

Gut microbiome identifies risk for colorectal polyps

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ABSTRACT

Objective To characterise the gut microbiome in subjects with and without polyps and evaluate the potential of the microbiome as a non-invasive biomarker to screen for risk of colorectal cancer (CRC).

Design Presurgery rectal swab, home collected stool, and sigmoid biopsy samples were obtained from 231 subjects undergoing screening or surveillance colonoscopy. 16S rRNA analysis was performed on 552 samples (231 rectal swab, 183 stool, 138 biopsy) and operational taxonomic units (OTU) were identified using UPARSE. Non-parametric statistical methods were used to identify OTUs that were significantly different between subjects with and without polyps. These informative OTUs were then used to build classifiers to predict the presence of polyps using advanced machine learning models.

Results We obtained clinical data on 218 subjects (87 females, 131 males) of which 193 were White, 21 African-American, and 4 Asian-American. Colonoscopy detected polyps in 56% of subjects. Modelling of the non-invasive home stool samples resulted in a classification accuracy >75% for Naïve Bayes and Neural Network models using informative OTUs. A naïve holdout analysis performed on home stool samples resulted in an average false negative rate of 11.5% for the Naïve Bayes and Neural Network models, which was reduced to 5% when the two models were combined.

Conclusion Gut microbiome analysis combined with advanced machine learning represents a promising approach to screen patients for the presence of polyps, with the potential to optimise the use of colonoscopy, reduce morbidity and mortality associated with CRC, and reduce associated healthcare costs.

INTRODUCTION

Colorectal cancer (CRC) is the third most common cancer and fourth most common cause of cancer death in the world.¹ Though a genetic component is clear, the pathogenesis of CRC is complex, involving a sequential transition of the normal mucosa to premalignant polyps, and eventually to CRC.² This ‘adenoma-carcinoma sequence’ is dependent on an interplay of factors such as diet, immune system dysfunction, chronic inflammation, and dysbiosis of the gut microbiome.^{3,4}

Summary box

What is already known about this subject?

- Colorectal cancer (CRC) is the third most common cancer and fourth most common cause of cancer death in the world.
- Many studies have reported gut microbiome dysbiosis as a factor in the aetiology of adenoma and the progression to CRC.
- Characterisation of these complex microbial changes could be used as a non-invasive biomarker to screen patients for premalignant lesions.

What are the new findings?

- A prospective study of subjects undergoing screening or surveillance colonoscopy was performed to determine if a unique microbiome pattern could be used to identify the presence of colorectal polyps.
- Advanced machine learning techniques were used to build classifying predictors for the presence of polyps.
- The predictive power of classifiers was greatest when informative operational taxonomic units that were significantly different in subjects with and without polyps were used in the model.
- A naïve holdout analysis performed on home collected stool samples had an average false positive rate of 12% and an average false negative rate of 11.5% using Naïve Bayes and Neural Network models.
- The false negative rate was reduced to 5% when data from the Naïve Bayes and Neural Network models were combined in a composite analysis.

How might it impact on clinical practice in the foreseeable future?

- Gut microbiome analysis combined with advanced machine learning methods could be used as a non-invasive biomarker to screen patients for polyps, enhance colonoscopy compliance and increase equitable access to CRC screening efforts.
- Larger studies in populations that are more ethnically diverse and with broader socioeconomic status need to be performed to improve model performance and clinical utility.

It is well accepted that increased participation in screening programmes can prevent disease by the timely removal of polyps, and



reduce CRC mortality with earlier diagnosis,⁵ yet recent data indicate that only 63% of eligible US residents are current with CRC screening recommendations, with rates further reduced in deprived populations such as the uninsured, ethnic minorities, and lower socioeconomic status.^{6–8}

The gut microbiota has been identified as a potential screening method for CRC,^{9,10} and many studies have reported dysbiosis as a factor in the aetiology of adenoma and CRC^{11–27} (online supplementary table S1), though to date no definitive bacterial species profile has been identified as a universal biomarker.

Currently, the 16S rRNA gene is used as a standard to determine phylogenetic relationships for bacteria and to detect and quantify specific bacterial populations.²⁸ The most challenging and time-consuming step in microbiome analysis is the bioinformatics analyses that define the operational taxonomic units (OTU) and their relative abundance from large numbers of NextGen sequence reads.²⁹ Non-parametric statistical approaches have been applied to identify associations between OTUs and clinical metadata, and machine learning classification techniques have been used in taxonomic and functional studies of microbiome data to improve the classifiers' predictive power.²⁹ We propose that preselection of informative OTUs combined with advanced machine learning methods could be used as a biomarker to identify at-risk patients with polyps, thereby enhancing colonoscopy compliance and offering a potential preventative, non-invasive, affordable screening tool. Here, we present the results of a prospective study with subjects undergoing screening or surveillance colonoscopy to determine if a unique microbiome pattern could be used to identify individuals with colorectal polyps via application of several machine learning techniques.

METHODS

Study overview

In this study we defined 'polyp' broadly to include non-neoplastic polyps, benign adenomas, advanced adenomas (greater than 10 mm or villus features), and high-risk adenomas (subjects with three or more adenomas).

The polyp and healthy control data sets were collected for a clinical trial sponsored and funded by Metabionics (Biosciences Park Center, Aurora, CO, USA). The study was conducted at the Metropolitan Gastroenterology Group/Chevy Chase Clinical Research (Chevy Chase, MD, USA) and the Microbiome Analysis Center at George Mason University (Manassas, VA, USA) between January 2014 and June 2015 under an Institutional Review Board-approved (Chesapeake IRB, Columbia, MD, USA) protocol. All subjects provided written, informed consent.

Study population

Samples were collected from male and female subjects aged 45–80 years. Patients undergoing polyp surveillance

or screening colonoscopy must have been American Society of Anesthesiologists class 1–3 (healthy or mild to severe systemic disease). Subjects were excluded if they had a history of inflammatory bowel disease, were unable to schedule the colonoscopy within 60 days of the initial stool sample, or had colonic pathology that could interfere with the accuracy of the colonoscopy (eg, colonic stricture, poor preparation, and obstructing tumour).

Sample collection and sequencing

Rectal swab and home stool samples were collected from subjects prior to routine bowel preparation and colonoscopy for polyp detection using Metabionics Home Microbiome Sampling Kit (Metabionics). These kits used Puritan Flock Swabs and prefilled collection tubes with RNALater as a preservative. Rectal swab samples were collected at the time of the initial screening visit and subjects were provided with the kits and instructions for home stool sampling. Biopsies were collected from subjects during colonoscopy and stored in RNALater. Samples were kept at -20°C in RNALater until extraction using FastDNA Spin Kit for Soil (MP Biomedicals, Solon, CA, USA). Sequencing was performed using tagged V1–V2 bacterial 16S rRNA primers (F21F-R355R) on the Ion Torrent Personal Genome Machine (Thermo Fisher Scientific, Waltham, MA, USA) located at the Microbiome Analysis Center, George Mason University.

Preprocessing and OTU selection

Based on colonoscopy results, subjects were categorised into two groups: polyp negative (polyp-N) and polyp positive (polyp-Y). Preprocessing, OTU clustering, and construction of an OTU abundance table were performed using UPARSE.³⁰ Further detail about the preprocessing step is available in the online supplementary methods.

Alpha and beta diversity

Alpha and beta diversity was analysed using *mothur*.³¹ After generating abundance tables, alpha (within subject) diversity measurements of richness and evenness and the identification of the presence or absence of specific taxa were performed. Rarefaction curves were drawn to analyse the sequencing depth. Samples with fewer than 5000 reads were removed. Alpha diversity indices such as Shannon, Simpson, *inv*simpson, and observed species (*sobs*) were calculated for all of the samples and compared between the polyp-Y and polyp-N groups using the Kruskal-Wallis test. The community diversity was compared between polyp-Y and polyp-N groups using permutational multivariate analysis of variance (PERMANOVA) and analysis of similarities (ANOSIM). Further detail about the beta diversity analysis (ie, unique fraction and principal coordinates analysis) is available in the online supplementary methods.

OTU ranking, classification, classifier validation, and predictions

Statistical tests such as Kruskal-Wallis, MetaStats,³² linear discriminant analysis (LDA) effect size (LEfSe),³³ and

indicator^{34 35} were used to identify informative OTUs or features that were significantly different between polyp-Y and polyp-N groups.

Several machine learning classification models were built (Naïve Bayes, decision tree, logistic regression, random forest, K-nearest neighbour, Neural Network, and support vector machine) using the Orange data mining tool, V.2.7 (<http://orange.biolab.si/>).³⁶ Classification was performed separately for the biopsy, stool, and rectal swab data sets. Using the fivefold cross-validation method, 80% of samples were chosen as the training set, and the rest were used as the test set. Classification was performed under two different conditions: (1) with all detected OTUs as classification features, and (2) with informative OTUs that were detected by the statistical methods described above. This cross-validation method was used to evaluate each of the classifiers and their classification accuracy, sensitivity, specificity, and area under the curve.

Naïve test data sets were generated using a Waikato Environment for Knowledge Analysis (Weka V.3.8.0)³⁷ module to assess the predictive power of the best performing classifiers for risk assessment. The generated classifiers were validated using the 10-fold cross-validation method and used to predict classes for the naïve test set. The classification accuracy was then averaged over all of the naïve test sets.

RESULTS

Participant characteristics and sample collection

From a cohort of 231 subjects in the Washington, DC, metro area undergoing screening or surveillance colonoscopy, we collected samples and clinical data from 218 subjects (male, n=131; female, n=87). The average age was 62 years and average body mass index (BMI) was 27 kg/m². Most subjects were White (n=193; 88%), 21 were African-American (10%), and 4 were Asian-American (2%). Over half of the subjects (n=124) had a history of polyps. Across all subjects, 552 samples were collected. Not all subjects submitted all types of specimens, which resulted in the collection of 138 biopsy, 183 home stool, and 231 rectal swab samples that were subsequently analysed. There was 79% compliance with submission of home stool samples after the initial rectal swab samples were collected.

Incidence of polyp pathology

Colonoscopy detected polyps in 56% of the subjects. All subjects presented with benign polyps. Adenomas, advanced adenomas, and high-risk adenomas were observed, respectively, in 50%, 2%, and 21% of the polyp-positive subjects. This incidence of high-risk adenomas (n=27, 11.8%) in the study was higher than would be expected in the general population, possibly because more than half of the study cohort (n=124) had a history of polyps and were undergoing surveillance colonoscopy.

Preprocessing and clustering

The number of original reads collected for the 552 samples (polyp-Y=316, polyp-N=236) was 12 646 278 and the number of reads after preprocessing used for OTU clustering was 4 377 359. The total number of OTUs detected by UPARSE was 2631.

Rarefaction plots indicated that sequencing depth was acceptable for the large majority of samples, and the reads should have adequately identified the number of species in the samples, online supplementary figure S1. In total, 13 biopsy, 15 home stool, and 20 presurgery rectal swab samples were omitted at this step, as samples with <5000 reads were removed.

Alpha and beta diversity

Simpson, invsimpson, and sobs indices were significantly different among the polyp-Y and polyp-N groups in all three data sets ($p < 0.001$). Shannon diversity had a significant change in median rank of samples' diversity between the groups only in the biopsy data set ($p = 0.039$), online supplementary figure S2. Comparison of alpha diversity and change of taxa abundance at the phylum and genera levels are shown in online supplementary tables S2 and S3.

PERMANOVA analysis indicated that there was a significant difference for the weighted UniFrac distances between the polyp-Y and polyp-N groups in the biopsy data set ($p = 0.03$). However, unweighted UniFrac was not statistically distinctive between groups in this data set. Moreover, there was no statistical difference in the Bray-Curtis distances plus weighted and unweighted UniFrac measurements for home stool and rectal swab samples based on PERMANOVA ($p > 0.05$), online supplementary figures S3, and S4.

Informative OTUs

We identified the informative OTUs that differed between the polyp-Y and polyp-N groups by performing statistical tests with 1000 permutations using MetaStats, Kruskal-Wallis, LEfSe, and indicator species analyses and used these informative features for classification.

MetaStats³² is a statistical approach designed to identify differentially abundant features in metagenomic and 16S rRNA sequence data sets. This programme uses the non-parametric t-test, Fisher's exact test, and the false discovery rate to provide users with a prioritised list of remarkable features that define differences between two classes.

The Kruskal-Wallis test uses a rank-ordered one-way analysis of variance and is a method for testing whether samples originate from the same distribution. It is used for comparing two or more independent samples of equal or different sample sizes. It extends to the Mann-Whitney U test when there are more than two groups. A significant Kruskal-Wallis test indicates that at least one sample stochastically dominates over at least one other sample.

The LEfSe³³ is an algorithm for high-dimensional biomarker discovery and detection of genomic features such as genes, pathways, and taxa that can characterise the differences between two or more biological classes. This algorithm is helpful to identify differentially abundant features that are also consistent with biologically meaningful categories (classes) by taking into account both statistical significance and biological relevance. It first detects statistically different features using the non-parametric Kruskal-Wallis sum-rank test and then uses another pairwise test (Wilcoxon) to determine whether the detected differences are consistent with biological behaviour. LDA is used to estimate the biological effect of each differentially abundant feature.

The indicator metric is another statistically based tool developed to find the indicator species (eg, OTUs) that define a distinctive aspect or characteristic of an environment. Indicator combines the species relative abundance with the relative frequency of occurrence in various classes. When all the individuals of a species are represented in one group, and all the species appear in all the samples of that group, the indicator index is defined as high. A randomisation method is used to find the statistical significance of the metric. The indicator index for each species is independent of the other species relative abundance and is independent of classification approaches.^{34 35}

These four approaches identified 109, 59, and 92 informative OTUs for biopsy, home stool, and rectal swab samples, respectively, from the original 2631 OTUs.

Online supplementary tables S4, S5 and S6 show the differentially detected OTUs for each of the three data sets. The informative OTUs at each taxonomic level were used as classification features to improve the classifiers' performance. Bar plots of the normalised abundance of

the informative OTUs are presented in online supplementary figures S5, S6 and S7 for biopsy, home stool, and rectal swab samples, respectively. It can be seen that some taxa are enriched while others are depleted in the polyp-Y group compared with the polyp-N group.

Some OTUs show the same pattern of change in all three sample types. For example, *Bacteroides* is enriched in the polyp-Y group in the biopsy, stool, and rectal swab samples; however, other OTUs show different patterns in the different sample types. For instance, *Blautia* shows enrichment in the polyp-Y group in stool and rectal swab samples and depletion in the polyp-Y biopsies, while *Faecalibacterium* was increased in the polyp-Y rectal swab and decreased in the polyp-Y stool samples.

Classification using all OTUs and informative OTUs

As shown in online supplementary table S7, in all specimen types (biopsy, stool, and rectal swab samples), the classification accuracy, sensitivity, specificity, and area under the receiver operating characteristic (ROC) curve improved by using informative OTUs for classification instead of all OTUs. For example, the Naïve Bayes classification accuracy for all OTUs for the home stool samples was 0.40 but increased to 0.75 when informative OTUs were used. Similarly, the Neural Network classification accuracy for all OTUs for the home stool samples was 0.50 but increased to 0.77 when informative OTUs were used. The ROC curves for biopsy, home stool, and rectal swab data sets are shown in figure 1. The home stool samples were chosen for the naïve predictions below.

The Naïve Bayes and Neural Network models appeared to be the best performing classifiers. Specifically, the classification accuracy of the Naïve Bayes model on the informative OTUs was 0.77, 0.75, and 0.72 for biopsy, home stool, and rectal swab samples, respectively. Similarly, the

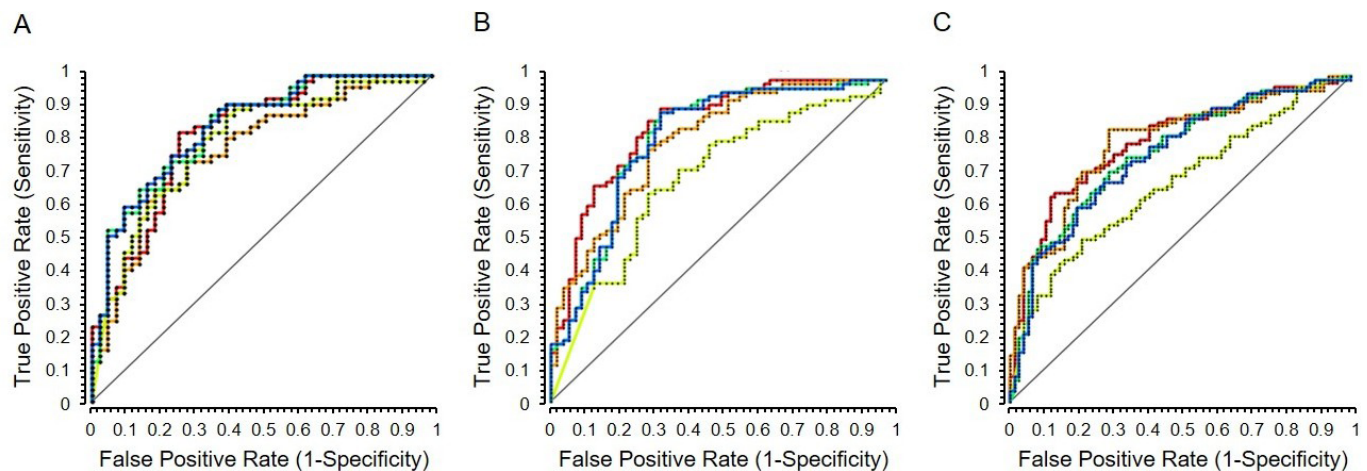


Figure 1 Receiver operating characteristic (ROC) curves for five classifiers using informative operational taxonomic units (OTU) for biopsy, home stool, and rectal swab data sets. The evaluated classifiers included Naïve Bayes (red), random forest (orange), K-nearest neighbour (yellow), logistic regression (green), and Neural Network (blue). The straight line represents the null model. (A) For the biopsy data set, the best performing classifier was Naïve Bayes with area under the curve (AUC) equal to 0.85. (B) For the home stool data set, the best performing classifiers were Naïve Bayes and random forest with AUC=0.83. (C) For the rectal swab data set, the best performing classifiers were random forest with AUC=0.81 and Naïve Bayes with AUC=0.80.

Table 1 Classification accuracy of the Naïve Bayes and Neural Network models for the home collected stool samples using naïve test sets

Model	Classification accuracy	Sensitivity (true positive rate)	Specificity (true negative rate)	AUC
Naive Bayes	79%	83%	72%	86%
Neural Network	82%	86%	75%	87%

AUC, area under the curve;

classification accuracy of the Neural Network model on the informative OTUs was 0.74, 0.77, and 0.67 for biopsy, home stool, and rectal swab samples, respectively. As such, these models were selected for the naïve predictions of the home stool samples.

Naïve prediction using informative features

Using the prediction pipeline that we developed using the Orange data mining tool, the predictive powers of the best performing classifiers (Naïve Bayes and Neural Network) were evaluated. For each of the sample types (biopsy, stool, and rectal swab), 90% of samples were used for training and 10% were used as the holdout test data set. From a total of 125 biopsy samples, 8 of 13 test samples (61.5%) were predicted correctly as shown in online supplementary table S8. From the total of 168 stool samples, 12 of 17 test samples (82.3%) were predicted correctly as shown in online supplementary table S9. From the total of 211 rectal swab samples, 18 of 22 test samples (81.8%) were predicted correctly as shown in online supplementary table S10.

Risk assessment of home collected stool samples using informative features

The classification results for the home stool samples were analysed in greater detail. Naïve test data sets were

generated using Weka. The Naïve Bayes and Neural Network classifiers were used to build models that were then used to predict classes for the naïve test set. This was repeated 10 times and the classification accuracy was then averaged over all of the naïve test sets. Table 1 shows the accuracy of the average classification of the stool samples using the naïve test sets. The Naïve Bayes and Neural Network classifiers have 79% and 82% classification accuracy, respectively, with an average false positive rate of 12% and an average false negative rate of 11.5%. However, all samples did not have the same result for each classifier, as shown in table 2, where there are different numbers of false positives and false negatives for each classification model. The more important issue in risk assessment is the false negative rate, as this risk assessment would result in a non-recommendation for colonoscopy for an at-risk individual.

Figure 2 is a box plot of the classification scores for the naïve predictions of the home stool samples. Classification score distributions for the Naïve Bayes true positives and the Neural Network true positives are very similar. Likewise, classification score distributions for the true negatives are comparable for the Naïve Bayes and Neural Network classifiers. However, there are differences between the classification score distributions of the

Table 2 Confusion matrix for the Naïve Bayes and Neural Network models for the home collected stool samples using naïve test sets

Model	Count	Score HS_Polyp_Y	Score HS_Polyp_N	Classification
Naïve Bayes	17**	27%	73%	FN
Naïve Bayes	19	82%	18%	FP
Naïve Bayes	50	10%	90%	TN
Naïve Bayes	82	90%	10%	TP
Neural Network	14††	22%	78%	FN
Neural Network	17	83%	17%	FP
Neural Network	52	11%	89%	TN
Neural Network	85	90%	10%	TP

*False negatives using Naive Bayes model

†False negatives using Neural Network model

AUC, area under the curve; FN, false negative; FP, false positive; HS, home collected stool sample; HS_Polyp_N, Home Stool from subjects without polyps; HS_Polyp_Y, Home Stool from subjects with Polyps; Polyp_N, polyp-negative group; Polyp_Y, polyp-positive group; TN, true negative; TP, true positive.

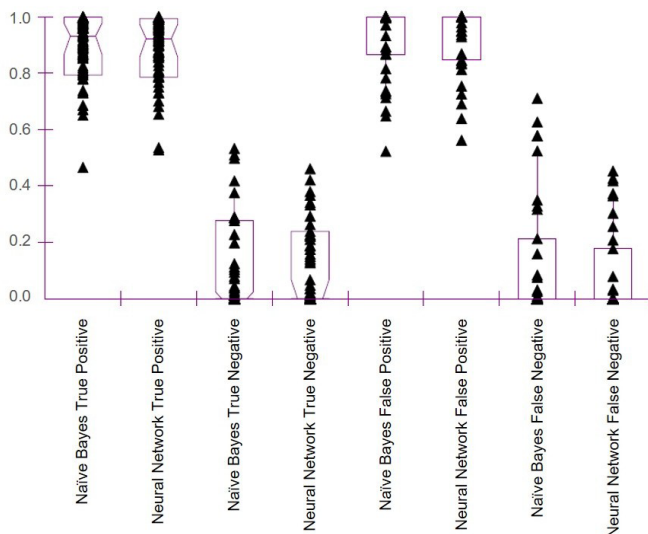


Figure 2 Naïve Bayes and Neural Network classification scores for the naïve predictions of the home stool samples.

false positives and false negatives compared with the true positives and true negatives. Thus, one cannot use the p values of either classifier alone to clarify the confusion matrix.

A total of 22 subjects were classified as false negative by either model; however, only nine subjects (5%) were classified as false negative by both models (tables 3 and 4), suggesting improved predictive accuracy of using a composite score from both models.

DISCUSSION

We sought to characterise the gut microbiome in a prospective cohort of subjects with and without colorectal polyps using home collected stool, presurgery rectal swab, and biopsy samples, and use statistical methods and advanced machine learning to build classifying predictors for the presence of polyps.

Although bacterial dysbiosis has been reported in virtually all CRC/adenoma microbiome studies as well as in our research, the microbial features that have been found to differ significantly are not the same, and are in some cases contradictory. We expected that the comparison of OTUs (ie, taxa) reported in previously published studies and those identified in our own work would have many common species and would change in abundance along with the appearance of polyps. Indeed, some bacterial taxa identified by our study were previously reported to be associated with adenoma/CRC. These include the Firmicutes, Bacteroidetes, and Proteobacteria phyla, *Bacteroides*, *Roseburia*, *Bifidobacterium*, *Faecalibacterium*, and *Blautia* genera, as well as *Bacteroides fragilis* and *Faecalibacterium prausnitzii* species. However, the direction of change was not collinear in all the studies. One possible explanation is the difference in species and strain composition between study populations and partial overlap between the biochemical functions of particular microbes. Another possible explanation is the presence of certain

clinical confounders (eg, differences in BMI, age, and medications), differences in ethnic backgrounds and dietary habits, or differences in sequencing methods employed, 16S variable region analysed, and analytical pipelines used which may influence the study outputs.

When individuals with polyps in our study were compared with those with normal colonoscopy results, their microbial profiles were different in all three types of the specimens. Even for the same individual, the microbial profiles of their biopsy, stool, and rectal swab samples differed. These observations are consistent with previous studies.^{14 21} A summary of alpha diversity results from this study and 17 other CRC and adenoma studies along with those phyla significantly changed are summarised in online supplementary table S11. Six of these 17 studies reported higher alpha diversity in adenoma or cancer groups, four studies observed lower diversity in the adenoma or cancer group, and three studies indicated no significant change in the diversity of the cancer or adenoma group compared with healthy control subjects.^{12 14 16 18 21 27 38 39}

At the phylum level, the most commonly reported significant differences of microbial abundancies among healthy control, adenoma, and CRC samples are for Firmicutes, Bacteroidetes, and Proteobacteria. Some studies have shown increased abundance of Firmicutes in adenoma/CRC samples while other studies reported relative depletion of this phylum.^{11 15 16 27 38–41} Similarly, a number of reports described an increase in abundance of Bacteroidetes in patients with adenoma/CRC while others reported a decrease in abundance of this phylum.^{11 12 15 16 18 21 38–41} In our polyp data set, Firmicutes and Bacteroidetes phyla were significantly more abundant in the polyp-Y samples compared with the polyp-N group.

Among the 17 studies of adenoma/CRC listed in online supplementary table S11, eight data sets contained information on Proteobacteria. In five out of six adenoma studies which reported Proteobacteria abundance, this phylum was represented at higher levels in the adenoma state.^{12 16 24 39 40} Among six CRC studies two detected higher Proteobacteria abundance with CRC, and two data sets reported lower abundance with CRC.^{23–26} In one study that analysed three types of samples—tumour, swab, and stool—an increase in Proteobacteria abundance in the stool of the CRC group and a decrease of this phylum in both the tumour and swab samples were reported.¹⁴ In our polyp data set, analysis of both rectal swab and stool samples revealed an increase in Proteobacteria abundance, but lower abundance of Proteobacteria in polyp biopsies compared with the normal colon biopsies.

At the genus level, the abundancies of *Bifidobacterium*, *Faecalibacterium*, and *Blautia* were decreased in our polyp biopsies as compared with normal colon mucosa, while in the rectal swab and stool samples of the subjects with polyps, their abundancies (except for *Faecalibacterium*) were higher than that in subjects with healthy colons. Possibly, the polyp-associated gut microbiota shifts

Table 3 Classification scores and predictions for the 22 subjects with polyps whose home stool samples were called false negative on Naïve Bayes and/or Neural Network models

Sample ID	Class	Classifier	Score HS_Polyp_Y	Score HS_Polyp_N	Predicted	Call
A. Subjects where both models call FN						
HS_23	HS_Polyp_Y	Naïve Bayes	0.007	0.993	HS_Polyp_N	FN
		Neural Network	0	1	HS_Polyp_N	FN
HS_341	HS_Polyp_Y	Naïve Bayes	0.159	0.841	HS_Polyp_N	FN
		Neural Network	0.177	0.823	HS_Polyp_N	FN
HS_372	HS_Polyp_Y	Naïve Bayes	0.213	0.787	HS_Polyp_N	FN
		Neural Network	0.208	0.792	HS_Polyp_N	FN
HS_381	HS_Polyp_Y	Naïve Bayes	0.005	0.995	HS_Polyp_N	FN
		Neural Network	0.373	0.627	HS_Polyp_N	FN
HS_384	HS_Polyp_Y	Naïve Bayes	0.026	0.974	HS_Polyp_N	FN
		Neural Network	0.256	0.744	HS_Polyp_N	FN
HS_386	HS_Polyp_Y	Naïve Bayes	0.35	0.65	HS_Polyp_N	FN
		Neural Network	0.418	0.582	HS_Polyp_N	FN
HS_413	HS_Polyp_Y	Naïve Bayes	0.328	0.672	HS_Polyp_N	FN
		Neural Network	0.427	0.573	HS_Polyp_N	FN
HS_423	HS_Polyp_Y	Naïve Bayes	0.01	0.99	HS_Polyp_N	FN
		Neural Network	0.002	0.998	HS_Polyp_N	FN
HS_461	HS_Polyp_Y	Naïve Bayes	0.578	0.422	HS_Polyp_N	FN
		Neural Network	0.303	0.697	HS_Polyp_N	FN
B. Subjects where one model calls FN and the other calls TP						
HS_363	HS_Polyp_Y	Naïve Bayes	0.779	0.221	HS_Polyp_Y	TP
		Neural Network	0.034	0.966	HS_Polyp_N	FN
HS_367	HS_Polyp_Y	Naïve Bayes	0.905	0.095	HS_Polyp_Y	TP
		Neural Network	0.365	0.635	HS_Polyp_N	FN
HS_373	HS_Polyp_Y	Naïve Bayes	0.578	0.422	HS_Polyp_N	FN
		Neural Network	0.992	0.008	HS_Polyp_Y	TP
HS_403	HS_Polyp_Y	Naïve Bayes	0.627	0.373	HS_Polyp_N	FN
		Neural Network	0.982	0.018	HS_Polyp_Y	TP
HS_407	HS_Polyp_Y	Naïve Bayes	0.076	0.924	HS_Polyp_N	FN
		Neural Network	0.991	0.009	HS_Polyp_Y	TP
HS_412	HS_Polyp_Y	Naïve Bayes	0.317	0.683	HS_Polyp_N	FN
		Neural Network	0.528	0.472	HS_Polyp_Y	TP
HS_417	HS_Polyp_Y	Naïve Bayes	0.894	0.106	HS_Polyp_Y	TP
		Neural Network	0.03	0.97	HS_Polyp_N	FN
HS_420	HS_Polyp_Y	Naïve Bayes	0.524	0.476	HS_Polyp_N	FN
		Neural Network	0.654	0.346	HS_Polyp_Y	TP
HS_427	HS_Polyp_Y	Naïve Bayes	0.084	0.916	HS_Polyp_N	FN
		Neural Network	0.536	0.464	HS_Polyp_Y	TP
HS_45	HS_Polyp_Y	Naïve Bayes	0.651	0.349	HS_Polyp_Y	TP
		Neural Network	0.079	0.921	HS_Polyp_N	FN
HS_507	HS_Polyp_Y	Naïve Bayes	0.711	0.289	HS_Polyp_N	FN
		Neural Network	0.682	0.318	HS_Polyp_Y	TP
HS_6	HS_Polyp_Y	Naïve Bayes	0.031	0.969	HS_Polyp_N	FN
		Neural Network	0.731	0.269	HS_Polyp_Y	TP
HS_62	HS_Polyp_Y	Naïve Bayes	0.686	0.314	HS_Polyp_Y	TP
		Neural Network	0.453	0.547	HS_Polyp_N	FN

Continued

**Table 3** Continued

Sample ID	Class	Classifier	Score HS_ Polyp_Y	Score HS_ Polyp_N	Predicted	Call
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Classification scores are presented for each model and subject where the true class (ie, Polyp-Y or Polyp-N) is tabulated along with the model scores and predictions.

FN, false negative; HS, home collected stool sample; Polyp_N, polyp-negative group; Polyp_Y, polyp-positive group; TP, true positive.

relative abundancies towards more harmful bacteria, while beneficial bacteria are displaced into the lumen and gradually shed with the stool.

At the species level, the pathogens *Fusobacterium nucleatum* and *B. fragilis* did not show enrichment in subjects with polyps in our study, as has been reported in other CRC data sets. As the origin and aetiology of CRC may be different based on the tumour location,^{42 43} it is possible that *F. nucleatum* and *B. fragilis* contribute to the development of polyps or malignant transformations of adenomatous polyps in some locations, but not others. Another confounding factor is that many of the subjects in our study were so-called ‘polyp producers’ who were monitored more frequently for removal of new polyps. Due to the possible genetic component, the aetiology of polyps in this group probably differed from that in the general population.

Supervised machine learning methods are useful for finding patterns in highly complex data sets like human microbiota surveys.⁴⁴ Moreover, we introduced informative feature selection as an additional step for classification to find a combination of feature subsets that would lead to better classifiers.⁴⁵ To decrease the complexity of the analysis in our study, we used independent non-parametric statistical tools to find significant differences between the polyp-Y and polyp-N groups to select OTUs that are associated with a shift from normal state to disease state.

Thus, we undertook a comparison of eight classification methods, four feature selection approaches, and four accuracy metrics. We focused on supervised classification methods, as unsupervised methods like clustering are not suitable for predictions and assigning naïve data to a specific class.^{46 47} We first performed classification with the complete relative abundance OTU table using all OTUs and then with relative abundance tables of just the informative OTUs. For all three data sets of biopsy, stool, and rectal swab samples, the accuracy of classification, sensitivity, and specificity of classification as well as

the area under the ROC curve were improved by using the informative features, demonstrating that most OTUs were not informative and removing them improved the model performance. As an added benefit, analysis of a reduced data set requires less computational power.

Widespread screening for CRC results in earlier diagnosis (when the disease is more easily treated) and primary prevention,⁶ yet remains underused. An affordable, non-invasive or minimally invasive tool for risk assessment for the presence of polyps would have the potential to increase acceptability of colonoscopy by individuals categorised as high risk for CRC,⁴⁸ that in turn could have a salient effect on CRC morbidity and mortality. Such a tool would have the additional benefit of reducing healthcare costs by avoiding screening colonoscopies in individuals without polyps.

In our study, advanced machine learning with Naïve Bayes and Neural Network classifiers resulted, respectively, in 79% and 82% classification accuracy of stool samples from subjects with and without polyps, although false positive and false negative classifications averaged 12% and 11.5%. False positive classifications are less problematic than false negative classifications; however, the number of subjects classified as false negative by both models was reduced to 5%, and it is likely that both sensitivity and specificity of the modelling could be improved by increasing cohort size. By comparison, existing in vitro diagnostics that have been recommended by the US Preventive Services Task Force for CRC screening have minimal or no reported sensitivity to colon polyps.^{49 50}

In summary, this study focused on the comparative investigation of the statistical analysis and machine learning methods applicable to colorectal microbiome studies. The informative features were selected a priori using Kruskal-Wallis, MetaStats, LEfSe, and indicator species in Mothur. This selection was independent from the machine learning classification. We expect that specific taxa will be identified in larger cohorts using this approach.

The key thrust of this study was to circumvent the overfitting inherent in machine learning methods by the independent selection of informative features using non-parametric techniques. Furthermore, the fact that this approach yielded higher classification accuracy on naïve data sets suggests that these informative features are robust and likely associated with disease progression. We currently are applying this approach in a meta-analysis of published data to verify the utility of the method.

Table 4 Summary for the adjusted composite confusion matrix for home stool samples

Call	False negative	False positive	True positive	True negative
n	9	22	90	47
Rate (of 168 subjects)	5%	13%	54%	28%

Subjects that had mixed false negative and true positive calls by the two models were binned as true positive.

By optimising the analytical pipeline, we were able to improve extraction of informative OTUs, thereby also improving the predictive power of resultant classifier models in identifying the presence of polyps in the human colon. It is possible that the best classifying features are also important in the aetiology of CRC. However, before microbiome-based classifiers could be introduced to clinical practice, additional biomarkers with predictive value will need to be identified and further validation in independent and much larger, ethnically diverse cohorts should be performed.

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Competing interests GK, TK, and PMG have founders' stock and LK, RH, and JB have stock options in Metabionics.

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Data availability statement The data sets analysed during the current study are available from the corresponding author on reasonable request and will be submitted to the Sequence Read Archive.

Author note The data for this manuscript has been deposited in Genbank. The accession number to the manuscript is PRJNA534511.

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