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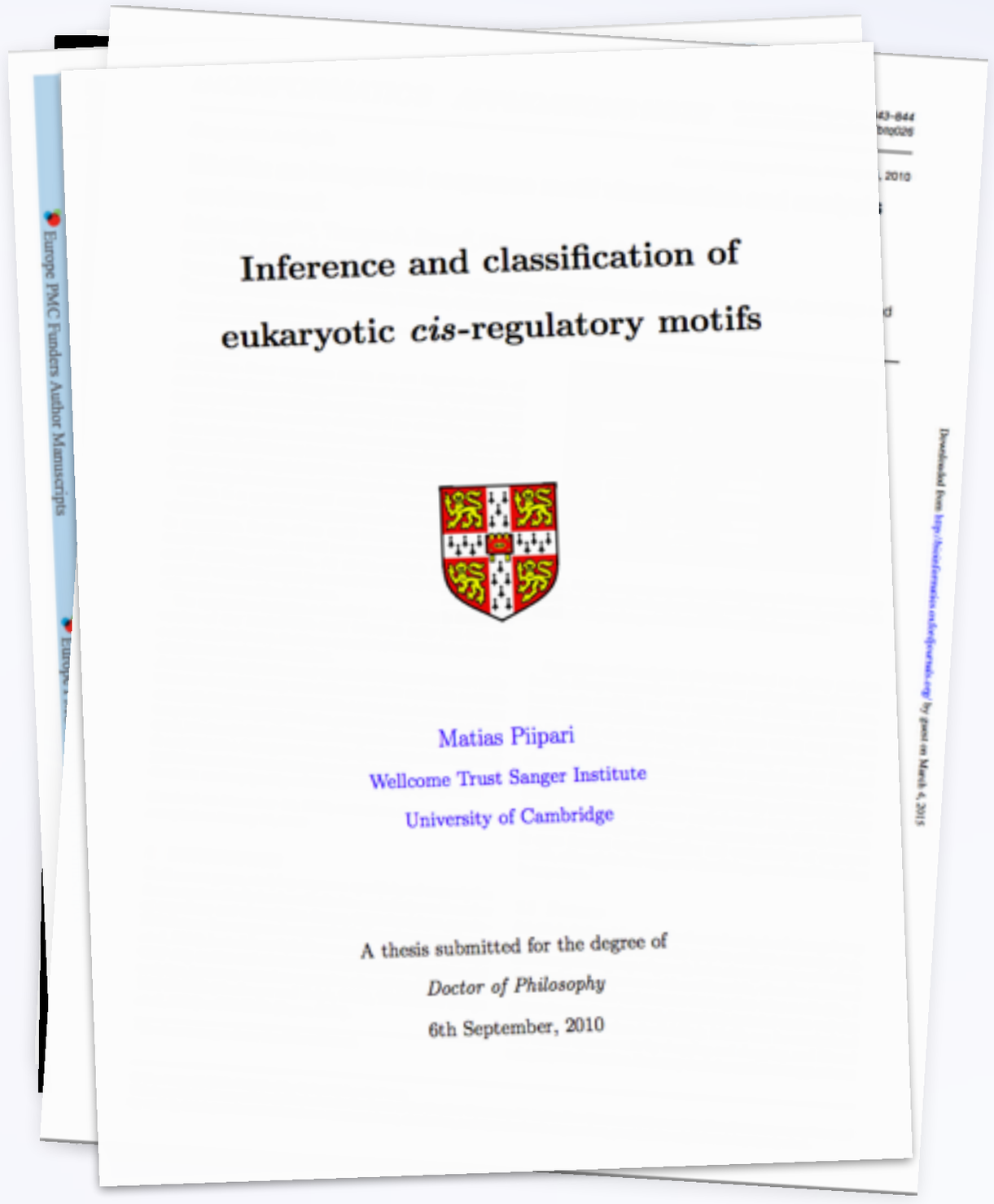

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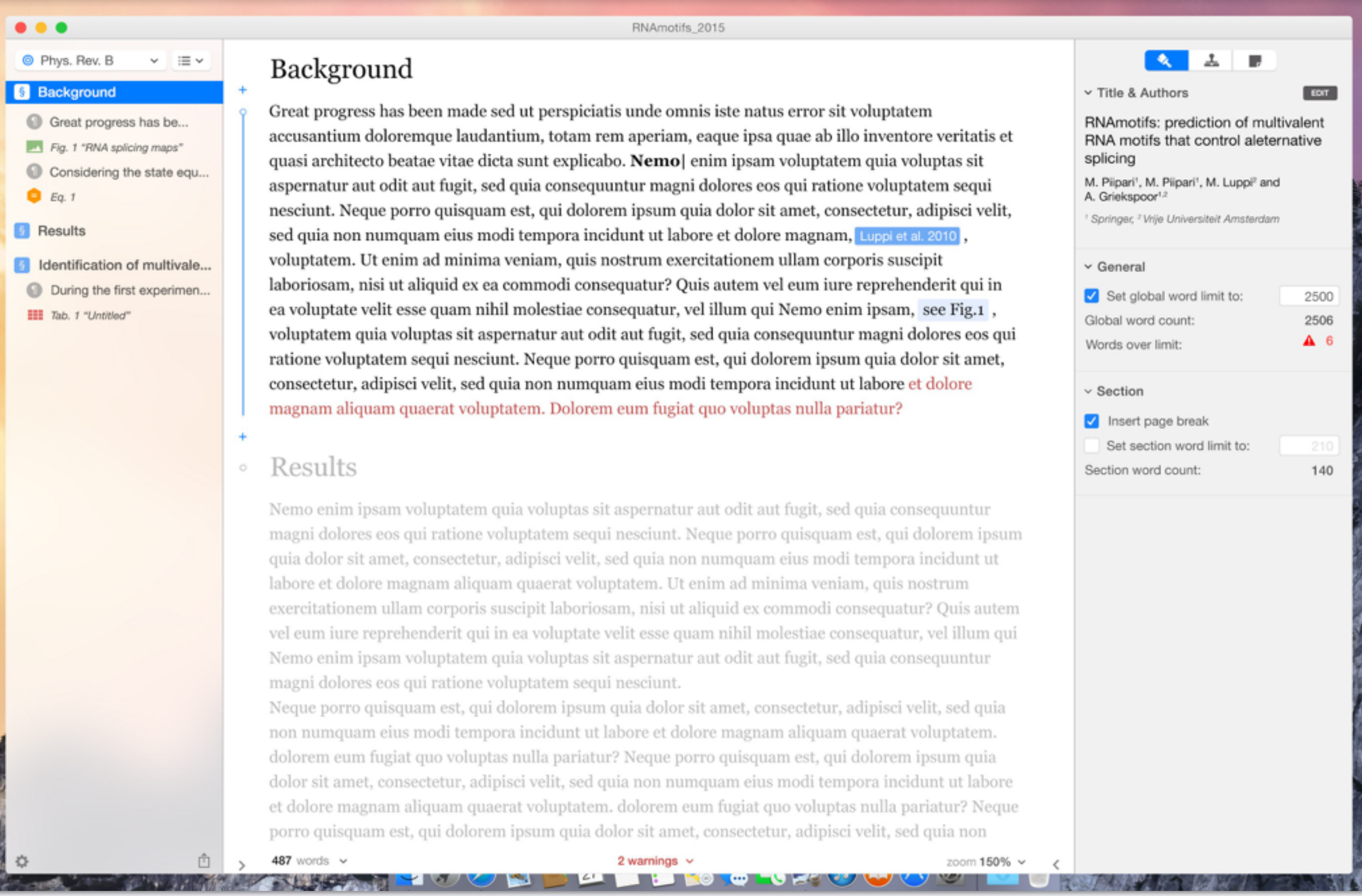

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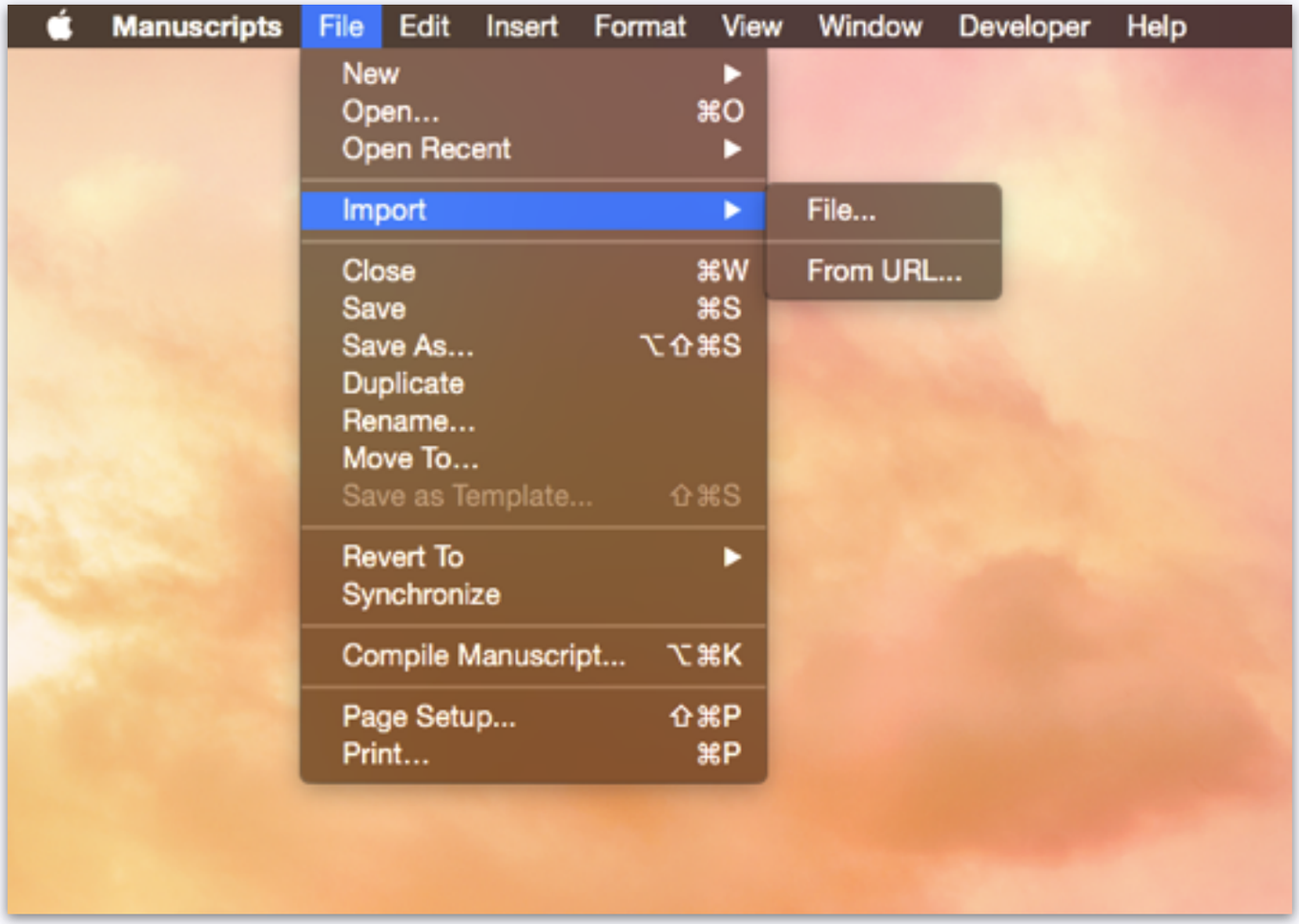

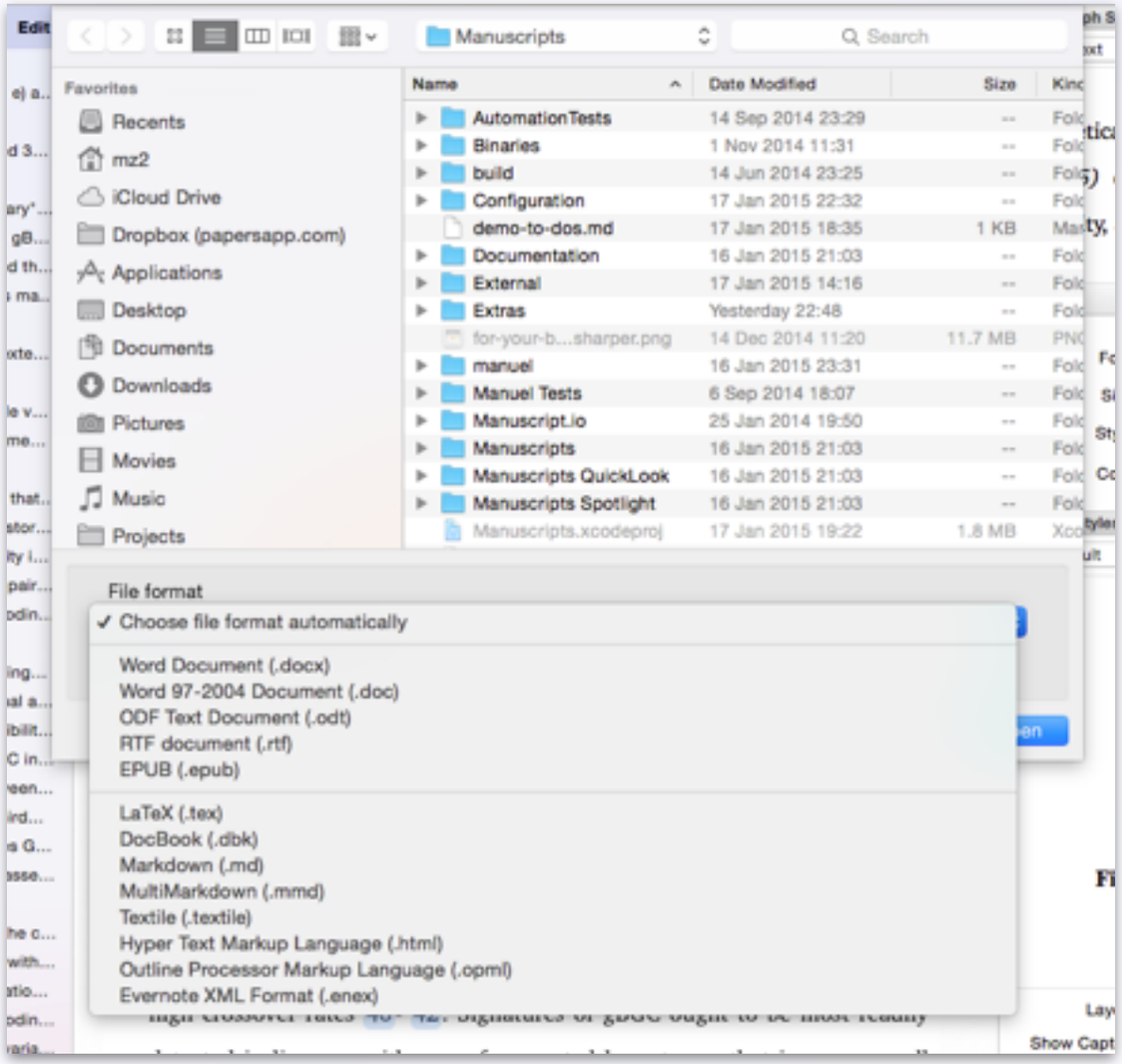

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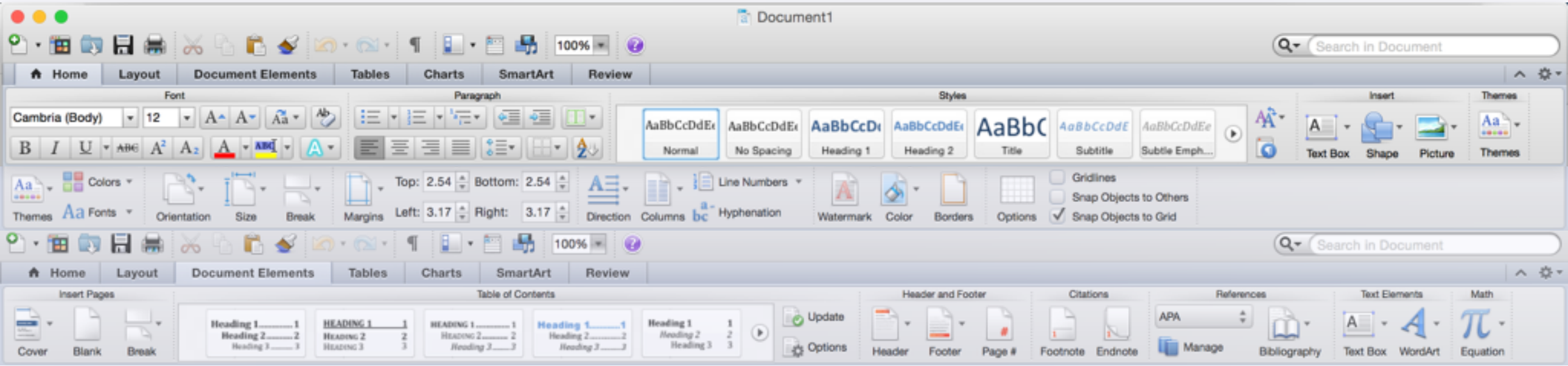

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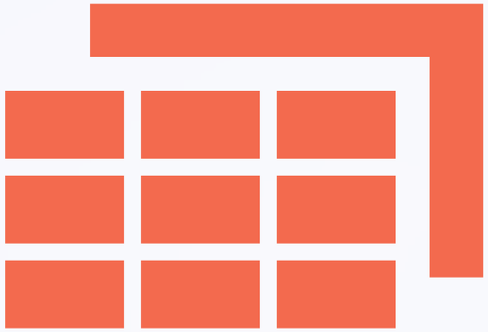

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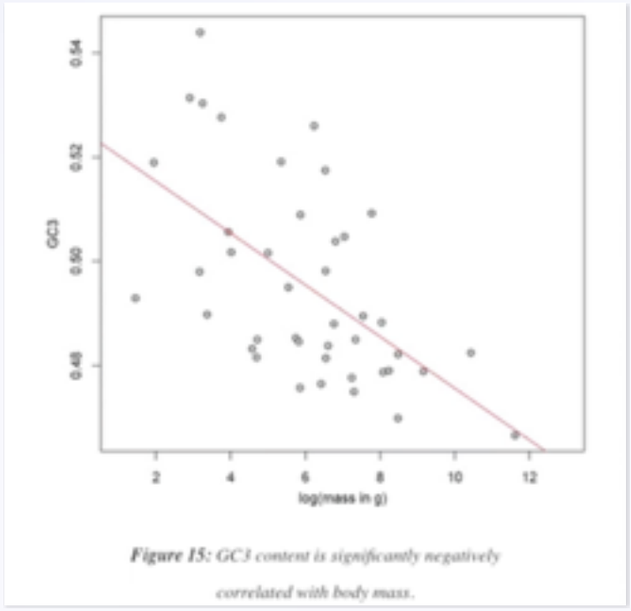

Figure 15: *GC3 content is significantly negatively correlated with body mass.*

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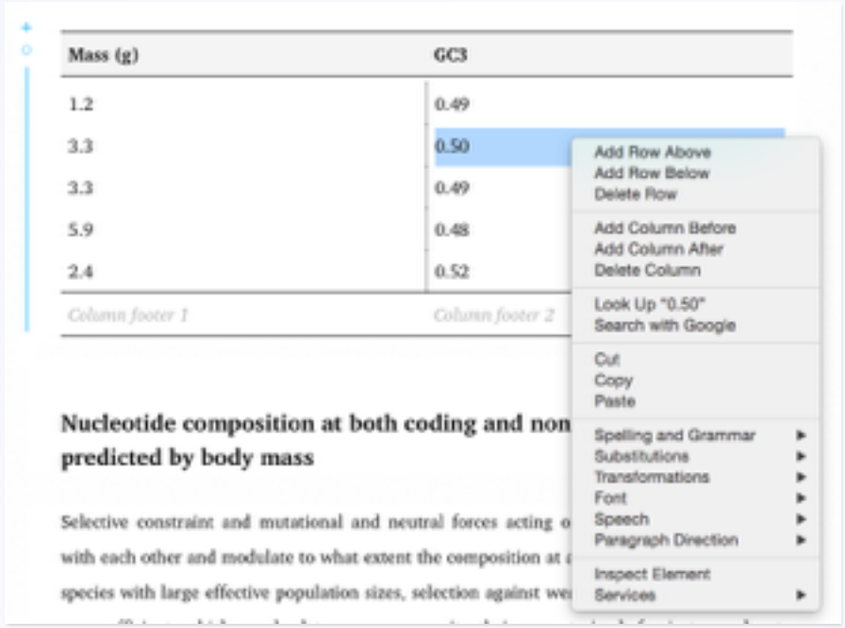

Mass (g)	GC3
1.2	0.49
3.3	0.50
3.3	0.49
5.9	0.48
2.4	0.52
Column footer 1	*Column footer 2*

Nucleotide composition at both coding and non
predicted by body mass

Selective constraint and mutational and neutral forces acting o
with each other and modulate to what extent the composition at
species with large effective population sizes, selection against we

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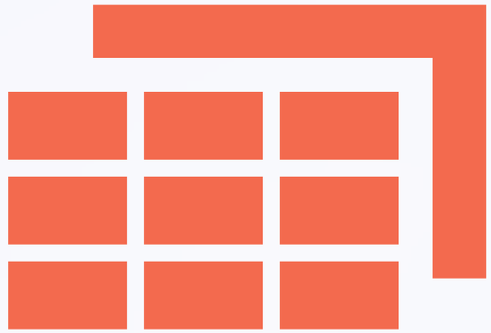

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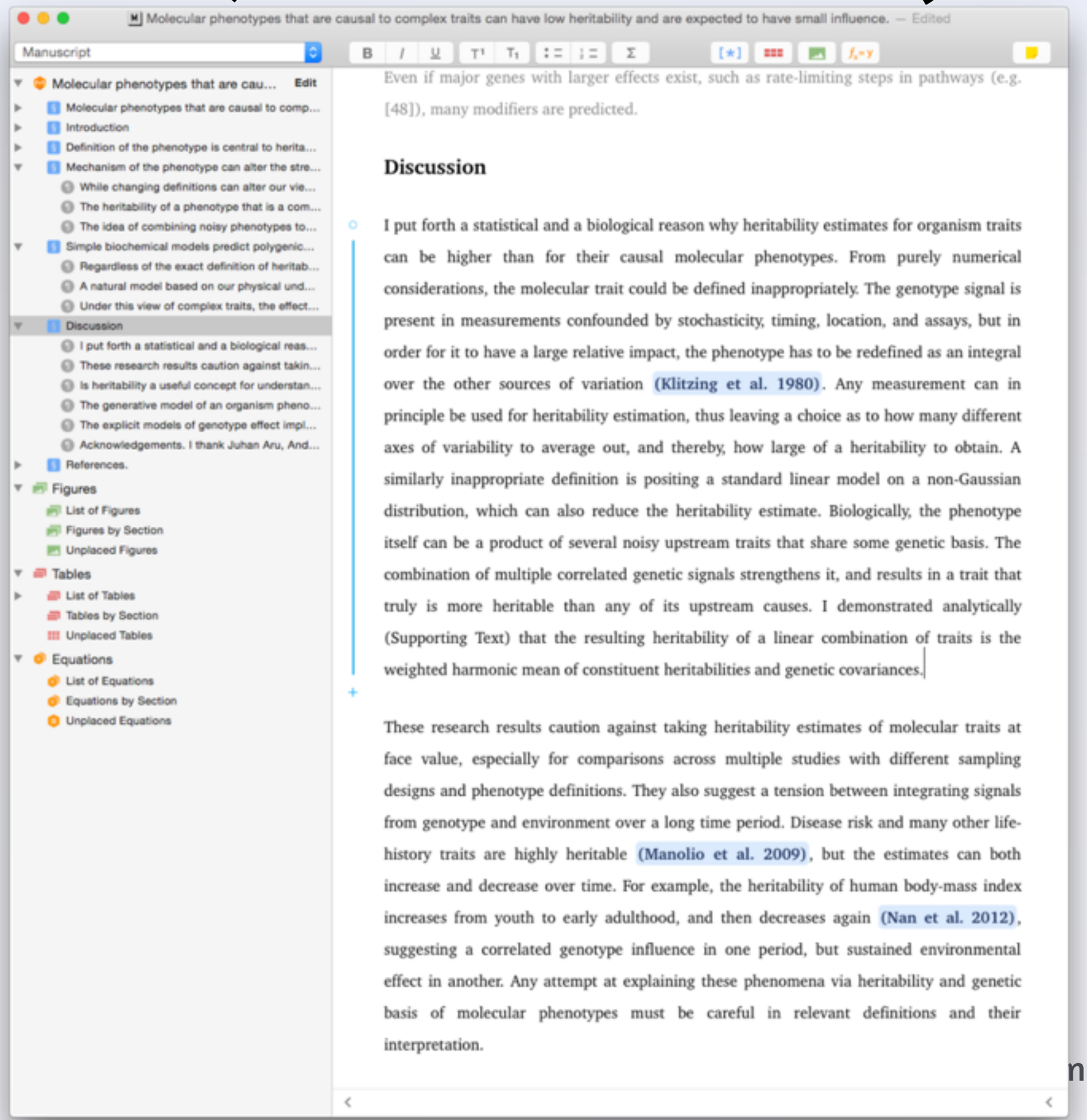

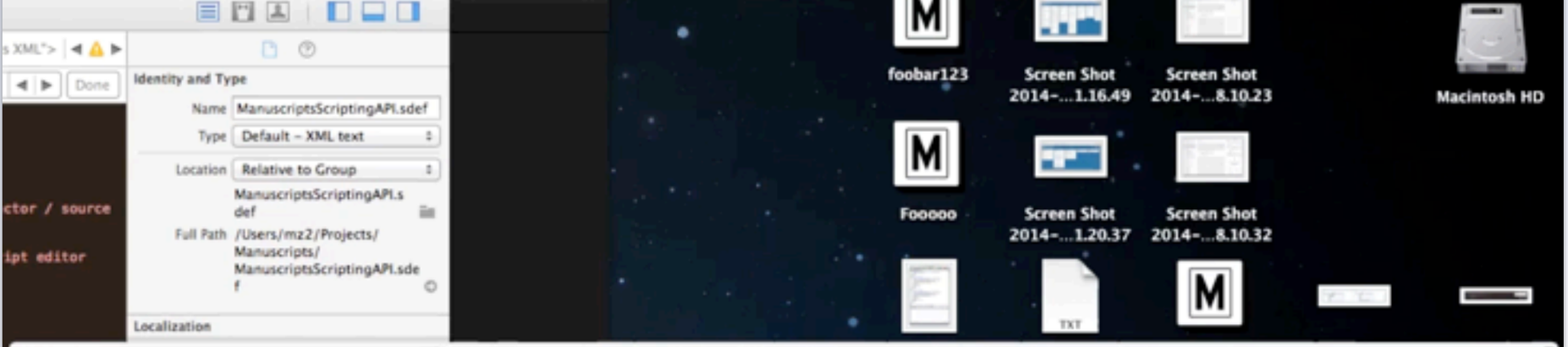

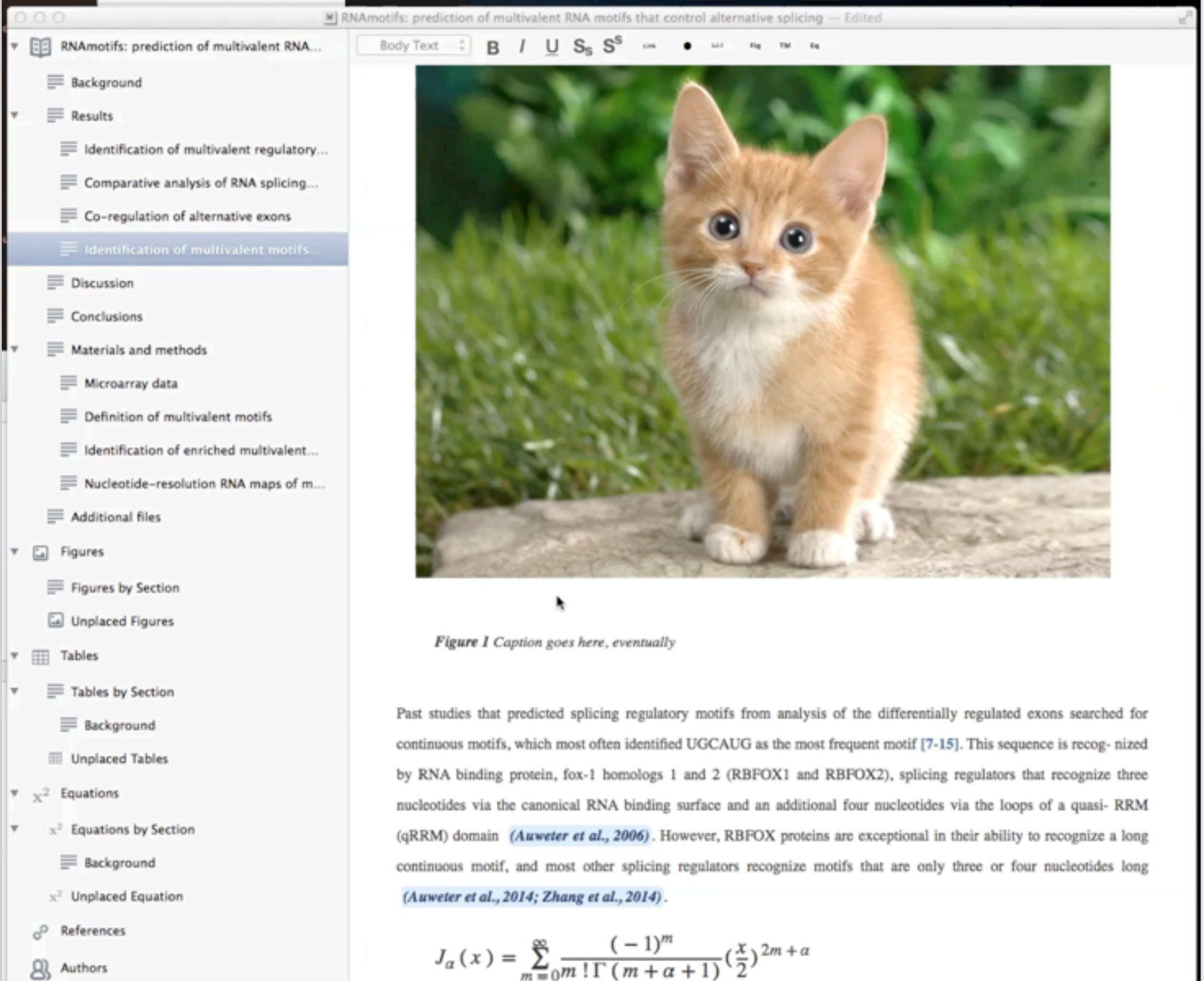

Figure 1 *Caption goes here, eventually*

Past studies that predicted splicing regulatory motifs from analysis of the differentially regulated exons searched for continuous motifs, which most often identified UGCAUG as the most frequent motif [7-15]. This sequence is recog- nized by RNA binding protein, fox-1 homologs 1 and 2 (RBFOX1 and RBFOX2), splicing regulators that recognize three nucleotides via the canonical RNA binding surface and an additional four nucleotides via the loops of a quasi- RRM (qRRM) domain ***(Auweter et al., 2006)***. However, RBFOX proteins are exceptional in their ability to recognize a long continuous motif, and most other splicing regulators recognize motifs that are only three or four nucleotides long ***(Auweter et al., 2014; Zhang et al., 2014)***.

$$J_\alpha(x) = \sum_{m=0}^{\infty} \frac{(-1)^m}{m!\,\Gamma(m+\alpha+1)} \left(\frac{x}{2}\right)^{2m+\alpha}$$

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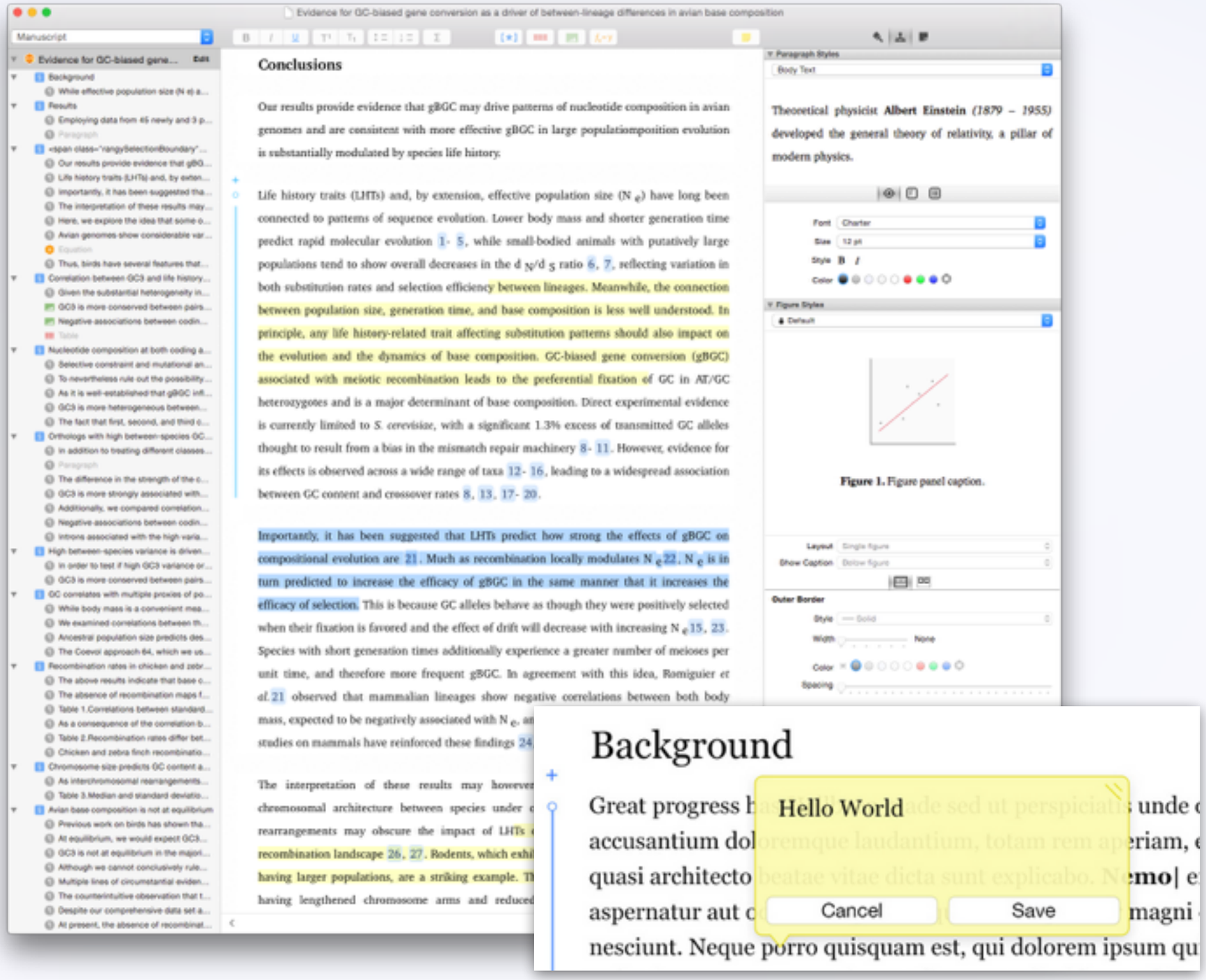

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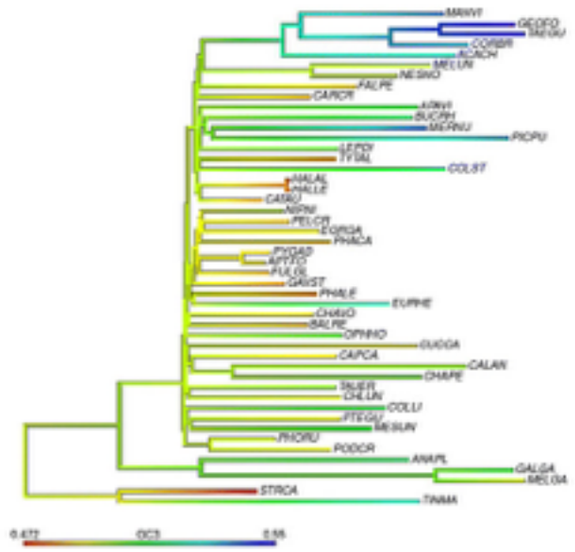
consider the degree to which different classes of sites are affected, how it corresponds to recombination rate estimates, and whether the impact of gBGC on the base composition of avian genomes is ongoing.

Correlation between GC3 and life history traits is consistent with stronger gBGC in large populations with short generation times

Given the substantial heterogeneity in GC3 content (the proportion of GC at third codon positions) between avian species 33, 47 (Figure 1), we asked whether there is evidence that third codon sites, which should be the least constrained coding positions, might be subject to the influence of recombination-associated gBGC. Species with smaller body mass are expected to have both shorter generation times and larger effective population sizes, increasing both the number of meioses per unit time and the efficacy of gBGC 21, 23. If gBGC is a factor in determining GC, small-bodied species ought then to have elevated GC. This is indeed what we observed, with species with greater body mass exhibiting lower GC3 than species with smaller body mass (Spearman's rho = -0.5866, P = 6.2e-05, n = 42; see Figure 2). Despite the limited number of species for which data are available, maximum longevity (rho = -0.3645, P = 0.0616, n = 27) and age of first female sexual maturity (rho = -0.5957, P = 0.0071, n = 19) showed similar trends, consistent with the possibility that short generation times lead to an increase in GC3 assuming equilibrium has not yet been reached. In the following we only examine body mass, as this maximizes the number of species we can consider.



1. GC3 content varies substantially between different avian lineages.

Figure 13: GC3 content varies substantially between different avian lineages.

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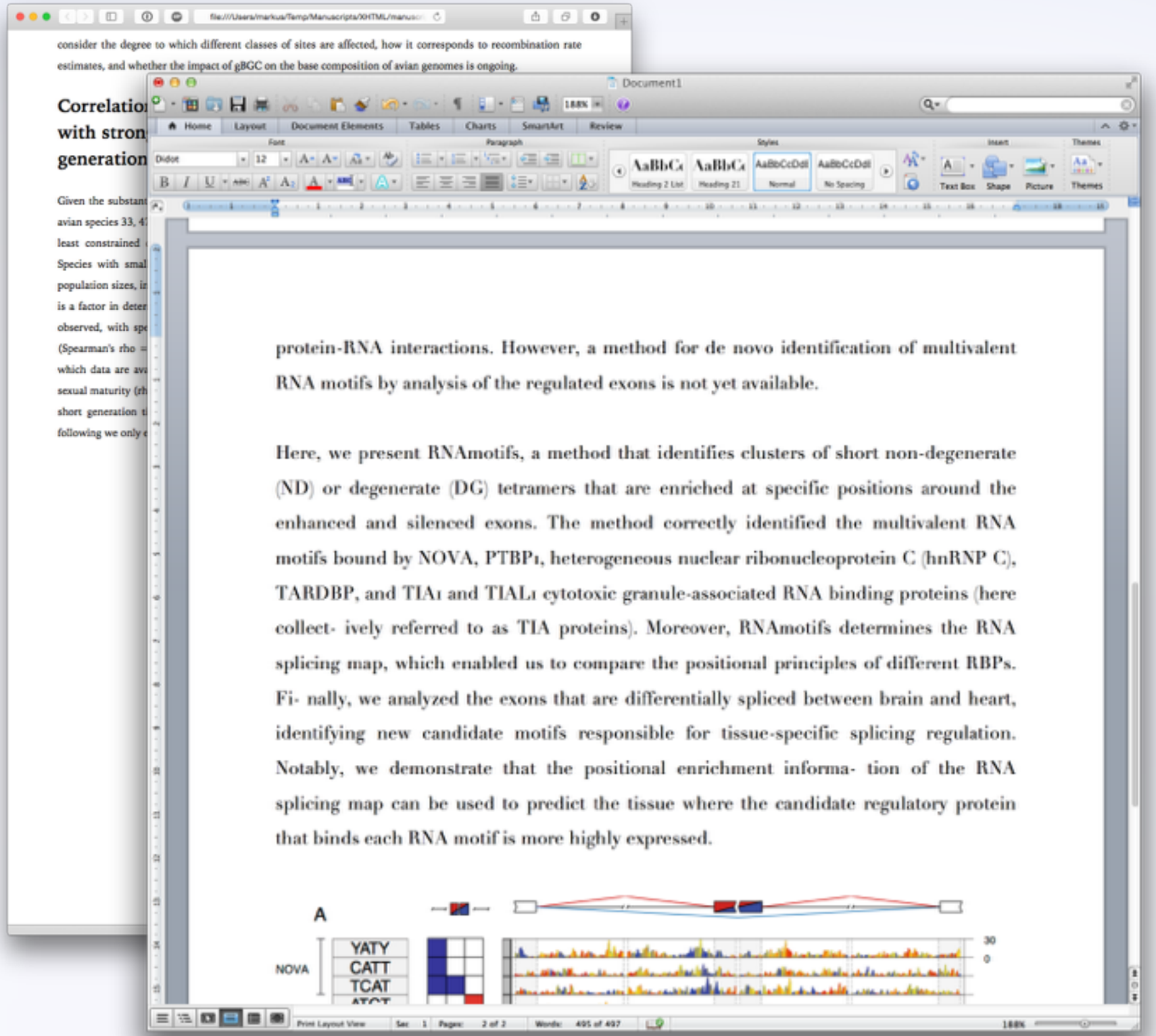

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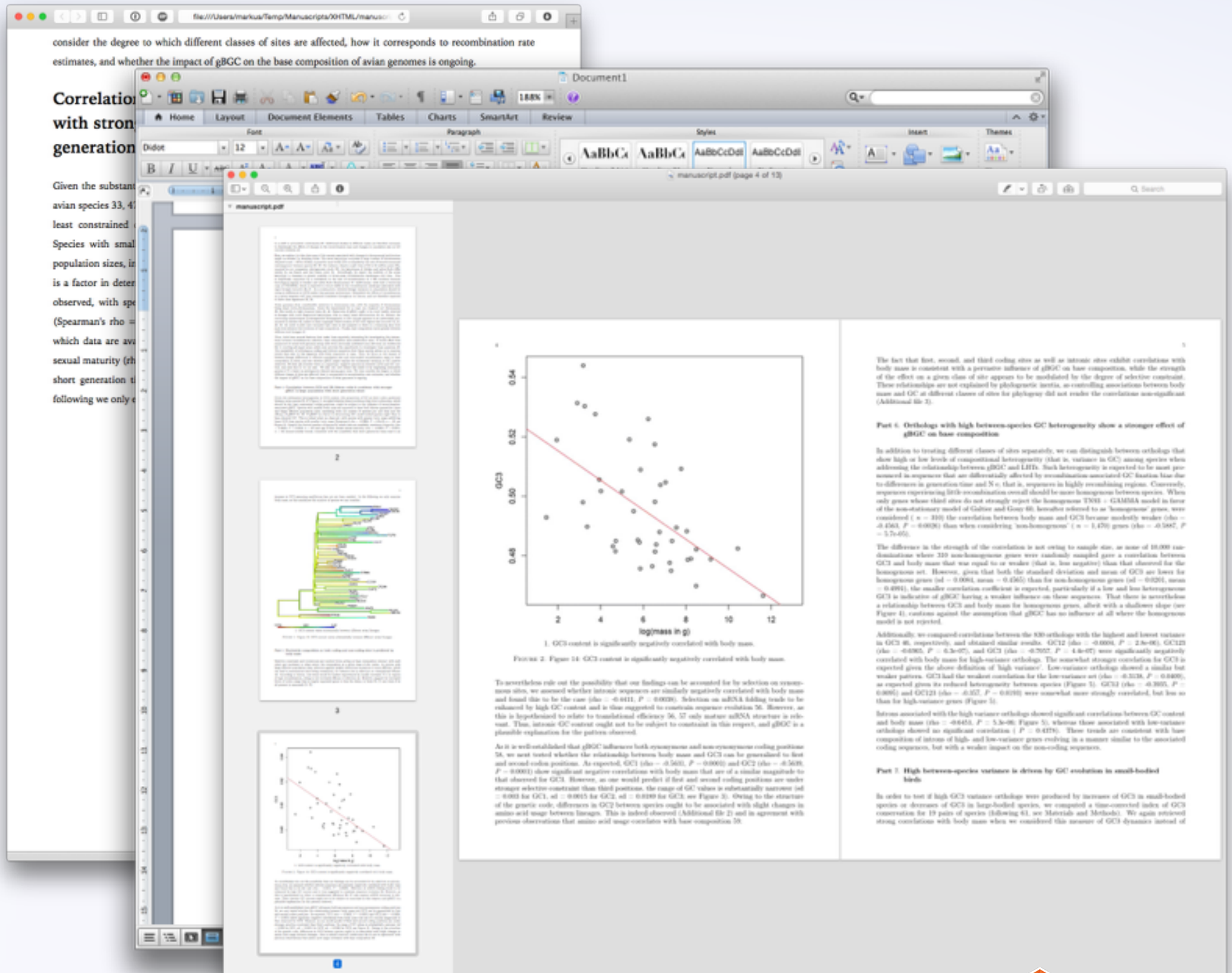

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iMotifs: an integrated sequence motif visualization and analysis environment.

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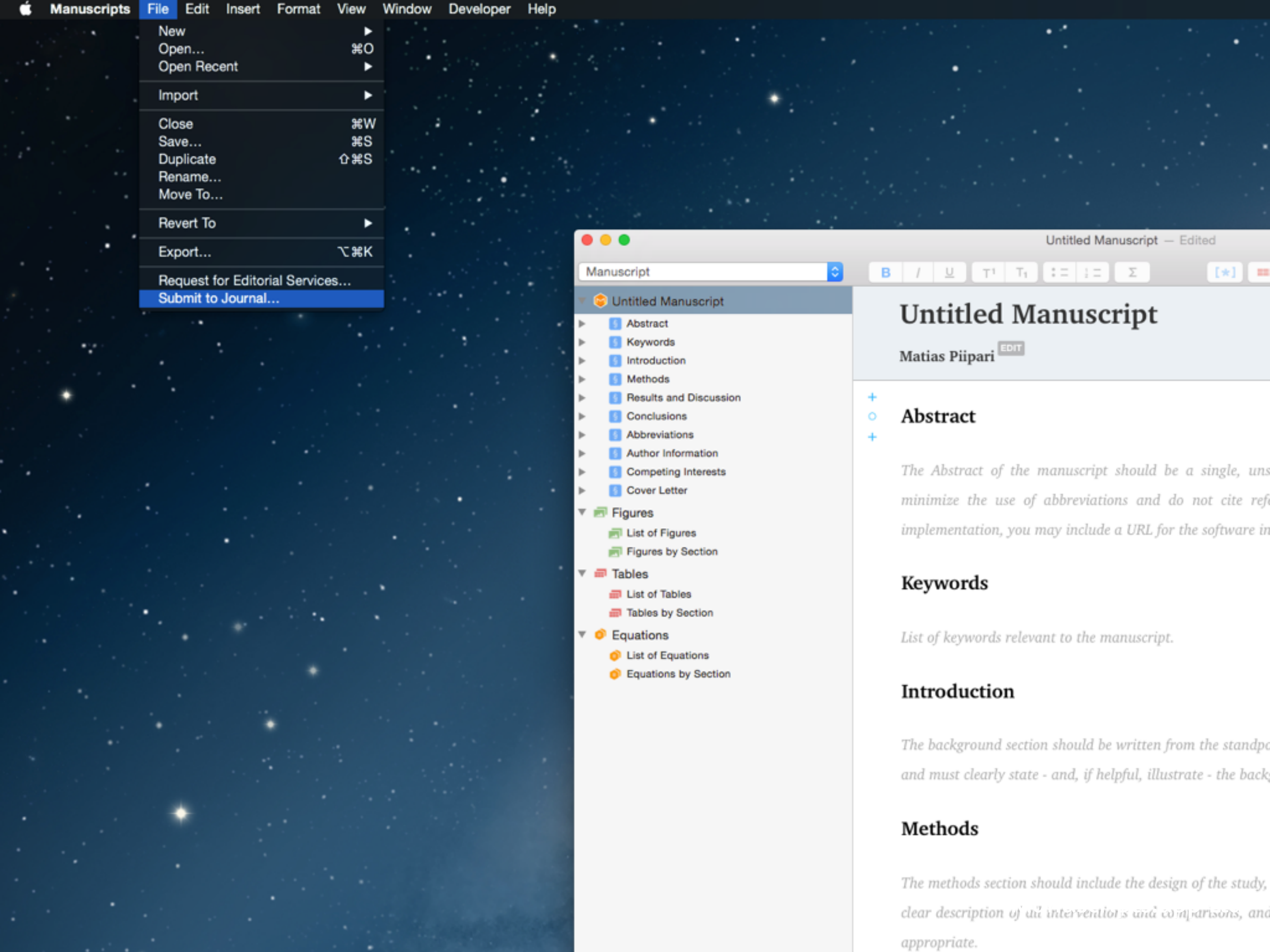
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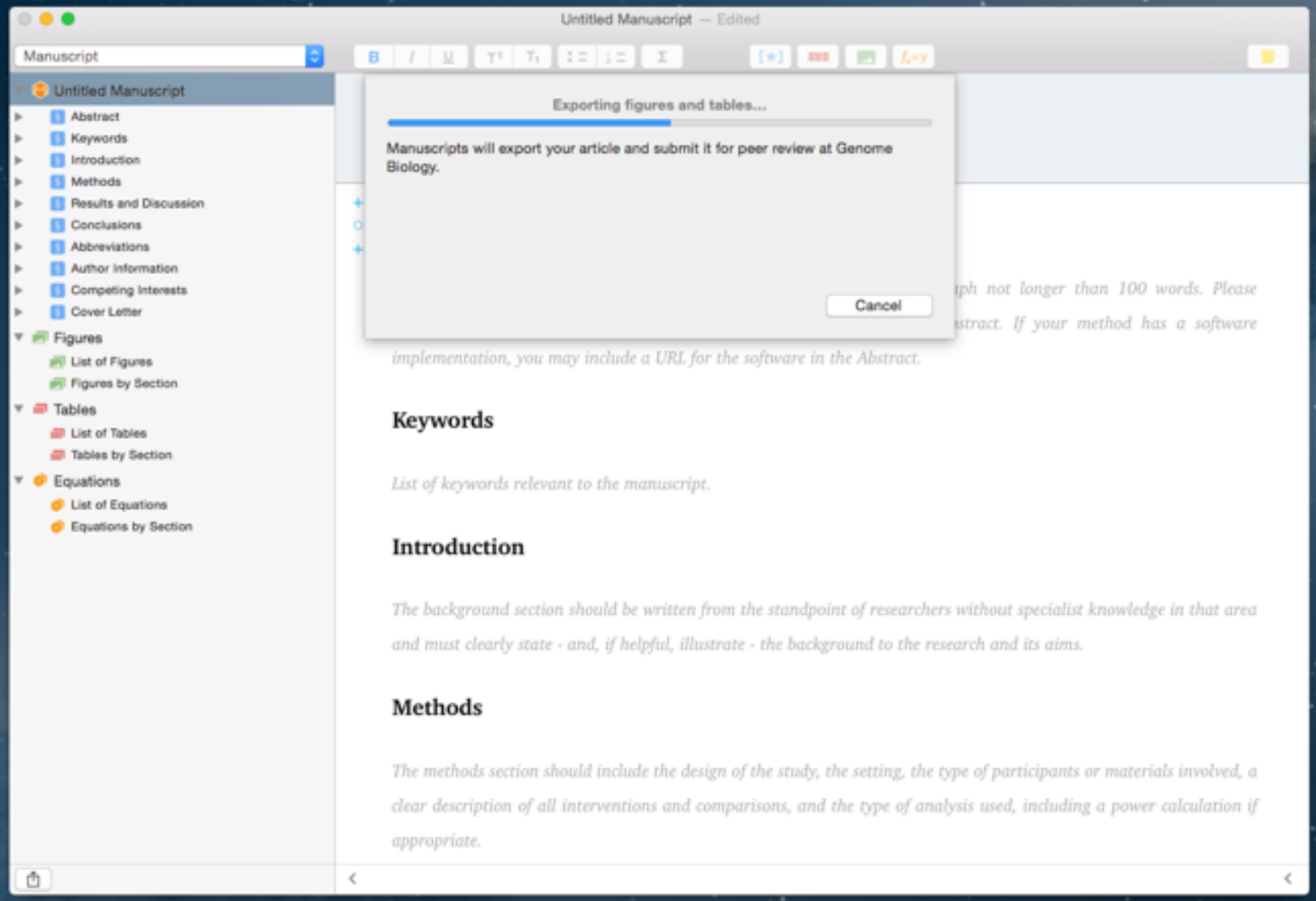

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