Investigation of gut microbiome association with inflammatory bowel disease and depression: a machine learning approach

Pedro Morell Miranda, Francesca Bertolini, Haja N. Kadarmideen
Department of Bio and Health Informatics, Technical University of Denmark, Kongens Lyngby, 2800, Denmark

Abstract
Background: Inflammatory bowel disease (IBD) is a group of chronic diseases related to inflammatory processes in the digestive tract generally associated with an immune response to an altered gut microbiome in genetically predisposed subjects. For years, both researchers and clinicians have been reporting increased rates of anxiety and depression disorders in IBD, and these disorders have also been linked to an altered microbiome. However, the underlying pathophysiological mechanisms of comorbidity are poorly understood at the gut microbiome level.

Methods: Metagenomic and metatranscriptomic data were retrieved from the Inflammatory Bowel Disease Multi-Omics Database. Samples from 70 individuals that had answered to a self-reported depression and anxiety questionnaire were selected and classified by their IBD diagnosis and their questionnaire results, creating six different groups. The cross-validation random forest algorithm was used in 90% of the individuals (training set) to retain the most important species involved in discriminating the samples without losing predictive power. The validation set that represented the remaining 10% of the samples equally distributed across the six groups was used to train a random forest using only the species selected in order to evaluate their predictive power.

Results: A total of 24 species were identified as the most informative in discriminating the 6 groups. Several of these species were frequently described in dysbiosis cases, such as species from the genus Bacteroides and Faecalibacterium prausnitzii. Despite the different compositions among the groups, no common patterns were found between samples classified as depressed. However, distinct taxonomic profiles within patients of IBD depending on their depression status were detected.

Conclusions: The machine learning approach is a promising approach for investigating the role of microbiome in IBD and depression. Abundance and functional changes in these species suggest that depression should be considered as a factor in future research on IBD.

Keywords
Inflammatory Bowel Disease, Depression, Microbiome, Machine Learning, Random Forest, Metagenomic, Metatranscriptomic.
Corresponding author: Haja N. Kadarmideen (hajak@dtu.dk)

Author roles: Morell Miranda P: Conceptualization, Formal Analysis, Investigation, Writing – Original Draft Preparation; Bertolini F: Supervision, Writing – Review & Editing; Kadarmideen HN: Supervision, Writing – Review & Editing

Competing interests: No competing interests were disclosed.


Copyright: © 2018 Morell Miranda P et al. This is an open access article distributed under the terms of the Creative Commons Attribution Licence, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited. Data associated with the article are available under the terms of the Creative Commons Zero "No rights reserved" data waiver (CC0 1.0 Public domain dedication).

Grant information: Authors thank funding from The Danish Independent Research Council (Technology and Production) grant number DFF – 6111-00471. P.M.M. thanks funding from Technical University of Denmark, DTU Bioinformatics for his research assistantship to conduct this study. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Introduction

Increased depression rates have been frequently reported on patients with inflammatory bowel disease (IBD) (Graff et al., 2009), which is a big concern from a clinical standpoint, since increased levels of stress and anxiety are major drivers of IBD relapse and severity (Mawdsley & Rampton, 2006). Both IBD and depression are heavily influenced by the gut microbiome structure, which controls anti-inflammatory processes and permeability in the gut, and communicates with the brain by a complex and close relationship with the Autonomous Nervous System that is known as the brain-gut axis (Foster & McVey Neufeld, 2013; Luna & Foster, 2015).

Altered microbiomes can have big impacts on the health and development of both the gut and brain, and alterations in the ecology of this microbiome, a process known as dysbiosis, have been separately linked to both depression and IBD (Kaur et al., 2011; Rogers et al., 2016). However, little is known about the role of the microbiome in the two diseases.

The availability of the large amount of data derived from the recent explosion in metagenomics and metatranscriptomics provides unique opportunities for investigation. However, it is sometimes difficult to identify informative species. Recently, machine learning algorithms have been successfully applied because they allow the identification of patterns in situations where large, multi-dimensional and heterogeneous datasets are available.

Among the several machine learning approaches available, random forest is an algorithm used for classification and regression based on an ensemble that builds a population of decision tree classifiers, such that the result of a prediction from a given set of features is the most frequent result from the different trees of the “forest” (Breiman, 2001). This is an efficient and generalist algorithm that has already been applied in several metagenomic investigations in human diseases, such as IBS (Saunier et al., 2011).

The aim of this work was to apply the random forest approach to identify the microbiome species that may be mostly involved in IBD and depression outcomes and that are responsible for the most relevant changes in the population structure between IBD, depression and patients comorbid for both conditions, and to provide insights on how the microbiome is involved in this comorbidity.

Methods

Database generation

The datasets used for the analyses were retrieved from the Inflammatory Bowel Disease Multi-Omics Database (IBDMDB) (Schirmer et al., 2018), which is part of the Integrative Human Microbiome Project (NIH HMP Working Group et al., 2009). The IBDMDB database contains a wide array of omics data (e.g., 16S and shotgun metagenomic, metatranscriptomic, proteomic and host genomes) of 132 individuals classified by IBD diagnostic in ulcerative colitis, Crohn’s disease and controls. Participants provided bi-weekly stool samples at five hospitals in the United States. Metagenomic and metatranscriptomic data was processed as described in Schirmer et al., 2018 (Abubucker et al., 2012; Truong et al., 2015).

Subject selection

From this dataset, the 70 unique participants who answered an additional self-reported depression and anxiety questionnaire during registration (the answers to which are listed in the HMP2 metadata, column EC to EL) were selected. As the questionnaire model was not specified, only individuals with raw scores over 6 on this test was considered as showing “signs of depression”. To calculate the raw scores, a severity scale was generated, with the following scores: 0, never; 1, rarely; 2, sometimes; 3, often; 4, always. The scores were then summed to give a final total. In the case of individuals undergoing multiple tests, the lower score was used. We selected a low threshold in order to be able to identify putative dysbiotic individuals that were not experiencing severe depression symptoms. All the others were classified as “no sign of depression”. The combination between the test and the IBD diagnosis divided the dataset in six groups: Crohn’s disease with no detectable sign of depression (CD; n=15), Crohn’s disease with signs of depression (CDD; n=20), ulcerative colitis with no sign of depression (UC; n=4), ulcerative colitis with signs of depression (UCD; n=11), signs of depression but no inflammation (nonIBD; n=7) and the control group: no inflammation/no depression (nonIBD; n=13).

Data analysis

For each of the six groups, abundance matrices of the metagenomic data, metatranscriptomic data, and the combination of metagenomics and metatranscriptomics were used for random forest classification. Each of the datasets was divided randomly into a training set (90% of the individuals) and a validation set (10% of the individuals). Random forest analysis were performed using the library Scikit-learn 0.19.1 (Pedregosa et al., 2011) on the training sets to identify the most important species involved in discriminating the samples without losing predicting power. A 1000-fold cross-validation for the combined dataset, and 500-fold for metagenomic and metatranscriptomic data, considering one model for each iteration was performed and only the most important species in the construction of this model was retained. Only models with a precision classification >80% were considered, and among the considered models, only species that appeared more than once were selected. Afterwards, the validation sets were run with the selected species only to measure the possible loss of predictive capability and computed the area under the receiver operating characteristic (auROC) curve for the prediction of the validation set classes as a performance metric.

Statistical analysis

In order to assess the significance of the differences between the abundances of the selected species, we performed a one-way ANOVA (Scipy 1.0.0, Jones et al., 2001) with a Tukey’s honest significant difference (HSD) post-hoc test. This test makes pair-wise comparisons between the different means to see which classes are different. For clarity, confidence intervals for Tukey’s HSD test can be found in Supplementary Materials (Supplementary Figure 1 and Supplementary Figure 2).
The functional activity of the selected species was retrieved from the HUMAnN metatranscriptomic analyses described above. Only the pathways in which the selected species are involved and those that were different between the groups from the ANOVA test were selected and the correlation between these species was calculated using Spearman’s correlation coefficient. A significance level of 0.05 was applied for all statistical tests.

**Results and discussion**

**Species selection and model validation**

The random forest cross-validation selection of the most informative species showed a combined list of 24 species, as can be seen in Figure 1. The validation models for DNA, RNA and the combined dataset shows micro-averaged auROC values of 0.96, 0.91 and 0.99, respectively (Supplementary Figure 3–Supplementary Figure 5). This metrics highlight the performance of the model that, even with a reduced subset of species, has not lost predictive power.

All species exhibited differences in at least one group in a one-way ANOVA (alpha=0.05, Supplementary Table 1), and no significant differences were found between DNA and RNA abundances for these species (Supplementary Table 2).

**The non-dysbiotic microbiome**

The analyses showed an increase in the number of species from the genus *Bacteroides* in dysbiotic groups compared with the control (nonIBD) (Figure 2), as has been reported in other dysbiotic samples (Bloom *et al.*, 2011), with the exception of *Bacteroides dorei*, which is more abundant in nonIBD than in any other group. Aside from *Bacteroides dorei*, nonIBD samples had a higher abundance of *Alistipes shahii* and *Ruminococcus bromii*, while a typical species associated with nonIBD, *Faecalibacterium prausnitzii*, was significantly decreased in nonIBDD and CD.

**Crohn’s disease abundance changes in depression**

Both of the Crohn’s disease-related groups (CD and CDD) showed higher abundances of *Bacteroides ovatus* and *Bacteroides uniformis*. However, CD samples exhibited higher abundances for several specific species, including *Bacteroides xylanisolvens*, *Parasutterella excrementihominis* and *Bacteroides fragilis*, compared with CDD, but decreased abundance of *Faecalibacterium prausnitzii*, which did not differ significantly in abundance between nonIBD and CDD groups.

**Ulcerative colitis changes in depression**

Ulcerative colitis samples had the most distinctive microbiome profile. Several species, including *Burkholderiales bacterium_1_1_47*, *Bacteroides eggerthii* and *Bacteroides finegoldii* were characteristic of this group, and absent in the others, except for *B. finegoldii*, which was also present in a lower abundance in nonIBD samples. Only UCD samples exhibited an increased abundance of *Bacteroides fragilis*, *Bacteroides vulgatus* and *Haemophilus pittmanii*, this last species being almost exclusive to the UCD group.

**Non-IBD changes in depression**

The nonIBDD was the group with the highest number of changes in microbiome diversity when compared with its non-depressed counterpart (Table 1). However, most of those changes followed a similar pattern in other dysbiotic groups.

---

**Figure 1.** Venn diagram for the species selected for each dataset.
Figure 2. DNA (A) and RNA (B) taxonomic abundances for the selected species. Abundances were quantified by the relative abundances of their sequences, and for each level they should sum to 1 (including unclassified sequences).
A notable change was observed in *Faecalibacterium prausnitzii*, which was present in almost the same abundances in nonIBD, UCD and CDD samples, and a high variability in UC while being significantly lower in CD and nonIBDD (Supplementary Table 3 and Supplementary Table 4). This is particularly interesting, since this species is considered to have anti-inflammatory activity. It seems counterintuitive to find a depleted population of one of the species most associated in the literature with a healthy microbiome compared to an IBD one in a group that doesn’t show any inflammatory process. However, *Parabacteroides goldsteinii* was increased in nonIBD and was depleted in all IBD groups in comparison with control samples. The *Parabacteroides* genus have been associated previously with anti-inflammatory activity (Neff et al., 2016; Schirmer et al., 2016), so the increase in abundance of this bacteria may explain why the nonIBDD microbiome is not associated with inflammation in the gut.

Other than *Parabacteroides goldsteinii*, nonIBDD samples did not contain other characteristic groups, and, more notably, none of the selected species was specific for depressed or non-depressed phenotypes.

### Microbial functional activity

Regarding the functional activity of these species, seven pathways that were more abundant in dysbiotic groups than in nonIBD were identified (Supplementary Figure 1) and were correlated between each other and inversely correlated with most of the others (Supplementary Figure 2 and Supplementary Table 5). Those pathways are folate transformations II, N10-formyl-tetrahydrofolate biosynthesis, *de novo* L-ornithine biosynthesis, superpathway of pyridoxal 5’-phosphate biosynthesis and salvage, phosphopantothenate biosynthesis I, preQ0 biosynthesis and queuosine biosynthesis. Folate (vitamin B9) and pyroxidal 5’-phosphate (vitamin B6) deficiencies have been linked both to depression (Coppen & Bolander-Gouaille, 2005; Hvas et al., 2004; Mitchell et al., 2014), as they are key for the synthesis of several neurotransmitters, and IBD (Pan et al., 2017; Yakut et al., 2010), although this association is not well understood and does not seem to be evidence of causation. Increased levels of L-ornithine derivatives have also been linked to depression (Zheng et al., 2010).

However, even if nonIBDD have the highest activity for almost all of these pathways, CD and UC were also significantly increased, while functional activity in CDD was generally lower.

<table>
<thead>
<tr>
<th>Species</th>
<th>CD</th>
<th>UC</th>
<th>nonIBD</th>
</tr>
</thead>
<tbody>
<tr>
<td>Alistipes shahii</td>
<td>-</td>
<td>-</td>
<td>Increase</td>
</tr>
<tr>
<td>Bacteroides ovatus</td>
<td>-</td>
<td>-</td>
<td>Increase</td>
</tr>
<tr>
<td>Subdunigranulum sp.</td>
<td>-</td>
<td>Decrease</td>
<td>-</td>
</tr>
<tr>
<td>Bacteroides xylanisolvens</td>
<td>Decrease</td>
<td>-</td>
<td>Increase</td>
</tr>
<tr>
<td>Parasutterella excrementominis</td>
<td>Decrease</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Burkholderiales bacterium 1_1_47</td>
<td>Decrease</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Alistipes putredinis</td>
<td>-</td>
<td>Decrease</td>
<td>Decrease</td>
</tr>
<tr>
<td>Bacteroides stercoris</td>
<td>-</td>
<td>-</td>
<td>Increase</td>
</tr>
<tr>
<td>Faecalibacterium prausnitzii</td>
<td>Increase</td>
<td>-</td>
<td>Decrease</td>
</tr>
<tr>
<td>Bacteroides uniformis</td>
<td>Decrease</td>
<td>-</td>
<td>Increase</td>
</tr>
<tr>
<td>Bacteroides fragilis</td>
<td>Decrease</td>
<td>Increase</td>
<td>-</td>
</tr>
<tr>
<td>Lachnospiraceae bacterium 7_1_58</td>
<td>Increase</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Bacteroides dorei</td>
<td>-</td>
<td>-</td>
<td>Decrease</td>
</tr>
<tr>
<td>Bacteroides vulgatus</td>
<td>-</td>
<td>Increase</td>
<td>Increase</td>
</tr>
<tr>
<td>Ruminococcus bromii</td>
<td>-</td>
<td>-</td>
<td>Decrease</td>
</tr>
<tr>
<td>Bacteroides finegoldii</td>
<td>Decrease</td>
<td>Decrease</td>
<td>-</td>
</tr>
<tr>
<td>Bacteroides eggerthii</td>
<td>-</td>
<td>Decrease</td>
<td>Increase</td>
</tr>
<tr>
<td>Parabacteroides goldsteinii</td>
<td>-</td>
<td>-</td>
<td>Increase</td>
</tr>
<tr>
<td>Haemophilus pittmaniae</td>
<td>-</td>
<td>Increase</td>
<td>-</td>
</tr>
</tbody>
</table>
and non-significant in some pathways. Moreover, UCD did not differ from nonIBD in any of them.

This difference in functional activity again highlights the lack of a concrete pattern of gut microbiome abundance between depressed groups.

**Conclusions**

The random forest approach was able to successfully identify informative changes in abundance at the species level, revealing specific patterns for the depressed and non-depressed groups without losing predictive power. This work provided, to our knowledge for the first time, an overview about the difference in the bacterial communities of patients with signs of depression and the combination with depression and inflammatory bowel disease. Our findings suggest a complex landscape of microbiome interactions, both at population structure and functional activity levels. However, the results showed that there are distinct taxonomic profiles within patients of IBD depending on their depression status, providing further input for future investigations.

**Data availability**

The datasets used for the analyses were retrieved from the Inflammatory Bowel Disease Multi-Omics Database (IBDMDB) (Schirmer et al., 2018), a part of the Integrative Human Microbiome Project (NIH HMP Working Group et al., 2009).

**Competing interests**

No competing interests were disclosed.

**Grant information**

Authors thank funding from The Danish Independent Research Council (Technology and Production) grant number DFF – 6111-00471. P.M.M. thanks funding from Technical University of Denmark, DTU Bioinformatics for his research assistantship to conduct this study.

*The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.*

**Supplementary material**

**Supplementary Figure 1.** Relative abundances of the pathways that showed significant differences between groups (alpha= 0.05).

Click here to access the data.

**Supplementary Figure 2.** Correlation between the different pathways contributed by the selected species. Color gradient shows positive (red) or negative (blue) correlation.

Click here to access the data.

**Supplementary Figure 3.** Receiver operating characteristic curves for the validation model with combined metagenomic and metatranscriptomic data.

Click here to access the data.

**Supplementary Figure 4.** Receiver operating characteristic curves for the validation model with metagenomic data.

Click here to access the data.

**Supplementary Figure 5.** Receiver operating characteristic curves for the validation model with metatranscriptomic data.

Click here to access the data.

**Supplementary Table 1.** ANOVA results for each of the selected species in metagenomic and metatranscriptomic data sets.

Click here to access the data.

**Supplementary Table 2.** A t-test was used to assess the difference between DNA and RNA abundances per species and a nested column per group.

Click here to access the data.

**Supplementary Table 3.** Tukey’s honest significant difference test for the metagenomic data. Results are organized by species with two nested columns, confidence intervals at 0.95 and the decision. Each row represents a pair-wise comparison.

Click here to access the data.
Supplementary Table 4. Tukey’s honest significant difference test for the metatranscriptomic data. Results are organized by species with two nested columns, confidence intervals at 0.95 and the decision. Each row represents a pair-wise comparison.

Click here to access the data.

Supplementary Table 5. Tukey’s honest significant difference test for the pathways correlated pathways. Results are organized by species with two nested columns, confidence intervals at 0.95 and the decision. Each row represents a pair-wise comparison.

Click here to access the data.

References


Open Peer Review

Current Referee Status:  

Yasir Suhail
Department of Biomedical Engineering, Yale University, New Haven, CT, USA

Overview

The paper's central thesis of the correlation, or putative causative mechanism of the gut microbiome on IBD and depression, is important. The application of machine learning techniques may be suitable because of the high dimensional structure of the data and lack of knowledge of a simple causal relationship between the microbiome and IBD/depression.

I have a number of concerns and suggestions about the article in its present form. Most of these concern the presentation of the data, methods, and results. Addressing these concerns will help bring the article into a shape where readers can better evaluate the results and contribution of this study.

Presentation of the methods and results

1. The article should explicitly specify the dimensions and form of the data/features that were fed to the random forest algorithm. Were they the estimates of each species abundance in each individual from the respective RNA and DNA sequences? Was it derived from ribosomal sequences only? How many species were included? What was the total dimension of this data set? Does it correspond to a specific table in the IBDMDB resource?

2. Since the intended audience may be researchers generally interested in IBD or metagenomics who are not experts in random forests, algorithmic details should be provided in terminology that is common to the broader field. N-fold cross-validation generally refers to using 1 out of N data samples as a hold out test sample. However, the article mentions 1000-fold and 500-fold cross-validation for a data-set with 70 individuals. Does this correspond to individual re-sampled bagging or feature bagging in the random forest? A more explicit explanation will make this comprehensible to more readers.

3. The supplementary figures and tables may have been mixed/corrupted. S. Figures 1 and 2 are described as corresponding to pathway analysis but are actually ROC curves. SF4 and 5 are supposed to be ROC curves but probably show pathway results. The resolution is too low to make out the text. The method of calculating the pathway abundances should also be described somewhere. Is it the total number of reads corresponding to genes in the pathway, does it depend on the species abundances or any other parameters?
4. Some of the ambiguity in the analysis may be removed by providing the code for any pre-processing, random forest analysis, feature selection, and pathway abundance analysis etc.

**Interpretation and Conclusion**

A machine learning algorithm can build an accurate prediction system, or generate hypotheses about the mechanisms at play or provide some other insight into the process. Here, I see two possible results of the ML analysis:

1. The prediction accuracy can be a measure of the amount of information contained in the microbiome about the diseases. Alternatively, how predictive is the gut microbiome, and does this imply evidence for the causative effect of the microbiome on the disease? These would be comparatively harder claims to make, and would probably require a few more calculations.

2. The random forests are used to arrive at the most important features (bacterial species) affecting bowel disease and depression. I think this is the main claim/result of the analysis. In this case, how much more does information does ML give us compared to simply finding the species whose abundance is most different between the disease and non-disease states (in terms of fold-change or p-value). For the case of the multi-class problem, ANOVA can provide p-values for the non-random abundances in the different classes of patients. The article describes the results of such t-tests and ANOVA results. A sufficient and logical argument for the ML approach supported by any relevant calculations will strengthen the case for this analysis.

Overall, I feel the discussion of the possible role of some of the species and metabolic pathways etiology of the disease is the most interesting for biologists and clinicians. The article is important in this regard and further development of this discussion can only add to its strength.

**Is the work clearly and accurately presented and does it cite the current literature?**

No

**Is the study design appropriate and is the work technically sound?**

Partly

**Are sufficient details of methods and analysis provided to allow replication by others?**

No

**If applicable, is the statistical analysis and its interpretation appropriate?**

Partly

**Are all the source data underlying the results available to ensure full reproducibility?**

Partly

**Are the conclusions drawn adequately supported by the results?**

Yes

**Competing Interests:** No competing interests were disclosed.

I have read this submission. I believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.
Discuss this Article

**Version 1**

Referee Response 25 Jun 2018

**Yasir Suhail**, Yale University, USA

Expanding on Prof. Waldron’s comment, the article states "Only models with a precision classification >80% were considered". If this precision is evaluated on the test/validation set then the validation set has already been used for training, biasing the estimate of accuracy.

I think part of the confusion might be phrases such as "running validation sets", or "validation models". If these refer to using the random forest models trained only on the training set to predict the disease labels on the test set, everything is fine. But people might understand a "validation model" to mean multiple things.

In the same vein, the article states "and among the considered models, only species that appeared more than once were selected". Does this mean that decision trees were pruned to only keep those that had these selected species as their initial steps? Or was a random forest re-trained using these selected species? In this case, either it was trained using the same training set used initially, or it was trained on the validation set.

**Competing Interests:** No competing interests were disclosed.

Author Response 14 Jun 2018

**Pedro Morell Miranda**, Technical University of Denmark, Denmark

Dear Prof. Waldron,

The "validation set" was only used for prediction. The validation model was still trained with the "training set". We did this in order to see how our model fits new data and to avoid the scenario described in Cawley & Talbot, 2010, in section 5.3, where we are testing on samples that the model has already "seen". As you correctly point out, training on a different dataset would left us with no way to estimate the predictive power of our model.

**Competing Interests:** Author

Reader Comment 12 Jun 2018

**Levi Waldron**, CUNY School of Public Health, USA

Please note that by training a random forest model in your 10% "validation set", this becomes a second training set, leaving you no way to estimate the predictive accuracy of the model. See for example section "5. Bias in Performance Estimation" of Cawley GC, Talbot NLC: *On Over-fitting in Model Selection and*

**Competing Interests:** No competing interests were disclosed.