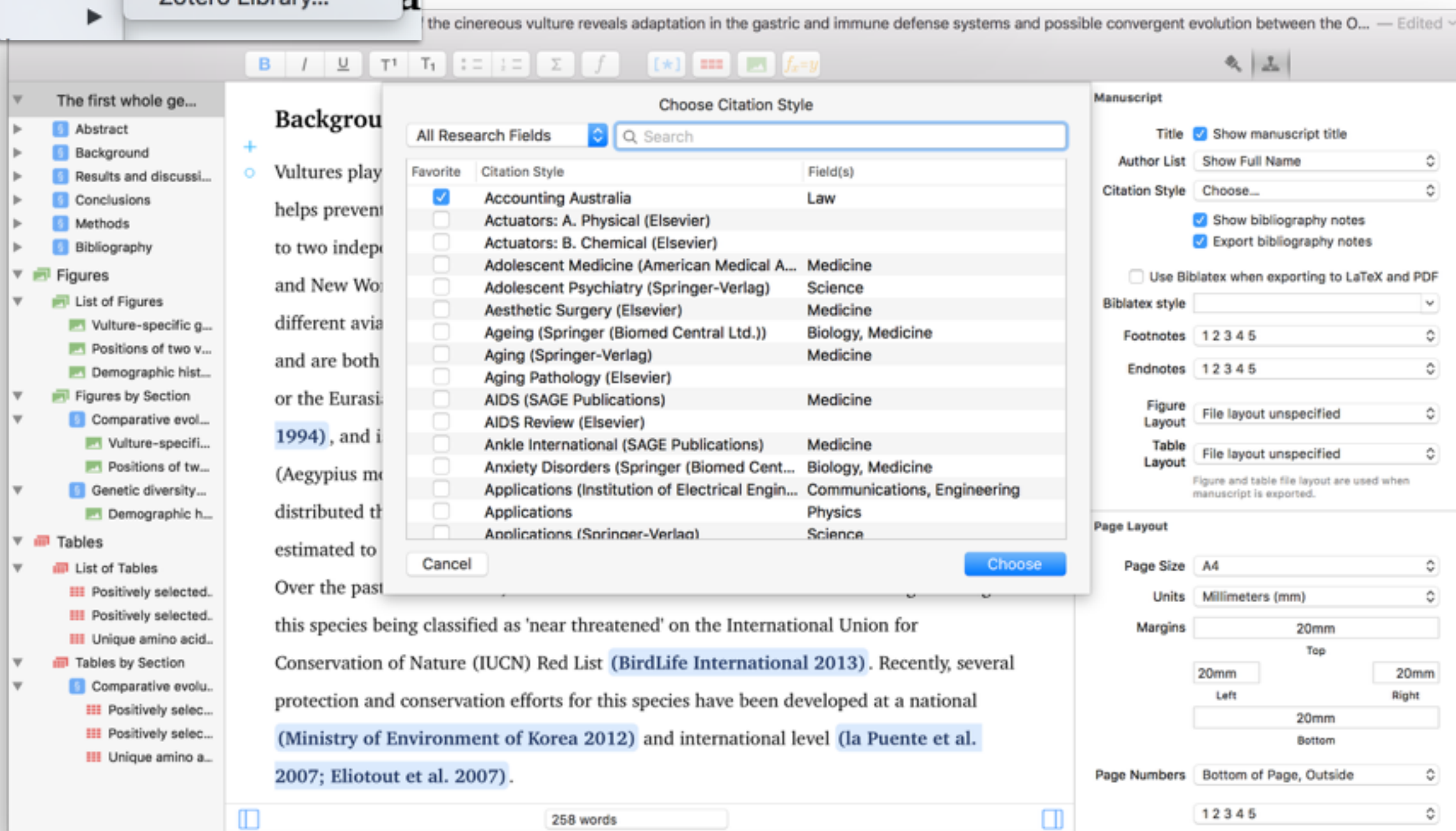
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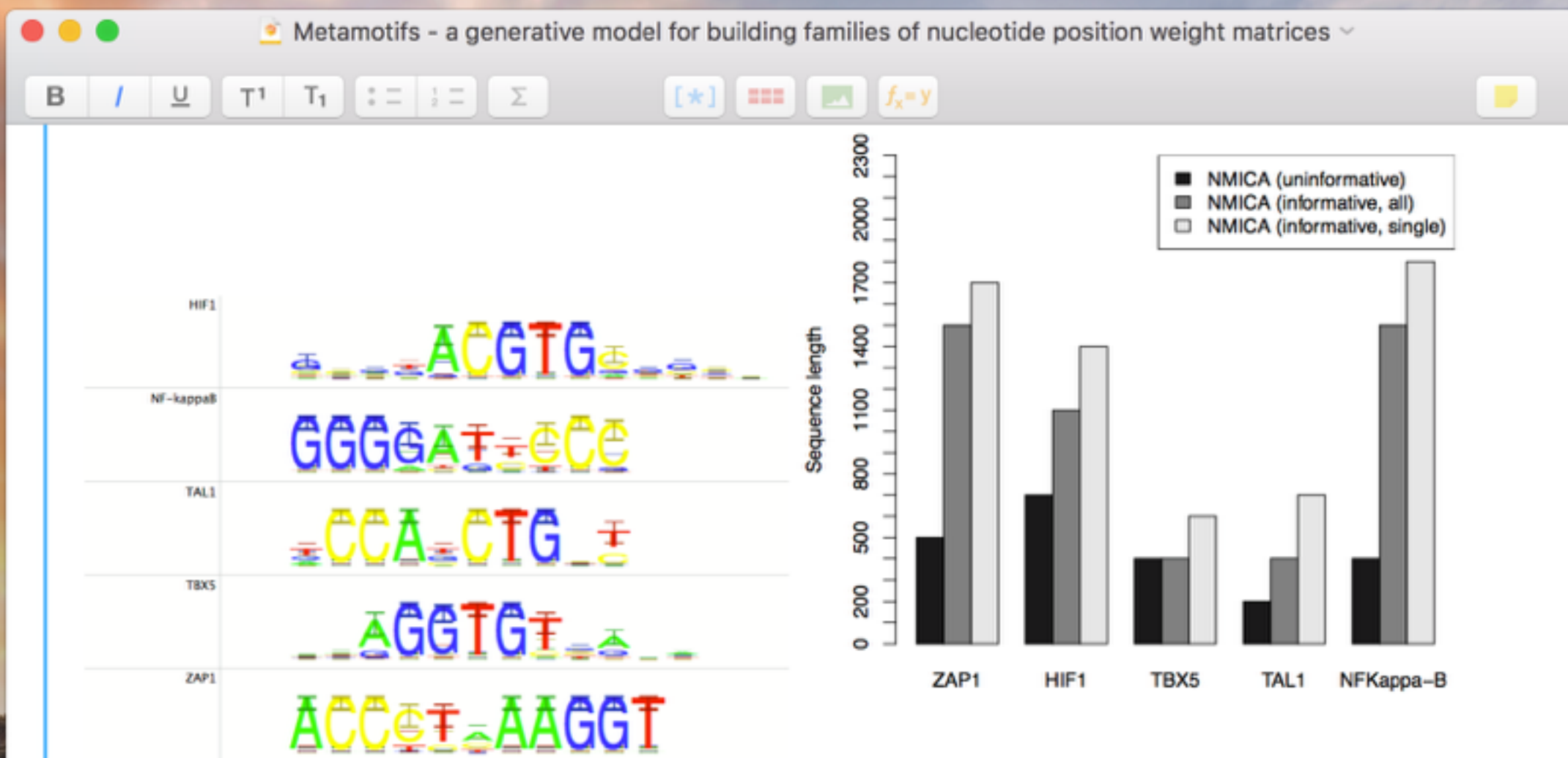
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1. Metamotifs used as the motif priors.

2. Weight matrix prior improves NMICA's sensitivity.

Figure 4: The effect of metamotif position weight matrix prior on motif discovery with NestedMICA.

+

- The informative motif prior function was shown to dramatically improve the capacity of the Nested-MICA algorithm to resolve weakly represented sequence motifs presented to it in longer nucleotide sequences, especially those with larger number of columns and higher information content (Figure 4). Both the baseline motif inference sensitivity and the effect of the informative weight matrix prior was seen to vary based on the length (likely due to the information content) of the motifs, ranging from as high as fourfold difference in the motif recovery length for TAL1 and NFKappa- β , to only a 1/3 improvement from 400 bp to

accuracy). Methods like metamattican however become increasingly relevant once more high-throughput TF DNA specificity data becomes available.

	Cys4	C2H2	bHLH	bZIP	Forkhead	Homeodomain	Class error
Cys4	39	0	0	0	0	1	0.025
C2H2	0	38	3	0	10	3	0.156
bHLH	0	2	22	5	0	0	0.24
bZIP	0	3	0	78	0	4	0.08
Forkhead	0	0	0	0	31	2	0.09
Homeodomain	2	1	1	3	0	37	0.16
Totals	41	43	26	86	32	47	

Table 2: Confusion matrix of the homeodomain motif specificity group classifier

Conclusions

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- We present a novel motif family model, the metamotif. We show its use as an informative prior in a motif discovery algorithm, and describe a motif classification method based on metamotif density features. We find that the method compares favourably to previously published related methods. Its performance with two novel experimental TFBS motif datasets is also found consistent with expected error estimates. The



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The metamotif

- A metamotif a is a matrix of L columns, each defining a Dirichlet distribution over \mathbb{R}^K where K is the alphabet size ([Equation 1](#)).

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$$\alpha = \begin{pmatrix} \alpha_{11} & \dots & \alpha_{1L} \\ \vdots & & \vdots \\ \alpha_{K1} & \dots & \alpha_{KL} \end{pmatrix}$$

Equation 1: A metamotif is a column Dirichlet distribution.

A motif $\mathbf{X} = (\mathbf{x}_1, \mathbf{x}_2, \dots, \mathbf{x}_n)$ is a set of column vectors over the same alphabet. The probability of observing the column \mathbf{x}_i from the metamotif a is given by the density of Dirichlet distribution with parameters a_i at weights \mathbf{x}_i ([Equation 2](#)). The normalising constant $B(a)$ is the multinomial beta function, expressed in [Equation 3](#) via the Gamma function.

$$\mathbb{P}(\mathbf{x}_i | \alpha_i) = \text{Dir}(\mathbf{x}_i; \alpha_i) = \frac{1}{B(\alpha)} \prod_{j=1}^K x_{ij}^{\alpha_{ij}-1}$$

Equation 2: A Dirichlet distribution with parameters alpha.

$$B(\alpha) = \frac{\prod_{j=1}^K \Gamma(\alpha_j)}{\Gamma(\sum_{j=1}^K \alpha_j)}$$

Equation 3: Beta distribution.

The log probability of observing a motif of length L is then given by Equation 4.



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246 # Highly expressed miRNAs are implicated in adipose and blood cell
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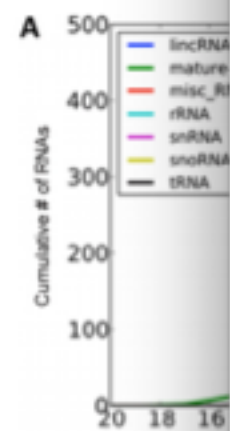
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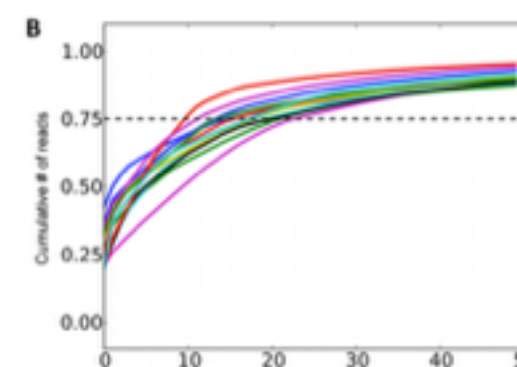
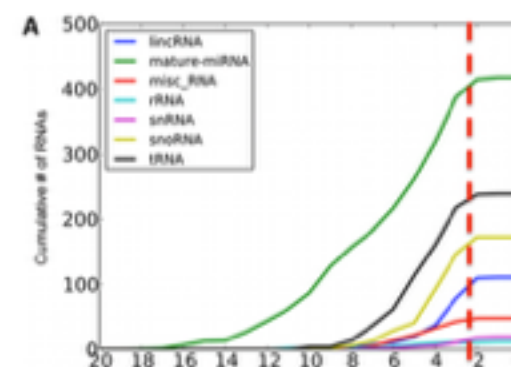
gene candidates (Dataset S1), and all samples (2 % DNase hypersensitive regions (Methods), which are enriched for transcripts (Kim et al., 2007) ($p < 10^{-10}$) and in the 5' sequence.



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Extent, Causes, and Consequences of Small RNA Variation in Human Adipos

30 base pair fragments, which excludes other functional RNA species except for degradation products. In addition, we found reads mapped to loci previously unannotated for noncoding RNA transcription. We identified 12 novel miRNA gene candidates using MapMi, which often harbour enhancer elements that are known to give rise to short transcripts. The rest overlapped exons (149/701, one-tailed binomial $p < 10^{-10}$) and introns (190/701, not significant), with 233 regions arising from intergenic sequence.



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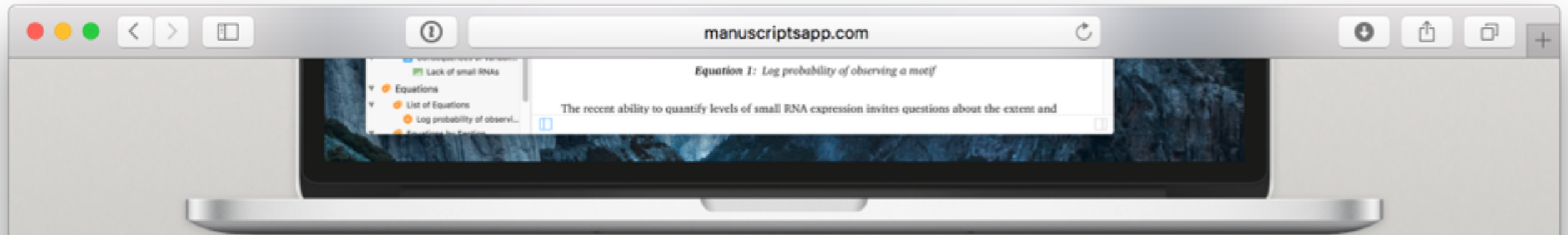


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