The hope and the despair of science and TDM

@chartgerink
(twitter and github)

The hope

Decreased mortality of the patients significantly, F(1, 39) = 2.43, p < .05.



Decreased mortality of the nations significantly

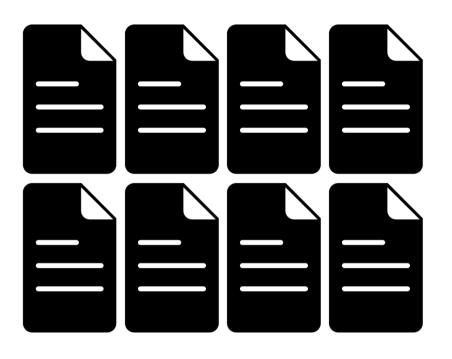
patients significantly, F(1, 39) = 2.43, p < .05.



Decreased mortality of the nations significantly

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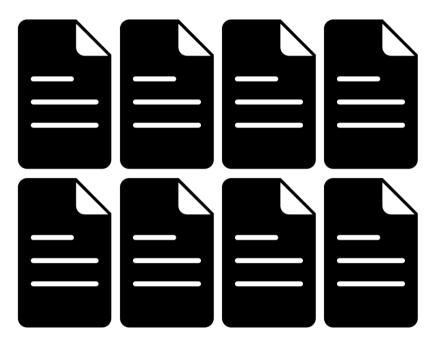








~2010

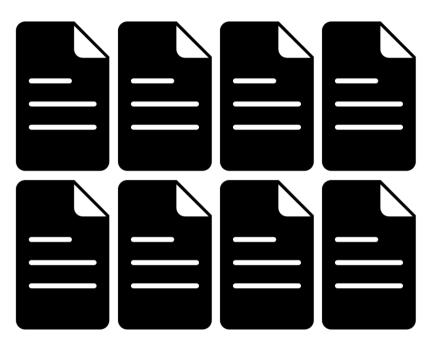










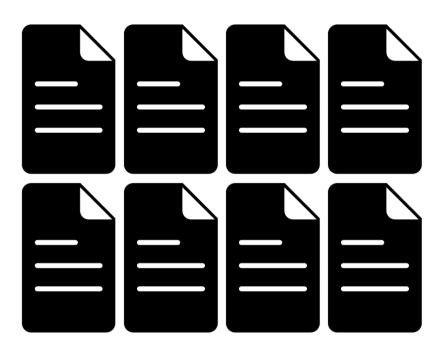












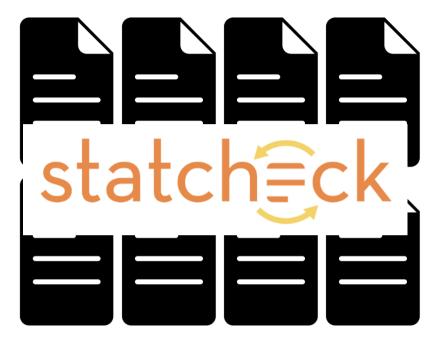
Not to worry! Computers can do it!





















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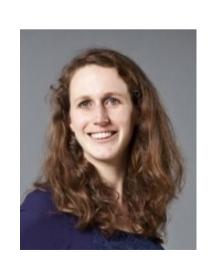






Now we just need more papers!

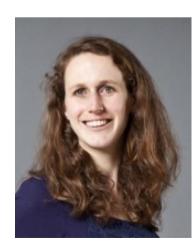
















Chris, download tens of thousand papers, manually









Chris, download tens of thousand papers, manually





The despair

UK has an exception since 2014

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Problem solved for researchers?

Return of the hope

(the conditional) Return of the hope

TDM not only has research potential

TDM can open up the market for information consumption

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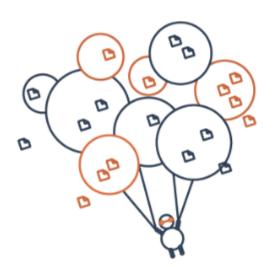
building on freely available data massive market value

Wide exception for TDM allows EU to become hub of innovation and economic growth

Businesses could break down publishing market by giving publishers the revenue they know is going away due to Open access

TDM no problem in Open Access

Gives us a glimpse into the future



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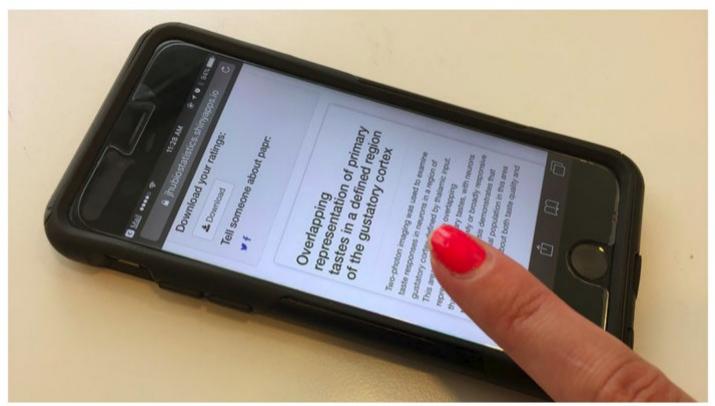
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Science/AAAS

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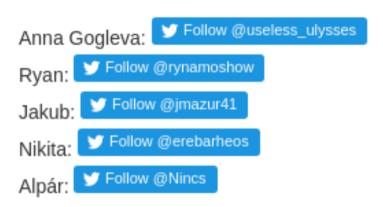
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Inference of cell-cell interactions from population density characteristics and cell trajectories on static and growing domains

A key feature of cell migration is how cell movement is affected by cell-cell interactions. Furthermore, many cell migratory processes such as neural crest stem cell migration [1, 2] occur on growing domains or in the presence of a chemoattractant. Therefore, it is important to study interactions between migrating cells in the context of domain growth and directed motility. Here we compare discrete and continuum models describing the spatial and temporal evolution of a cell population for different types of cell-cell interactions on static and growing domains. We suggest that cell-cell interactions can be inferred from population density characteristics in the presence of motility bias, and these population density characteristics for different cell-cell interactions are conserved on both static and growing domains. We also study the expected displacement of a tagged cell, and show that different types of cell-cell interactions can give rise to cell trajectories with different characteristics. These characteristics are conserved in the presence of domain growth, however, they are diminished in the presence of motility bias. Our results are relevant for researchers who study the existence and role of cell-cell interactions in biological systems, so far as we suggest that different types of cell-cell interactions could be identified from cell density and trajectory data.

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