




# 1 AlgarMIC: a Python package for automated 2 interpretation of agar dilution minimum inhibitory 3 concentration testing

4 **Alessandro Gerada** <sup>1,2</sup>, **Nicholas Harper** <sup>1</sup>, **Alex Howard** <sup>1,2</sup>, and **William  
5 Hope** <sup>1,2</sup>

6 **1** Antimicrobial Pharmacodynamics and Therapeutics Group, Department of Pharmacology and  
7 Therapeutics, Institute of Systems, Molecular & Integrative Biology, University of Liverpool, United  
8 Kingdom **2** Department of Infection and Immunity, Liverpool Clinical Laboratories, Liverpool University  
9 Hospitals NHS Foundation Trust, Liverpool, United Kingdom

DOI: [10.xxxxxx/draft](https://doi.org/10.xxxxxx/draft)

## Software

- [Review](#) 
- [Repository](#) 
- [Archive](#) 

Editor: 

Submitted: 12 April 2024

Published: unpublished

## License

Authors of papers retain copyright  
and release the work under a  
Creative Commons Attribution 4.0  
International License ([CC BY 4.0](https://creativecommons.org/licenses/by/4.0/))

## 10 Summary

11 Minimum inhibitory concentration (MIC) is a laboratory test used to estimate the susceptibility  
12 of a microorganism to an antibiotic. The result is used to determine whether it is possible to  
13 use that same drug to treat a patient's infection. Agar dilution is a reference method for MIC  
14 testing. However, the interpretation of agar dilution plates is time-consuming and prone to intra-  
15 and inter-operational error when read by laboratory personnel. AIgarMIC is a Python package  
16 for automated interpretation of agar dilution methodology. AIgarMIC processes laboratory  
17 images to identify bacterial growth on each position on solid agar containing different dilutions  
18 of an antimicrobial agent to generate a 3-dimensional growth matrix. The growth matrix is  
19 then used to identify the antimicrobial concentration at which microbial growth is inhibited –  
20 defining the minimum inhibitory concentration. AIgarMIC can be imported for use in Python  
21 scripts, or can be run through a command-line interface. Users can customise AIgarMIC to their  
22 workflow with bespoke models, or use the pre-trained models provided. AIgarMIC automates  
23 the collection of multiple data and minimizes measurement error.

## 24 Statement of need

25 Antimicrobial susceptibility testing (AST) is required to ensure timely and appropriate an-  
26 timicrobial therapy worldwide. AST is also used to quantify the incidence and prevalence of  
27 antimicrobial resistance in hospitals, regions and countries. Agar dilution is a standard AST  
28 method – it has the advantage of being relatively inexpensive, and enables high throughput.  
29 However, the implementation of agar dilution is often limited by the time required to interpret  
30 plates, a process that is also subject to significant intra- and inter-observer variability.

31 The aim of AIgarMIC is to standardise and automate the interpretation of agar dilution plates.  
32 Typical users of AIgarMIC are likely to include:

- 33 ▪ Laboratories that are currently performing agar dilution MIC testing, but wish to automate  
34 and standardise the interpretation of their results,
- 35 ▪ Laboratories that have a need for moderate–high throughput MIC testing, but do not  
36 have access to other automated assays and systems.

## 37 Related resources

38 Users of AIgarMIC may also be interested in the following related resources and software:

- 39     ▪ Laboratory protocols for agar dilution MIC testing, such as those published by the  
40       European Committee on Antimicrobial Susceptibility Testing (EUCAST) ([EUCAST,](#)  
41       [2000](#)) or by Wiegand et al ([Wiegand et al., 2008](#)).
- 42     ▪ Software such as [cellprofiler](#) as a general biological image analysis tool that can be  
43       used for tasks beyond the scope of AIgarMIC ([Lamprecht et al., 2007](#)).

44 Additionally, AIgarMIC also comes with a collection of [assets](#) (example images and pre-trained  
45 models) to help users get started with the software ([Gerada, Harper, Howard, Reza, Hope, &](#)  
46 [Liverpool Clinical Laboratories, 2024](#)).

## 47 Laboratory validation

48 AIgarMIC has undergone research validation against a wide range of antimicrobials, against  
49 a gold standard of manual annotation. It has mainly been tested on clinical *Escherichia coli*  
50 strains ([Gerada, Harper, Howard, Reza, & Hope, 2024](#)).

## 51 Funding and acknowledgements

52 AIgarMIC was funded, in part, by UKRI Doctoral Training Program (AG) [grant ref: 2599501]  
53 and the Wellcome Trust [grant ref: 226691/Z/22/Z]. The bacterial strains used in this study  
54 were provided by Liverpool Clinical Laboratories.

## 55 References

- 56 EUCAST. (2000). Determination of minimum inhibitory concentrations (MICs) of antibacterial  
57 agents by agar dilution. *Clinical Microbiology and Infection*, 6(9), 509–515. <https://doi.org/10.1046/j.1469-0691.2000.00142.x>
- 59 Gerada, A., Harper, N., Howard, A., Reza, N., & Hope, W. (2024). Determination of minimum  
60 inhibitory concentrations using machine-learning-assisted agar dilution. *Microbiology*  
61 *Spectrum*, e04209–23. <https://doi.org/10.1128/spectrum.04209-23>
- 62 Gerada, A., Harper, N., Howard, A., Reza, N., Hope, W., & Liverpool Clinical Laboratories.  
63 (2024). *Image and model assets for AlgarMIC (agar dilution minimum inhibitory con-*  
64 *centration software)* [Data set]. [object Object]. [https://doi.org/10.17638/DATACAT.](https://doi.org/10.17638/DATACAT.LIVERPOOL.AC.UK/2631)  
65 [LIVERPOOL.AC.UK/2631](https://doi.org/10.17638/DATACAT.LIVERPOOL.AC.UK/2631)
- 66 Lamprecht, M. R., Sabatini, D. M., & Carpenter, A. E. (2007). CellProfiler: Free, versatile  
67 software for automated biological image analysis. *BioTechniques*, 42(1), 71–75. <https://doi.org/10.2144/000112257>
- 69 Wiegand, I., Hilpert, K., & Hancock, R. E. W. (2008). Agar and broth dilution methods to  
70 determine the minimal inhibitory concentration (MIC) of antimicrobial substances. *Nature*  
71 *Protocols*, 3(2), 163–175. <https://doi.org/10.1038/nprot.2007.521>