



# Corrigendum: IDLDA: An Improved Diffusion Model for Predicting LncRNA–Disease Associations

Qi Wang<sup>1,2</sup> and Guiying Yan<sup>1,2\*</sup>

## OPEN ACCESS

**Edited and reviewed by:**  
Alfredo Pulvirenti,  
University of Catania, Italy

**\*Correspondence:**  
Guiying Yan  
yangy@amss.ac.cn

**Specialty section:**  
This article was submitted to  
Bioinformatics and  
Computational Biology,  
a section of the journal  
Frontiers in Genetics

**Received:** 18 December 2019  
**Accepted:** 04 February 2020  
**Published:** 26 February 2020

**Citation:**  
Wang Q and Yan G (2020)  
Corrigendum: IDLDA: An Improved  
Diffusion Model for Predicting  
LncRNA–Disease Associations.  
*Front. Genet.* 11:137.  
doi: 10.3389/fgene.2020.00137

<sup>1</sup> Academy of Mathematics and Systems Science, Chinese Academy of Sciences, Beijing, China, <sup>2</sup> School of Mathematical Sciences, University of Chinese Academy of Sciences, Beijing, China

**Keywords:** long non-coding RNA, disease, association prediction, computational prediction model, diffusion model

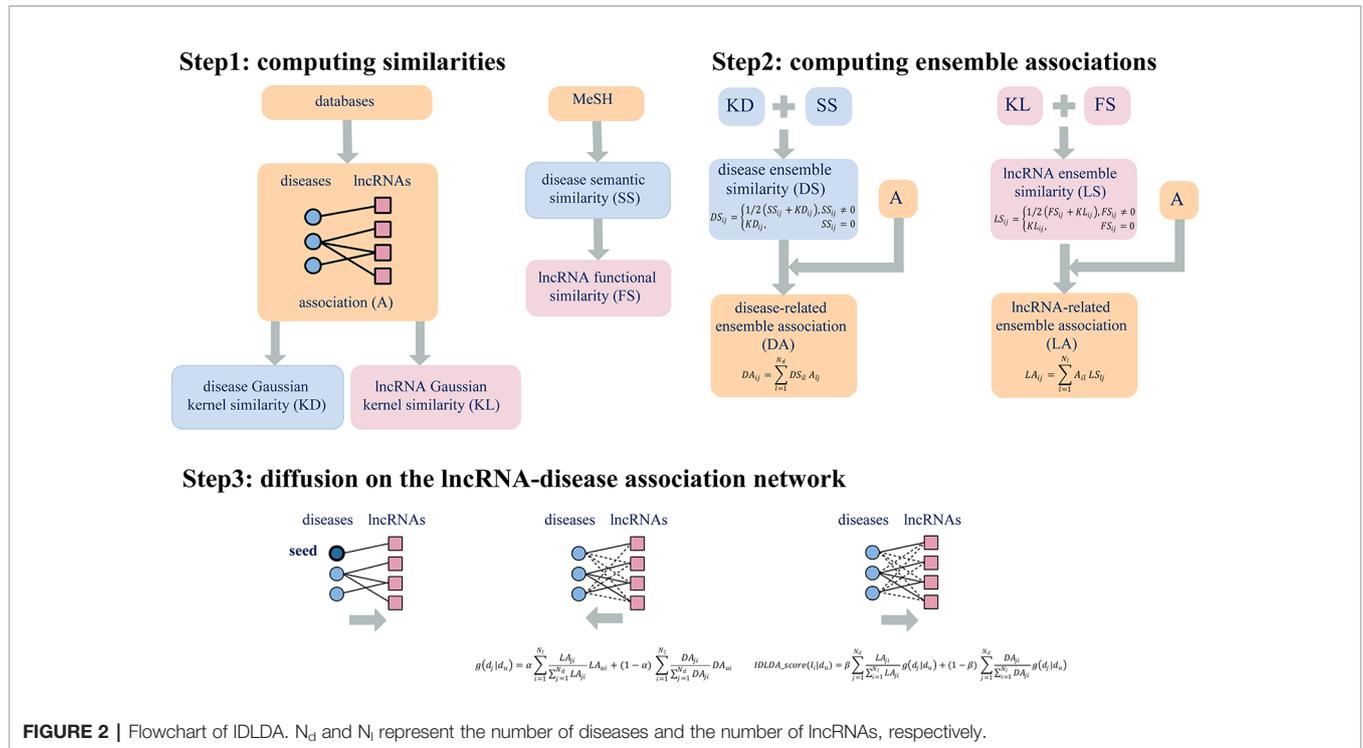
## A Corrigendum On

**IDLDA: An Improved Diffusion Model for Predicting LncRNA–Disease Associations**  
by Wang Q and Yan G (2019). *Front. Genet.* 10:1259. doi: 10.3389/fgene.2019.01259

In the original article, there was a mistake in the legend for **Figure 2** published as an explanation of what  $N_d$  and  $N_l$  represent was missing. The correct legend appears below.

Also in **Figure 2** the diagrams shown in Step 2 are incorrect as the formulas were omitted. The corrected **Figure 2** and its legend appear below. The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

Copyright © 2020 Wang and Yan. This is an open-access article distributed under the terms of the Creative Commons Attribution License (CC BY). The use, distribution or reproduction in other forums is permitted, provided the original author(s) and the copyright owner(s) are credited and that the original publication in this journal is cited, in accordance with accepted academic practice. No use, distribution or reproduction is permitted which does not comply with these terms.



**FIGURE 2 |** Flowchart of IDLDA.  $N_d$  and  $N_l$  represent the number of diseases and the number of lncRNAs, respectively.