1 **Method for evaluating genomic material**

2 **purity using whole genome sequencing**

3 **data.**

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6 **ABSTRACT**

7

Dummy abstract text.

8 Keywords: Biodetection, Test material, Reference material, Purity, Bioinformatics

9 **INTRODUCTION**

10 Rapid, sensitive and accurate assays for detecting bacterial pathogens in food, water, clinical samples,

11 and suspicious biothreats is critical to public health and safety. Biodetection assays must be evaluated for

12 assay sensitivity and specificity prior to deployment as well in the hands of the user to instill confidence

13 in the actions made based on assay results ([Ieven et al.](#_bookmark15), [2013](#_bookmark15); [Coates et al.](#_bookmark9), [2011](#_bookmark9); [EPA](#_bookmark10), [2004](#_bookmark10); [ISO/TS](#_bookmark16),

14 [2010](#_bookmark16); [Guide](#_bookmark13), [1998](#_bookmark13); [Feldsine et al.](#_bookmark11), [2002](#_bookmark11)). Test materials are used to validate assay performance. Test

15 materials can be either purified cultures, genomic DNA or whole cells spiked into a matrix [(EPA](#_bookmark10), [2004](#_bookmark10);

16 [ISO/TS](#_bookmark16), [2010](#_bookmark16); [CLSI](#_bookmark8), [2010](#_bookmark8)). Before being used to evaluate a biodetection assay the material itself must

17 be validated in terms of purity and identity to eliminate false positive results due to test material contami-

18 nants or false negatives due to the test material being the wrong strain [(CLSI](#_bookmark8), [2010](#_bookmark8)). There are a number

19 of potential sources of microbial contaminants including the stock culture, preservation medium, as well

20 as airborne and laboratory contaminants [(Marron et al.](#_bookmark20), [2013](#_bookmark20); [Shrestha et al.](#_bookmark28), [2013](#_bookmark28); [Tanner et al.](#_bookmark29), [1998](#_bookmark29)).

21 Currently polymerase chain reaction (PCR) assays are the most commonly use method for evalu-

22 ating test material purity. Though other methods to detect contaminants in whole genome sequencing

23 datasets have been developed but not currently used to evaluate test material purity. A PCR assay was

24 developed to analyze protist cultures. This assay uses endpoint PCR for prokaryotes and eukaryotes

25 with template dilutions ([Marron et al.](#_bookmark20), [2013](#_bookmark20)). The benefit to PCR-based approaches is that they can

26 be cost effective and fast if an applicable protocol exists. While PCR assays can detect contaminants,

27 this approach does not scale to multiple contaminants and test materials. More importantly, PCR assays

28 can only target specific contaminants thus biases the purity assessment to known potential contaminants.

29 The bioinformatics tools developed to identify contaminants in metagenomic datasets, which include

30 sequencing data from all organisms in a sample, can also be used to evaluate test material purity. For

31 example DeconSeq ([Schmieder and Edwards](#_bookmark24), [2011](#_bookmark24)) and a similar method QC-Chain ([Zhou et al.](#_bookmark32), [2013](#_bookmark32))

32 were developed to identify contaminants based on analysis of 16S ribosomal ribonucleic acid (rRNA)

33 gene sequences or comparison of a subset of reads to a reference database using Basic local alignment

34 search tool (BLAST). Metagonomic-based methods are able to identify contaminants without any prior

35 knowledge or assumptions regarding the identity of the organism(s). However, methods based on 16S

36 rRNA gene identification have limited resolution, as 16S rRNA sequences can only provide genus level

37 taxonomic resolution at best. The benefit to using metagenomic tools developed is that prior knowledge

38 of the identity of the contaminant is not required; however this method is unable to identify contaminants

39 to the species level or higher.

40 Another approach to evaluating test material purity is through shotgun whole genome sequencing,

41 sequence all DNA in a single organism sample. There are a number of metagenomic read classifica-

42 tion algorithms developed to determine the taxonomic composition of a sequence dataset of unknown

43 composition. These algorithms tend to use one of three primary strategies for taxonomic assignment.

44 The first method consist of aligning reads to an reference database([Buchfink et al.](#_bookmark6), [2015](#_bookmark6); [Francis et al.](#_bookmark12),

45 [2013](#_bookmark12)). This approach while exaustive is computationally expensive. The second type of method focuses

46 on marker genes, genes common to different phylogenetic groups, which reduces the computational cost

47 [(Segata et al.](#_bookmark27), [2012](#_bookmark27); [Liu et al.](#_bookmark19), [2011](#_bookmark19)). The decrease in computational cost comes at a price at infor-

48 mation required to discriminate closely related genomes may not be present in the marker genes. The

49 third method uses a *k*-mer based approach, where taxonomic composition is determined based the abun-

50 dance of DNA sequences of length *k* in the sequence dataset and a reference database ([Ounit et al.](#_bookmark22), [2015](#_bookmark22);

51 [Menzel et al.](#_bookmark21), [2016](#_bookmark21); [Wood and Salzberg](#_bookmark31), [2014](#_bookmark31)).

52 In this work, we present the results of a proof of concept study to measure the purity of single

53 organism test materials using whole genome sequencing data combined with a metagenomic read classi-

54 fication algorithm. We choose to use *Pathoscope*, a sequence alignment based method, developed use in

55 detecting pathogens and identify strains using whole genome sequencing data [(Francis et al.](#_bookmark12), [2013](#_bookmark12)), as

56 the pathogen detection problem is similar to contaminant detection as the organism of interest is likely

57 present at low concentrations. *Pathoscope* benefits from the large sample size obtained using all sequence

58 data for higher sensitivity(compared to marker gene based methods) and leverages algorithmic advances

59 for whole genome sequence mapping. We will first present the specificity of the method using simulated

60 data for single organisms. Then, evaluate sensitivity of the method using simulated contaminanted test

61 material datasets.

62 **METHODS**

63 To test the suitability of using whole genome sequence data and metagenomic taxonomic classifica-

64 tion methods for evaluating material purity we first simulated whole genome sequence data from single

65 genomes and also simulated contaminanted datasets. Simulated data from single genomes was used to as-

66 sess method specificity and simulated contaminant datasets method sensitivity. Simulated datasets were

67 generated using the ART sequencing read simulator [(Huang et al.](#_bookmark14), [2012](#_bookmark14)). The datasets were generated

68 using the Illumina MiSeq error models for 230 paired end base pair reads and 20 X mean coverage with

69 an average insert size of 690 base pairs with standard deviation of 10 bp for each strain, the seed number

70 for the random number generator was randomly assigned and recorded for each dataset.

71 The taxonomic composition of simulated datasest was assessed using the Pathoscope metagenomic

72 taxonomic classifier [(Francis et al.](#_bookmark12), [2013](#_bookmark12)). This method uses an expectation maximization algorithm

73 where the sequence data are first mapped to a database comprised on all sequence data in the Genbank

74 nt database, then through an iterative process re-assigns ambiguously mapped reads to based on the

75 proportion of reads mapped unambigously to individual taxa in the database. The PathoScope 2.0 taxo-

76 nomic read classification pipeline includes an initial read filtering step (PathoQC), followed by mapping

77 reads to a reference database (PathoMap) - a wrapper for bowtie2 ([Langmead and Salzberg](#_bookmark18), [2012](#_bookmark18))), then

78 an expectation-maximization classification algorithm (PathoID). The annotated Genbank nt database pro-

[79](ftp://pathoscope.bumc.bu.edu/data/nt_ti.fa.gz) vided by the PathoScope developers was used as the reference database ([ftp://pathoscope.bumc.](ftp://pathoscope.bumc.bu.edu/data/nt_ti.fa.gz)

80 [bu.edu/data/nt\_ti.fa.gz](ftp://pathoscope.bumc.bu.edu/data/nt_ti.fa.gz)).

81 **Specificity**

82 Method specificity was defined as the proportion of reads in a single organism simulated dataset assigned

83 to a different taxonomy then the taxonomy of the test material. Sequence data was simulated for 406

84 strains, from 9 genera (Table [1](#_bookmark0)). We will refer to the genome used to generate the reads as the target

85 genome. The genomes included in the simulation study were limited to the number of closed genomes

86 in the Genbank database (<http://www.ncbi.nlm.nih.gov/genbank/>, accessed 10/18/2013)

87 belonging genera of interest (Table [1](#_bookmark0)). Due to the large number of closed genomes genomes from the gen-

88 era *Bacillus*, *Escherichia*, and *Salmonella* were limited to thefollow species *Bacillus cereus*, *Escherichia*

89 *coli*, *Salmonella enteria*. The taxononomic heirarchy for the target genome and simulated read assign-

90 ment match levels were determined using the R package ([Scott Chamberlain and Eduard Szocs](#_bookmark26), [2013](#_bookmark26);

91 [Chamberlain et al.](#_bookmark7), [2016](#_bookmark7)).

92 **Sensitivity**

93 We simulated datasets with contaminants to evaluate method sensitivity. Representative genomes for

94 8 of the 9 genus were used to generate the simulated contaminant datasets (Table [2](#_bookmark4)). An *Escherichia*

95 *coli* strain was selected as a representative of both *Eschericha coli* and *Shigella*. For each pairwise

96 combination of representative genomes for the simulated contaminant dataset was subsampled at 0*.*1 to

97 10*−*8 (contaminant proportion), at 10 fold dilutions, the target genome dataset was subsamples at 1 -

98 contaminant proportion, resulting in 512 simulated contaminant datasets. This approach simulates the

99 proportions of cells in a test material and not the amount of DNA, assuming unbiased DNA extraction.

100 To speed up processing the aligned sequence files were subsampled instead of the simulated sequence

101 files.

102 **Reproducibility**

103 To facility reproducibility and transparency a Docker ([www.docker.com](http://www.docker.com/)) container is available with

104 installed pipeline dependencies ([www.registry.hub.docker.com/u/natedolson/docker-pathoscop](http://www.registry.hub.docker.com/u/natedolson/docker-pathoscope/)

[105](https://github.com/nate-d-olson/genomic_purity) The script used to run the simulations were available at [https://github.com/nate-d-olson/](https://github.com/nate-d-olson/genomic_purity)

106 [genomic\_purity](https://github.com/nate-d-olson/genomic_purity). Pathoscope results were processed using using the statistical programing language

107 R [(R Core Team](#_bookmark23), [2016](#_bookmark23)) and intermediate analysis and data summaries were organized using ProjectTem-

[108](https://github.com/nate-d-olson/genomic_purity_analysis) plate ([White](#_bookmark30), [2014](#_bookmark30)) and archived in a github repository ([https://github.com/nate-d-olson/](https://github.com/nate-d-olson/genomic_purity_analysis)

109 [genomic\_purity\_analysis](https://github.com/nate-d-olson/genomic_purity_analysis)).

110 **RESULTS AND DISCUSSION**

111 **Specificity**

112 Simulated sequence data from individual isolates was used to assess the genomic purity assessment

113 method specificity. Here we define specificity as the ability of the method to correctly assign reads to

114 the taxonomy of the genome the sequencing reads were simulated from, the target genome. Method

115 specificity was evaluated by characterizing the read assignment results based on the level of agreement

116 between the genome and assigned taxonomy (Fig. [1](#_bookmark1)). Overall high proportion of matches at species and

117 genus level. The cumulative match proportions do not always reach 1.00, for example *Staphylococcus*

118 genomes. This might be due to exclusion of unclassified and unknown matches (NCBI taxid 12908 and

119 0 respecitively) from match level analysis. Some genus have high levels of family and higher matches.

120 For *Shigella* most likely due to matches with *Escherichia* (Fig. [2](#_bookmark2)).

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| --- | --- | --- |
| Genus | N | Genome Size (Mb) |
| *Bacillus* | 76 | 5.05 (3.07-7.59) |
| *Escherichia* | 62 | 5.11 (3.98-5.86) |
| *Pseudomonas* | 57 | 6.18 (4.17-7.01) |
| *Staphylococcus* | 49 | 2.82 (2.69-3.08) |
| *Salmonella* | 44 | 4.88 (4.46-5.27) |
| *Listeria* | 39 | 2.97 (2.78-3.11) |
| *Clostridium* | 32 | 4.02 (2.55-6.67) |
| *Yersinia* | 19 | 4.73 (4.62-4.94) |
| *Francisella* | 18 | 1.89 (1.85-2.05) |
| *Shigella* | 10 | 4.74 (4.48-5.22) |

**Table 1.** Breakdown of the number of genomes by genus used to generate single genome simultated datasets. N indicates the number of genomes, and Genome Size is presented as the median and range (minimum to maximum) genome size

121 Most of the genus had genus level or higher match proportions excluding a few outliers (Fig. [3](#_bookmark3)).

122 *Escherichia*, *Shigella*, and *Staphylococcus* are noteable exceptions. As discussed previously the taxo-

123 nomic ambiguities for *Shigella* and *Escherichia* are responsible for the overall lower genus level match

124 proportions. Another example of low genus level matches is the *Bacillus* genome with genus match pro-

125 portion close to zero, *Bacillus infantis* string NRRL B 14911. While the *B. infantis* strain was originally

126 classified as *Bacillus* the species is phylogenetically distinct from other members of the genus ([Ko et al.](#_bookmark17),

127 [2006](#_bookmark17)). It is important to consider the strain and genome being characterized as taxonomic ambiguities

128 (e.g. *Shigella* and *Escherichia*) can lead to lower than expected specificity and the identification of false

129 positive contaminants.

130 **Sensitivity**

131 To evaluate genomic purity assessment methods we generated simulated contaminant datasets as pair-

132 wise combinations of representative genomes from 8 of the genus used in the specificity section of the

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| *Bacillus* | | | | | | | |  | *Clostridium* | | | | | | | |  | *Escherichia* | | | | | | | |
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Cumulative Match Proportion

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| *Listeria* | | | | | | | |
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| *Pseudomonas* | | | | | | | |
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| *Salmonella* | | | | | | | |
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| *Shigella* | | | | | | | |
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| *Staphylococcus* | | | | | | | |
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| *Yersinia* | | | | | | | |
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species genus family order class phylum

superkingdom

species genus family order class phylum

superkingdom

species genus family order class phylum

superkingdom

# Taxonomic Level

**Figure 1.** Cumulative taxonomic match results for genomic purity assements of simulated sequence data from single genomes. Each line represents the cumulative proportion of simulated reads with taxonomic assignments matching at or above the specified taxonomic level. Genomes are grouped by genus.

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0.95

Cumulative Match Proportion

0.90

0.85

genus

family

class

# Taxonomic Level

species

superkingdom

**Figure 2.** Cumulative taxonomic match results for genomic purity assement for *Shigella* considering matches to *E. coli* as species level matches. Each line represents the cumulative proportion of simulated reads with taxonomic assignments matching at or above the specified taxonomic level. Genomes are grouped by genus.

1.00

0.75

0.50

Genus Match Proportion

0.25

0.00

*Bacillus*

*Clostridium*

*Escherichia*

*Listeria*

*Salmonella*

*Shigella*

*Yersinia*

Query Genus

*Pseudomonas*

*Staphylococcus*

**Figure 3.** Distribution of the proportion of reads assigned to the source genome at or above the genus level. Horizontal grey line highlights a match proportion of 0.95. Boxplots hinges represent the 25th and 75th percentiles, line through box represent is the median, whiskers are the 95% confidence interval, and the black dots are outliers.

133 study (Table [2](#_bookmark4)). Due to the overall high proportion of reads matched to the correct genome in the method

134 specificity study the simulated contaminant datasets were evaluated at the genus level. For all the uncon-

135 taminated representative set of target genomes the proportion of simulated reads that matched at species

136 level or higher was 0.98 (Table [2](#_bookmark4)).

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| --- | --- | --- | --- | --- | --- |
| Representative Strain | Species | C Mb | C Acc | P Mb | P Acc |
| Bacillus anthracis str. Ames | 1.00 | 5.23 | AE016879.1 |  |  |
| Clostridium botulinum A str. Hall | 1.00 | 3.76 | CP000727.1 |  |  |
| Escherichia coli O157:H7 str. EC4115 | 0.98 | 5.57 | CP001164.1 | 0.13 | CP001163.1, CP001165.1 |
| Francisella tularensis subsp. tularensis SCHU S4 | 1.00 | 1.89 | AJ749949.2 |  |  |
| Pseudomonas aeruginosa PAO1 | 1.00 | 6.26 | AE004091.2 |  |  |
| Salmonella enterica subsp. enterica serovar Typhimurium str. D23580 | 1.00 | 4.88 | FN424405.1 |  |  |
| Staphylococcus aureus subsp. aureus ED133 | 0.98 | 2.83 | CP001996.1 |  |  |
| Yersinia pestis CO92 | 1.00 | 4.65 | AL590842.1 | 0.18 | AL109969.1, AL117189.1, AL117211.1 |

**Table 2.** Represenative strains used in simulated contaminant datasets. Species indicates the proportion of simulated reads assigned to the correct taxa at the species level or higher. DNA size (Mb) and Genbank accession numbers (Acc) are indicated for chromosomes (C) and plasmids (P). Escherichia coli O157:H7 str. EC4115 and Yersinia pestis CO92 have two and three plasmids respecitively.

137 While the proportion of contaminant reads in the simulated datasets was not equal to defined con-

138 taminant proportion the proportion of reads assigned to the contaminant genus was comparable to the

139 expected proportion (Fig. [4](#_bookmark5)). This was especially true for datasets containing mixtures of *B. anthracis*,

140 *Y. pestis*, *E. coli*, and *S. enteria* as they had similar sized genomes (Table [2](#_bookmark4)). Three contaminants were

141 detected when spiked in at contaminant proportions of 10*−*8, *B. anthracis* in *E. coli* as well *S. enteria*

142 and *E. coli* in *Y. pestis*. Interestingly the proportion of assigned reads did not decrease with decreasing

143 contaminant proportions after 10*−*4.

144 The lowest proportion of simulated contaminant detected varied by both contaminant and taget

145 genome. All organisms had comparable minimum contamination levels for which reads were assigned

146 to the contaminat genome. Two notable exceptions are *Escherichia* and *Yersinia*, where *Bacillus*, and

147 *Salmonella* and *Escherichia* were detected at the lowest contaminant levels respectively. As the results

148 are from simulated data and based on proportions of simulated reads, these values do not indicate a limit

149 of dection for the method.

150 **CONCLUSIONS**

151 • Proof of concept study additional work required to validate use in assessing the purity of a test

152 material.

153 • Use of other taxonomic classification methods are likely to have different sensitivity and specificity

154 results.

155 • Need to evaluate the suitablility of the reference database for used the genome and contaminant of

156 interest.

157 • Work to further expand the taxonomic database to include genomes from uncultured organism us-

158 ing either metagenome datasets for single cell datasets along with efforts to address issues related

159 to taxnomic ambiguities will help to improve the method applicability.

1e+00

1e−02

1e−04

1e−06

1e+00

1e−02

1e−04

1e−06

Proportion of Matched Reads

1e+00

1e−02

1e−04

1e−06

1e+00

1e−02

1e−04

1e−06

1e+00

1e−02

1e−04

1e−06

1e+00

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1e−04

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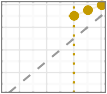
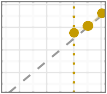
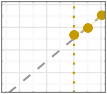
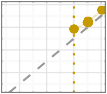
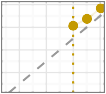
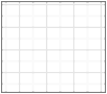
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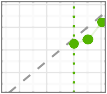
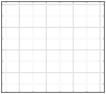
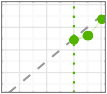
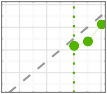
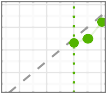
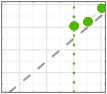
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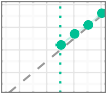
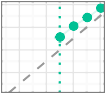
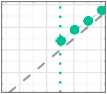
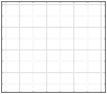
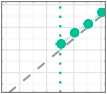
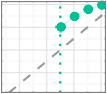
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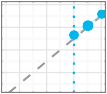
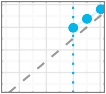
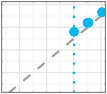
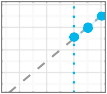
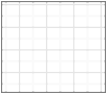
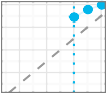
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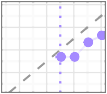
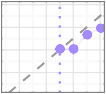
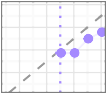
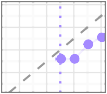
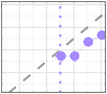
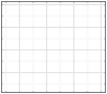
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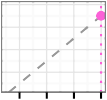
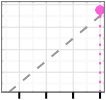
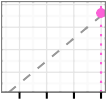
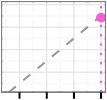
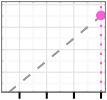
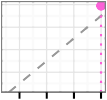


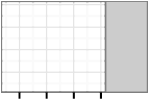
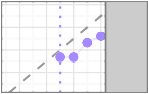
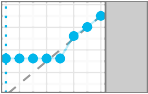
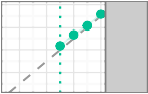
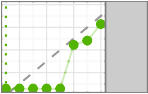
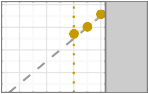
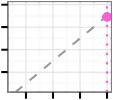
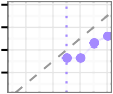
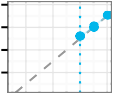
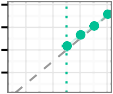
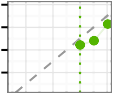
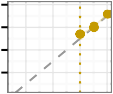
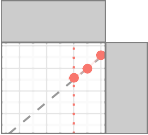
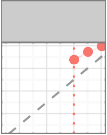
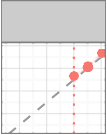
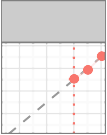
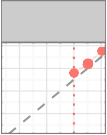
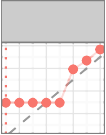
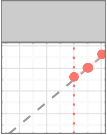
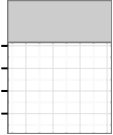
     

Contaminant Proportion

Baci

Clos

Esch

Pseu

Salm

Stap

Yers

1e−07

1e−05

1e−03

1e−01

1e−07

1e−05

1e−03

1e−01

1e−07

1e−05

1e−03

1e−01

1e−07

1e−05

1e−03

1e−01

1e−07

1e−05

1e−03

1e−01

1e−07

1e−05

1e−03

1e−01

1e−07

1e−05

1e−03

1e−01

1e−07

1e−05

1e−03

1e−01

Contaminant

Bacillus anthracis Ames Clostridium botulinum A Hall Escherichia coli O157 H7 EC4115 Pseudomonas aeruginosa

Salmonella enterica serovar Typhimurium Staphylococcus aureus ED133

Yersinia pestis CO92

**Figure 4.** Relationship between the proportion of contaminant reads simulated per dataset and the proportion of reads matched to the contaminant genus.

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164 (NIST). Opinions expressed in this paper are the authors and do not necessarily reflect the policies and

165 views of DHS, NIST, or affiliated venues. Certain commercial equipment, instruments, or materials are

166 identified in this paper in order to specify the experimental procedure adequately. Such identification

167 is not intended to imply recommendations or endorsement by NIST, nor is it intended to imply that the

168 materials or equipment identified are necessarily the best available for the purpose. Official contribution

169 of NIST; not subject to copyrights in USA.

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