

# THE PROGRAMMING OF THE HOMOLOGY CALCULATION OF DIHEDRAL QUANDLES R VERSION

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ABSTRACT. This paper aims to serve both as a documentation and an explanation of the implementation in R of the algorithm for the calculation of the homology of racks, quandles and their biversions as detailed in [1]

## 1. INTRODUCTION

This paper is divided into two parts. The first chapter comprises the commented code. The second chapter explains the thinking behind the implementation, in particular where there are differences to the algorithm defined in [1]. The notation does also follow the notation in the aforementioned paper. Please note that this will hopefully also be coded in C in order to a) speed up the runtime and b) lower memory usage.

## 2. THE CODE

The code is organised into (currently) three different files. The first consists of two subroutines for the calculation of the Smith Normal Form and to find the matrix X. Then there is the main function to calculate the homology. The input, degree, k, degenerate, are used for dihedral quandles in particular and only used for the calculation of the boundary matrices <sup>1</sup> and the subsequent output of the calculation result.

```
1 #first load the packages necessary for third-party functions.
2 library(Matrix)
3 library(schoolmath)
4 library(MASS)
5 library(numbers)
6
7 #first define the subfunctions
8
9 #this is used to calculate the left elementary matrix X
10 findX <- function(A){
11   X <- diag(nrow(A))      #create Identity matrix
12   G_X <- cbind(A,X)       #combine identity matrix with original matrix for Gaussian
                             elimination
13   GX_res <- GaussianElimination(G_X) #Gaussian elimination
14   X <- GX_res[, (ncol(GX_res)-nrow(A)+1):ncol(GX_res)] #extract the left matrix, X
```

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<sup>1</sup>to do

```

15   return(X)
16 }
17
18 #this calculates the smith normal form based on the calculation of the Hermite
   Normal Form.
19 #In particular, HNF((HNF(A))^T)
20 smith <- function(A){
21   HF <- hermiteNF(A)$H
22   S <- hermiteNF(t(HF))$H
23   return(S)
24 }
25 #here is the main function to calculate the homology
26 homology <- function(degree,k,degenerate){
27   boundary_F <- matrix(nrow=12,ncol=6,byrow=T,data=c
      (1,-1,0,0,1,0,1,-1,-1,0,0,0,-1,1,1,0,0,-1,1,0,0,0,1,-1,0,1,-1,0,1,-1,0,0,0,0,-1,1,0,
      )#a matrix - Matrix(,sparse=TRUE)
28   boundary_G <- matrix(c(-1,0,1,-1,1,0,0,-1,1,1,-1,0,0,1,-1,1,0,-1),ncol=3,nrow=6,
      byrow=T)#another matrix
29   rho <- rankMatrix(boundary_G)[1] #first, this calculates the rank of the matrix G
      . This removes the need to calculate D and Y later.
30   q <- nrow(boundary_G)
31   r <- ncol(boundary_G)
32   q_rho <- q - rho
33   X <- findX(boundary_G)
34   Z <- X[(rho + 1):q, ] #only take the rows that map to zero (i.e. only the
      boundaries)
35   B <- GaussianElimination(boundary_F) #identify the cycles, i.e. remove the
      boundaries via Gaussian elimination
36   B <- B[which(rowSums(abs(B))!=0), ] #remove the boundaries in order to lower
      memory allocation
37   N <- round(Z %*% ginv(B)) #calculate N. Details in documentation
38   S <- smith(N)
39   Delta <- diag(S) #Extract the values necessary for the output.
40   s <- length(Delta)
41   l <- 0
42   ones <- 0
43   output <- c()
44   for(i in 1:s){
45     if(Delta[i]==1){
46       ones <- ones + 1 #count number of ones
47     }
48     else if(Delta[i]!=0){
49       l <- l + 1
50       output <- append(output,Delta[i]) #count and extract nonzero and non-one
      values in the diagonal
51     }
52     else{
53       break
54     }
55   }
56
57   #the following is the output depending on the number of zeroes.
58   if(s>l+ones){#check if there are any values not equal to one or zero

```

# THE PROGRAMMING OF THE HOMOLOGY CALCULATION OF DIHEDRAL QUANDLES R VERSION3

```

59     print(paste0("The ",degree,ifelse((degree%%10)==1,"st",ifelse((degree%%10)==2,"
      "nd",ifelse((degree%%10)==3,"rd","th")))," homology group of R_",k," is
      isomorphic to Z^",s-(k+ones)," plus the following:"))
60 } else{
61     print(paste0("The ",degree,ifelse((degree%%10)==1,"st",ifelse((degree%%10)==2,"
      nd",ifelse((degree%%10)==3,"rd","th")))," homology group of R_",k," is
      isomorphic to the following:"))
62 }
63 if(l>0){ #if so, print out the resulting Z_n groups
64     for(i in 1:l){
65         print(paste0("Z_",Delta[ones+i],ifelse(i!=1," plus","")))
66     }
67 }
68 else{
69     print("0")
70 }
71 }

```

. ../R\_code/homology\_calculation.R

The second file collects two functions written by other people. In particular, the function for Gaussian Elimination is used.

```

1 #this is a collection of other peoples function, used for the homology calculation.
2 #in particular, the Gaussian elimination is used.
3
4 GaussianElimination <- function(A, B, tol=sqrt(.Machine$double.eps),
5                                verbose=FALSE, fractions=FALSE){
6     # A: coefficient matrix
7     # B: right-hand side vector or matrix
8     # tol: tolerance for checking for 0 pivot
9     # verbose: if TRUE, print intermediate steps
10    # fractions: try to express nonintegers as rational numbers
11    # If B is absent returns the reduced row-echelon form of A.
12    # If B is present, reduces A to RREF carrying B along.
13    if (fractions) {
14        mass <- require(MASS)
15        if (!mass) stop("fractions=TRUE needs MASS package")
16    }
17    if ((!is.matrix(A)) || (!is.numeric(A)))
18        stop("argument must be a numeric matrix")
19    n <- nrow(A)
20    m <- ncol(A)
21    if (!missing(B)){
22        B <- as.matrix(B)
23        if (!(nrow(B) == nrow(A)) || !is.numeric(B))
24            stop("argument must be numeric and must match the number of row of
25                A")
26        A <- cbind(A, B)
27    }
28    i <- j <- 1
29    while (i <= n && j <= m){
30        while (j <= m){
31            currentColumn <- A[,j]
32            currentColumn[1:n < i] <- 0
33            # find maximum pivot in current column at or below current row

```

```

34     which <- which.max(abs(currentColumn))
35     pivot <- currentColumn[which]
36     if (abs(pivot) <= tol) { # check for 0 pivot
37         j <- j + 1
38         next
39     }
40     if (which > i) A[c(i, which),] <- A[c(which, i),] # exchange rows
41     A[i,] <- A[i,]/pivot # pivot
42     row <- A[i,]
43     A <- A - outer(A[,j], row) # sweep
44     A[i,] <- row # restore current row
45     if (verbose) if (fractions) print(fractions(A))
46     else print(round(A, round(abs(log(tol,10))))))
47     j <- j + 1
48     break
49 }
50 i <- i + 1
51 }
52 # 0 rows to bottom
53 zeros <- which(apply(A[,1:m], 1, function(x) max(abs(x)) <= tol))
54 if (length(zeros) > 0){
55     zeroRows <- A[zeros,]
56     A <- A[-zeros,]
57     A <- rbind(A, zeroRows)
58 }
59 rownames(A) <- NULL
60 if (fractions) fractions (A) else round(A, round(abs(log(tol, 10))))
61 }
62
63 rref <- function(A, tol=sqrt(.Machine$double.eps),verbose=FALSE,
64                 fractions=FALSE){
65     ## A: coefficient matrix
66     ## tol: tolerance for checking for 0 pivot
67     ## verbose: if TRUE, print intermediate steps
68     ## fractions: try to express nonintegers as rational numbers
69     ## Written by John Fox
70     if (fractions) {
71         mass <- require(MASS)
72         if (!mass) stop("fractions=TRUE needs MASS package")
73     }
74     if ((!is.matrix(A)) || (!is.numeric(A)))
75         stop("argument must be a numeric matrix")
76     n <- nrow(A)
77     m <- ncol(A)
78     for (i in 1:min(c(m, n))){
79         col <- A[,i]
80         col[1:n < i] <- 0
81         # find maximum pivot in current column at or below current row
82         which <- which.max(abs(col))
83         pivot <- A[which, i]
84         if (abs(pivot) <= tol) next # check for 0 pivot
85         if (which > i) A[c(i, which),] <- A[c(which, i),] # exchange rows
86         A[i,] <- A[i,]/pivot # pivot
87         row <- A[i,]
88         A <- A - outer(A[,i], row) # sweep

```

```

89   A[i,] <- row                                # restore current row
90   if (verbose)
91     if (fractions) print(fractions(A))
92   else print(round(A,round(abs(log(tol,10))))))
93 }
94 for (i in 1:n)
95   if (max(abs(A[i,1:m])) <= tol)
96     A[c(i,n),] <- A[c(n,i),] # 0 rows to bottom
97   if (fractions) fractions (A)
98   else round(A, round(abs(log(tol,10))))
99 }

```

. ../R\_code/found\_functions.R

The third file contains the function to calculate boundary matrices for (bi)racks and (bi)quandles based on the Switch equation and in  $\mathbb{Z}_k$ , in particular the dihedral quandles. The up and down actions are called in their respective functions and can easily be changed.<sup>2</sup>

```

1 #this collects all the functions necessary for the calculation of boundary matrices
  of (bi)quandles
2
3 up_action <- function(a,b,k){
4   result <- (2 * b - a) %% k
5   return(result)
6 }
7
8 down_action <- function(a,b,k){
9   return(a)
10 }

```

. ../R\_code/boundary\_calculations.R

### 3. EXPLANATION

The code mostly follows the algorithm as laid out in [1]. There are a few differences, as follows:

- We do calculate neither XGY nor Y itself. This is due to the fact that XGY is only used as a proxy to calculate the rank and that Y is never used again. We think it faster and more memory effective to calculate the rank directly.
- We do not have XGY with D in the lower right, but rather in the top left corner. Thus, we do not use the first  $q - \rho$  rows but rather the last  $q - \rho$  rows.
- We also use Gaussian elimination to calculate the span of the rowspace of F or Z, depending on Notation.
- The  $N \vdash \text{round}(Z \% \% \text{ginv}(B))$  equation<sup>3</sup> follows by simple arithmetic.
- Finally, instead of coding a Smith Normal Form Algorithm (of which there are plenty!), we use the Hermitian Normal Form function from the numbers package in R.

<sup>2</sup>this is still in progress

<sup>3</sup> $\% \%$  is matrix multiplication in R,  $\vdash$  is equivalent to  $=$  and  $\text{ginv}$  is the general inverse of a  $m \times n$  matrix

## 4. USED SOFTWARE

This programme was written in R and used the following packages:

- R base installation, version 3.0.1 (2013-05-16) "Good Sport", [2].
- Matrix, [3].
- schoolmath, [4].
- MASS, [5].
- numbers, [6].

## REFERENCES

- [1] R. Fenn, *How to Calculate Homology*, 2013, unpublished.
- [2] R Core Team (2013). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL <http://www.R-project.org/>.
- [3] D. Bates & M. Maechler (2013). Matrix: Sparse and Dense Matrix Classes and Methods. R package version 1.0-12. <http://CRAN.R-project.org/package=Matrix>.
- [4] J. Schlarmann & J. Wienand (2012). schoolmath: Functions and datasets for math used in school. R package version 0.4. <http://CRAN.R-project.org/package=schoolmath>
- [5] W. N. Venables & B. D. Ripley (2002) Modern Applied Statistics with S. Fourth Edition. Springer, New York. ISBN 0-387-95457-0
- [6] H. W. Borchers (2012). numbers: Number-theoretic Functions. R package version 0.3-3. <http://CRAN.R-project.org/package=numbers>