

# Next generation text-mining applied to toxicogenomics data analysis = Next-generation text-mining toegepast op toxicogenomics data analyse

Citation for published version (APA):

Hettne, K. M. (2012). *Next generation text-mining applied to toxicogenomics data analysis = Next-generation text-mining toegepast op toxicogenomics data analyse*. [Doctoral Thesis, Maastricht University]. Universiteit Maastricht. <https://doi.org/10.26481/dis.20121220kh>

## Document status and date:

Published: 01/01/2012

## DOI:

[10.26481/dis.20121220kh](https://doi.org/10.26481/dis.20121220kh)

## Document Version:

Publisher's PDF, also known as Version of record

## Please check the document version of this publication:

- A submitted manuscript is the version of the article upon submission and before peer-review. There can be important differences between the submitted version and the official published version of record. People interested in the research are advised to contact the author for the final version of the publication, or visit the DOI to the publisher's website.
- The final author version and the galley proof are versions of the publication after peer review.
- The final published version features the final layout of the paper including the volume, issue and page numbers.

[Link to publication](#)

## General rights

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal.

If the publication is distributed under the terms of Article 25fa of the Dutch Copyright Act, indicated by the "Taverne" license above, please follow below link for the End User Agreement:

[www.umlib.nl/taverne-license](http://www.umlib.nl/taverne-license)

## Take down policy

If you believe that this document breaches copyright please contact us at:

[repository@maastrichtuniversity.nl](mailto:repository@maastrichtuniversity.nl)

providing details and we will investigate your claim.

Download date: 23 Apr. 2024

## Stellingen

Behorende bij het proefschrift

### **Next-generation text mining applied to toxicogenomics data analysis**

1. Knowledge-based filtering and disambiguation rules have a dramatic positive effect on the precision of dictionary-based biomedical and chemical term identification in scientific literature.
2. A dictionary of chemical terms is not enough to identify all chemical terms in scientific literature.
3. Gene sets based on concept profile matching provide a broader scope than gene sets based on manually curated databases.
4. There is not one perfect gene set analysis tool that fits every data set.
5. Until bioinformaticians are forced to accompany their journal publications with a preserved and executable implementation of their experiment, the discipline will continue to produce methods that almost no biologist will use.
6. A bioinformatics toolbox that does not include text mining is incomplete.
7. Publishing a bioinformatics method in a high impact journal without an accompanied new, exciting, and experimentally confirmed biological finding is practically impossible, and something that is holding back scientific progress in the field.
8. Data mining can be defined according to the principle of "my data is mine, and your data is mine". *With reference to C. Goble, The Seven Deadly Sins of Bioinformatics, 2007.*
9. Continuous application of pressure on the gas pedal will inevitably cause a crash.