

# Modeling of Yarn Hairiness

Jiří Militký<sup>1)</sup>, Sayed Ibrahim<sup>2)</sup> and Dana Křemenáková<sup>2)</sup>

<sup>1)</sup>Dept. of Textile Materials, <sup>2)</sup>Dept. of Textile Technology, Technical University of Liberec, 46117 Liberec, Czech Republic.

## ABSTRACT:

*Hairiness is defined as the sum of fiber ends and loops protruding out from the main compact yarn body. Beside other instruments, there are two major testing equipments available on the market used for evaluating the yarn hairiness. The most popular instrument is the Uster hairiness system, which characterizes the hairiness by H value, and is defined as the total length of all hairs within one centimeter of yarn. The hairiness H is an average value and giving no indication of the distribution of the length of hairs. Main aim of this contribution is to analyze the yarn hairiness distribution for compact yarns according to the possibility of fitting bimodal function; i.e. dividing the hairiness to two types of hairiness. The individual values of yarn hairiness were extracted from Uster tester 4 and fed to a computer program HYARN written in Matlab code for complex characterization of yarn hairiness. The results show that in general, the fiber hair distribution has a bi-modal shape and comprises a mixture of two Gaussian distributions. Also the data was used for complex evaluation of yarn hairiness in time and frequency domain.*

## 1. INTRODUCTION

Yarn hairiness is a complex concept, which generally cannot be completely defined by a single figure. The hairiness occurs because some fiber ends protrude from the yarn body, some looped fibers are out from the yarn core and some wild fibers appear on the yarn surface. Hairiness of yarns has been discussed for many years, but it always remained a fuzzy subject. With the advent of compact yarns and their low hairiness compared to conventional yarns, the issue of measuring hairiness and the proper interpretation of the values has become important again. Generally speaking, long hairs are undesirable, while short hairs are desirable.

The effect of yarn hairiness on the textile operations following spinning, especially weaving and knitting, and its influence on the characteristics of the product obtained and on some fabric faults has led to the introduction of measurement of hairiness.

The most popular instrument for hairiness evaluation is the Uster hairiness system, which characterizes the hairiness by H value defined as the total length of all hairs within one centimeter of yarn. The hairiness H is an average value giving no indication of the distribution of the length of hairs. The spectrogram of hairiness is also available. The second major used instrument is the Zweigle hairiness tester. The numbers of hairs of different lengths are counted separately. In addition to the S3 value is given as the sum of the number of hairs 3 mm and longer. The information obtained from both systems is limited. The available methods compress the data into a single value (deletion of the important information about statistical behavior) or convert the entire data set into a spectrogram. Other methods dealing with image processing are time consuming.

Modern USTER devices have possibility to give raw data about whole yarn hairiness in the length interval of hundreds meters. The raw data  $H_i$  are in fact realization of spatial process (hairiness spatial process - HSP) and can be used for more complex evaluation of hairiness characteristics in the space and frequency domain.

Main aim of this contribution is to identify the yarn hairiness distribution shape. The individual values of yarn hairiness (HSP curve) are extracted from Uster tester 4. The standard and special techniques of data visualization and uni-modality testing are shown. The simple methods for complex characterization of HSP statistical behavior (stationarity,

independence, linearity etc.) are presented. The computer program HYARN written in Matlab code is used for complex characterization of yarn hairiness stochastic behavior. Many as 45 yarns spun on different systems, namely classical Ring spun, compact, Siro spun, plied yarns, and vortex spun yarns were tested. The yarn counts was ranging between 14.6 to 30 tex. All yarns were cotton, except the vortex yarns, which was spun from viscose staple fibers. The results show that in general, the yarn hairiness distribution obeys a bi-modal shape (short and long hairs) and can be described by a mixture of two Gaussian distributions.

## 2. DATA DISTRIBUTION VISUALIZATION

For graphical visualization of data distribution many simple techniques as stem-leaf plot, histogram, Q-Q plot and kernel density estimators have been proposed [3].

The simplest is estimation of quantile function based on the so-called order statistics

$$x_{(1)} \leq x_{(2)} \leq \dots \leq x_{(i)} \dots \leq x_{(N)}$$

which are the sample values (assumed to be distinct) arranged the in increasing order. Let  $F_e(x)$  is the distribution function from which values  $x_i$  has been sampled. It is well known that the transformed random variable

$$z_{(i)} = F_e(x_{(i)}) \quad (1)$$

has independently on distribution function  $F_e$  the Beta distribution  $Be[i, N-i+1]$ . Corresponding mean value is

$$E(z_{(i)}) = \frac{i}{N+1} \quad (2)$$

where  $E(.)$  is operator of mathematical expectations. The elements  $V_{ij}$  of covariance matrix  $V$  for all pairs  $z_{(i)}, z_{(j)}$   $i, j = 1, \dots, N$  are simple functions of  $i, j$  and  $N$  only. Using back transformations of  $E[z_{(i)}]$  the relation

$$E(x_{(i)}) = F_e^{-1}(z_{(i)}) = Q_e(P_i) \quad (3)$$

is obtained. In eqn. (3) the  $Q_e(P_i)$  denotes quantile function and

$$P_i = \frac{i}{N+1}$$

is cumulative probability. Description of quantile function properties and its advantages for constructing of empirical sample distribution are given in the book [5]. Generally, the quantile function is inversion of distribution function. When  $F(x) = P$  is continuous distribution function and  $f(x)$  is corresponding probability density function is  $Q(P) = x$  quantile function. It is simple to prove that  $F(Q(P)) = P$  for all  $0 \leq P \leq 1$  and  $f(Q(P)) * q(P) = 1$ . The  $q(P) = dQ(P)/dP$  is so called quantile density function and  $f(Q(P)) = 1/q(P)$  is density quantile function.

From eqn. (3) it is obvious that the order statistic  $x_{(i)}$  is raw estimate of the quantile function  $Q_e(P_i)$  in position of  $P_i$ . For estimation of quantile  $x_p = Q_e(P)$  at value  $P$  for which

$i/(n+1) < P < (i+1)/(n+1)$  the piecewise linear interpolation

$$x_{(p)} = (N+1) \left( \frac{PN + P - i}{N+1} \right) (x_{(i+1)} - x_{(i)}) + x_{(i)} \quad (4)$$

can be used. Variance  $D(x_p)$  can be computed from equation

$$D(x_p) = \frac{P(1-P)}{N f^2(x_p)}$$

Symbol  $f_e(x_p)$  means the probability density function corresponding to distribution function  $F_e$ . The asymptotic distribution of  $x_p$  is normal with mean  $Q(P)$  and variance defined by eqn. (5).

The interpolation (4) can be used for estimation of sample quantiles  $x_{P_i}$  or  $x_{1-P_i}$  for  $P_i = 2^{-i}$  for  $i = 1, \dots, N$ . These quantiles are called letter values [4]. All letter values except for  $i=1$  (median) are in pairs. For example we can estimate lower quartile  $x_{0.25}$  ( $P_i = 0.25$ ) and upper quartile  $x_{0.75}$  ( $P_i = 0.75$ ) etc.

Some proposals for more precise definitions of  $P_i$  are presented in paper [4]. For characterization of location the median  $x_{0.5}$  can be evaluated as the middle of order statistics. Variation is expressed as difference between upper quartile  $x_{0.75}$  ( $P_i = 0.75$ ) and lower quartile  $x_{0.25}$  ( $P_i = 0.25$ ). The so-called quantile deviation has the form

$$DQ = 2 * (x_{0.75} - x_{0.25}) \quad (5)$$

$DQ$  is justified as numerical derivative of  $Q(P)$  at  $P = 0.5$  which roughly approximate so called density quantile deviation

$$DfQ = 1 / f(Q(0.5)) = 1 / f(x_{0.5}) = q(0.5)$$

By using of these estimators of spread and location is possible to standardize data probability distribution to have  $DQ = 1$  and median  $x_{0.5} = 0$ . Standardized quantile function is called shape identification quantile function  $QI_e(P)$ . The sample form of  $QI_e(P)$  is defined as [5]

$$QI_e(P) = \frac{(x_{(i)} - x_{0.5})}{2 * (x_{0.75} - x_{0.25})} \quad (6)$$

The **shape identification quantile function  $QI_e(P)$  plot** is simply dependence of  $QI_e(P_i)$  on the  $P_i$ .

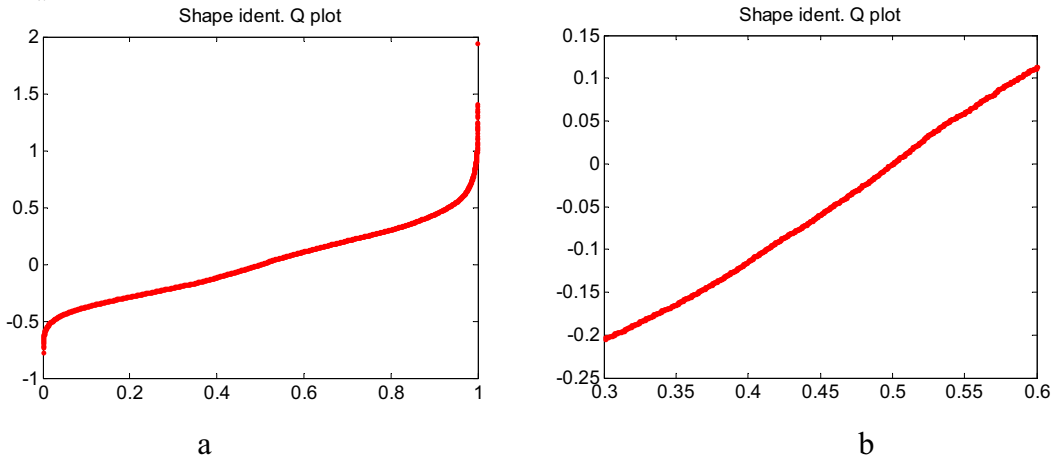


Fig. 1  $QI_e(P)$  for sample yarn C 30 tex (a.. full scale, b.. detail)

The shape identification quantile function  $QI_e(P)$  for sample yarn Compact 30 tex is shown on the fig. 2. The sigmoidal form in the central region is typical for bimodal distribution. There are present some outlying points in the upper part of plot.

Values  $|QI_e(P)| \geq 1$  are identified as outliers (for normal distribution) or as indicators of long tailed distribution. Values  $QI_e(P)$  can be easily used for specification of skewness and tail length. As a measures of skewness the  $SQ = QI_e(0.25) + QI_e(0.75)$  can be used (for symmetric distribution is this quantity equal to zero). Measures of tail length are  $QI_e(0.05)$  and  $QI_e(0.95)$ :

short tail is for  $QI_e(0.95) < 0.5$ ,

long tail is for  $QI_e(0.95) > 1$

medium tail is for  $0.5 < QI_e(0.95) < 1$ .

**Empirical quantile plot  $Q(P)$**  is constructed as dependence of  $x_{(i)}$  on  $P_i$ . From patterns of points some statistical features of data as a symmetry, local concentration and rough normality can be simply recovered. Detailed interpretation of  $QP$  is described in the book [4].

quantile functions of normal distribution

$$Q_N(P) = \mu + \sigma * u_p$$

are superimposed to  $QP$ . In the above equation the  $u_p$  are quantiles of standard normal distribution

$N(0, 1)$ . Parameters  $\mu$  and  $\sigma$  are estimators of location and scale.

Two various normal quantile functions are graphed. The first one is based on the moment estimators i.e. sample mean  $x_M$  and sample standard deviation  $s$ . The second one uses robust quantile estimator median  $x_{0.5}$  and quartile based standard deviation

$$s_M = \frac{x_{0.75} - x_{0.25}}{1.349}$$

This variant of  $QP$  enables to compare deviation of sample values from assumed normal distribution. For data from skewed distribution the normal quantile function can be replaced by assumed distribution. These diagnostics are very simple and can be used for crude evaluation of data distribution type.

The simple estimator of **cumulative density function** (CDF) is created as sum of order statistics.

$$cdf(x) = \frac{\sum_{i=1}^i x_{(i)}}{\sum_{i=1}^N x_{(i)}} , \quad \text{for } x_{(i)} \leq x \leq x_{(i+1)} \quad (7)$$

This estimator of CDF for sample yarn C 30 tex is shown on the fig. 3.

For comparative purposes are on the same fig the CDF for normal and rectangular distributions. The typical “bump” oh empirical CDF indicates bimodality.

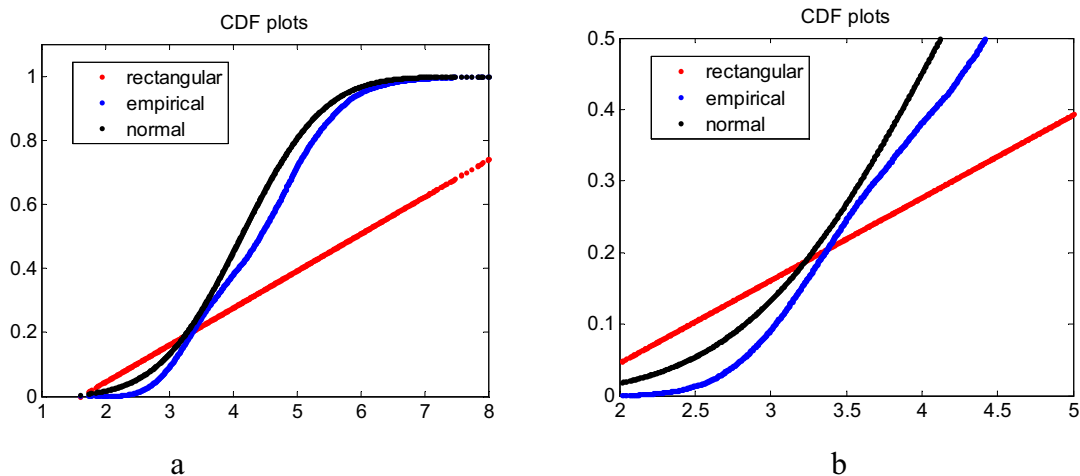


Fig. 2 CDF for sample yarn C 30 tex (a.. full scale, b.. detail)

The comparison of the empirical sample distribution and suitable theoretical one the variants of **Q-Q plot** are useful. Classical **Q-Q plot** is based on comparison of empirical quantile function  $Q_e(P_i) \cong x_{(i)}$  with chosen theoretical quantile function  $Q_T(P_i)$ . For theoretical distribution functions of type  $F_T((x-T)/S)$  is attractive to use standardized quantile function

$Q_{TS}(P_i)$  (see[4]) or shape identification quantile function  $QI_T(P_i)$ . When empirical and theoretical distributions are in coincidence, the relationship

$$x_{(i)} = T + S Q_{TS}(P_i) \quad (8)$$

is valid. Here usually  $T$  is the location parameter and  $S$  is the parameter of scale. For some three-parameter distribution the shape factor is usually a parameter of the plot. Due to strong dependence among order statistics and their non-constant variance the  $Q-Q$  plot gives a much-patterned appearance and the degree of linearity is often hard to quantify.

The  $Q-Q$  plot using normal theoretical quantile function for sample yarn C 30 tex is shown on the fig. 3.

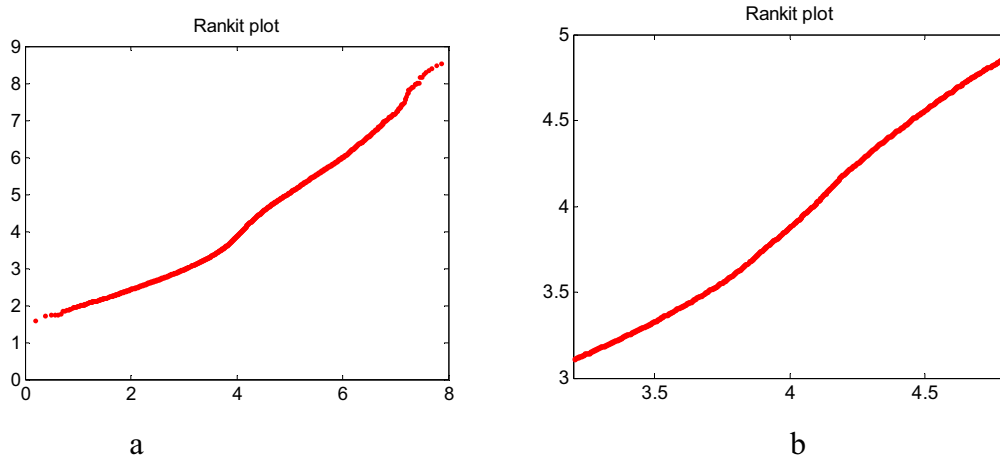


Fig. 3 Empirical quantile plot for sample yarn C 30 tex (a.. full scale, b.. detail)

The bend in the central region is here indication of bimodality. For better interpretation the ***P-P (or Probability-Probability) plot*** is useful for determining how well a specific theoretical distribution fits the observed data. In the  $P-P$  plot, the observed cumulative distribution function (estimated by probability  $P_i$ ) is plotted against a theoretical cumulative distribution function  $F_T(x_{(i)})$  in order to assess the fit of the theoretical distribution to the observed data. If all points in this plot fall onto a diagonal line (with intercept 0 and slope 1), then can be concluded that the theoretical cumulative distribution approximates the observed distribution well. If the data points do not all fall on the diagonal line, then can be used this plot to visually assess where the data do and do not follow the distribution (e.g., if the points form an S shape along the diagonal line, then the data may need to be transformed in order to bring them to the desired distribution pattern).

In order to create this plot, the theoretical distribution function must be completely specified. Therefore, the parameters for the distribution must either be defined by the user or computed from the data (see the specified distribution for more information on the respective parameters). Parzen [5] proposed for this purpose so called comparison distribution function

$$CDD = F_T(Q_e(P_i)) \quad (9)$$

The  $CDD$  is roughly equal to the theoretical distribution function in point  $x_{(i)}$ . Plot of  $CDD$  against  $P_i$  is therefore for sample data equal to the  $P-P$  plot. For comparative purposes is better to use **comparative  $P-P$**  plot. In this plot  $CDD$  is replaced by the difference  $CDD - P_i$ . In the ideal case of univariate normality is this plot horizontal line having level equal to zero. The comparative  $P-P$  plot for sample yarn Compact 30 tex is shown on the fig. 4.

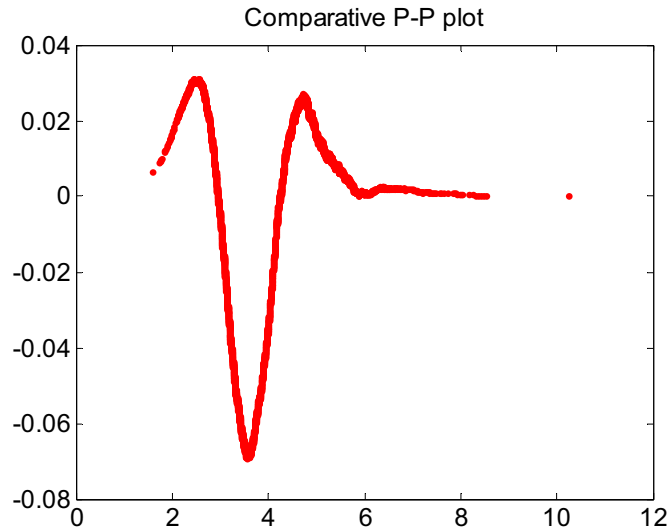


Fig. 4 Comparative P-P plot for sample yarn C 30 tex

The typical pattern for bimodal distribution is clearly visible on this fig. Combining of  $Q-Q$  and  $P-P$  plots leads to the best diagnostics.

As simplest estimator of probability density function (PDF) the **histogram** with constant or variable bins (number of bins is  $M$ ) is often constructed. Histogram is piecewise constant estimator of sample probability density. Histogram height in  $j$ -th class bounded by values  $(t_{j-1}, t_j)$  is calculated from the relationship

$$f_H(x) = \frac{C_N(t_{j-1}, t_j)}{N h_j} \quad (10)$$

where the function  $C_N(a, b)$  denotes the number of sample points within interval  $\langle a, b \rangle$  and  $h_j = t_j - t_{j-1}$  is the length of the  $j$ -th bin (interval). Now, the problem encountered is the choice of boundary values  $\{t_j\}$   $j=1, \dots, M$ , the number of class intervals  $M$  and their lengths  $h_j$  with respect to the histogram quality. For nearly normal data the constant bin length

$$h = 3.49 * (\min(s, Dq / 2) / 1.34) / n^{1/3} \quad (11)$$

Histogram for sample yarn Compact 30 tex and  $h$  computed from eqn. (11) is shown on the fig. 5.

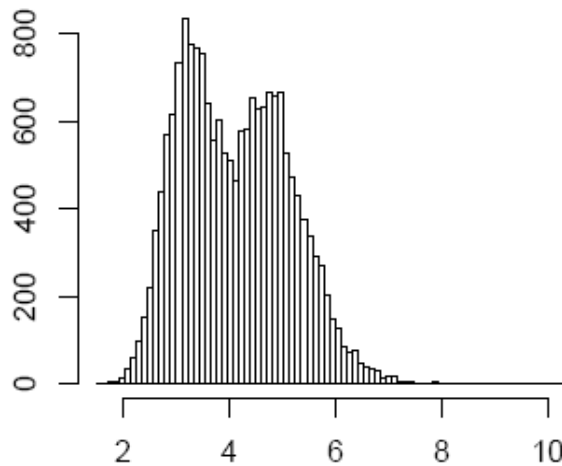


Fig. 5 Histogram with constant bin length ( $h=0.134$ ) for sample Compact yarn 30 tex.

For the case of non-constant bin length the simple data based two-stage technique can be used. In the first stage the number of class intervals

$$M = \text{int}[2.46 (N - 1)^{0.4}] \quad (12)$$

is computed. Here  $\text{int}[x]$  is integer part of number  $x$ . The optimal number of bins computed from eqn. (12) is for sample yarn C 30 tex is equal to  $M = 125$ .

In the second stage the individual lengths  $h_j$  are determined. The estimation of  $h_j$  is based on the requirement of equal probability in all classes. For this purpose the empirical quantile function  $Q(P_i)$  based on the order statistics  $x_{(i)}$  is used.

In practice the P-axis is divided into identical intervals having the size of  $1/M$ . For these intervals the corresponding quantile estimates  $t_j = x_{(j/M)}$  are constructed by using of eqn. (4).

Practical experiences have hitherto proven that this construction be suitable even for strongly skewed sample distributions [3].

Smooth **kernel type density estimator** is natural generalization of histogram. The kernel type nonparametric estimator of sample probability density  $f(x)$  can be constructed on the basis of constant or variable bandwidth  $h$  (analogy with bin width). The final estimator for constant  $h$  has the form

$$\hat{f}(x) = \frac{1}{N} \sum_{i=1}^N K \left[ \frac{x - x_i}{h} \right] \quad (13)$$

Selection of kernel function  $K[x]$  and computation of bandwidths  $h$  is described in [3]. The simple biquadratic kernel function  $K[x]$  has the form

$$K(x) = 0.9375 * (1 - x^2)^2 \quad \text{for } -1 \leq x \leq 1 \quad (14)$$

The suitable  $h$  can be computed from eqn (11).

Kernel type density estimator defined by eqn. (13) and kernel defined by eqn. (14) for sample yarn C 30 tex is shown on the fig. 6.

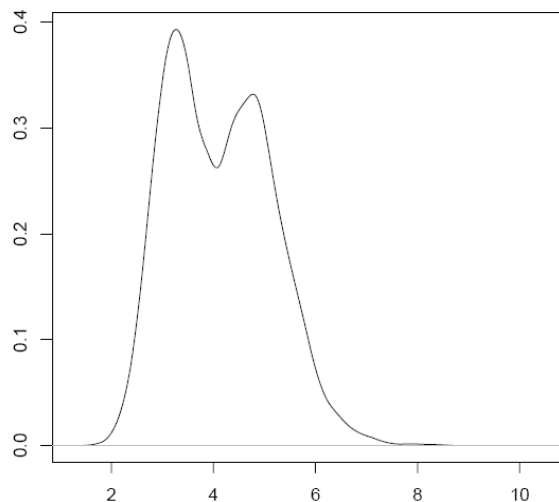


Fig. 6 Kernel density estimator with constant bin length ( $h = 0.128$ ) for sample yarn C 30 tex

In the case when the normality of data can be accepted but there is suspicion of bimodality (mixture of normal distributions) the parameters for unimodal (one Gaussian) distribution

$$f_u(x_i) = A0 * \exp \left( -\frac{(x_i - B1)^2}{2 * C1^2} \right) \quad (15)$$

and bimodal distribution (mixture of two Gaussians)

$$f_B(x_i) = A1 * \exp\left(-\frac{(x_i - B1)^2}{2 * C1^2}\right) + A2 * \exp\left(-\frac{(x_i - B2)^2}{2 * C2^2}\right) \quad (16)$$

can be computed. Here A1, A2 are proportions of smaller hairiness (first Gaussian having index 1) or higher hairiness (second Gaussian having index 2). Parameters B1 and B2 are mean H values for individual component and parameters C1, C2 correspond to standard deviations.

Mixture of two normal distribution can be unimodal or bimodal. For the case of unimodality the following relation should be valid.

$$|B1 - B2| < 2 * \min(C1, C2) \quad (17)$$

The parameters of unimodal normal distribution are A1 = sample mean value, B1= sample standard deviation. To obtain the coefficient estimates (A1, A2, B1, B2, C1 and C2), the least squares method minimizing the residual sum of squares can be used. The residual for the  $i$  th data point  $r_i$  is defined as the difference between the observed response values (see eqn.(13)) and the fitted response values (see eqn.(16))

$$r_i = \hat{f}(x_i) - f_B(x_i)$$

The residual sum of squares is given by

$$S = \sum_{i=1}^N r_i^2 \quad (18)$$

where N is the number of data points included in the fit. Assumption leading to the minimization of S is given in the book [3]. Model of two Gaussian mixture is a nonlinear regression model. Nonlinear models are more difficult to fit than linear models, because the coefficients cannot be estimated using simple matrix techniques. Instead, an iterative approach is required. The MATLAB toolbox used in HYARN provides these algorithms:

- Trust-region -- This is the default algorithm. It can solve difficult nonlinear problems more efficiently than the other algorithms and it represents an improvement over the well-known Levenberg-Marquardt algorithm.
- Levenberg-Marquardt -- This algorithm has been used for many years and has proved to work most of the time for a wide range of nonlinear models and starting values. If the trust-region algorithm does not produce a reasonable fit, and there are no coefficient constraints, the Levenberg-Marquardt is good starting algorithm.

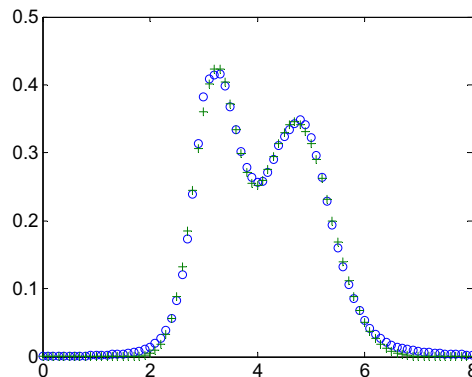


Fig. 8 Approximation of empirical PDF (circles) by two Gaussian terms (crosses) for sample yarn Compact 30 tex



For comparison of unimodal and bimodal models the likelihood ratio

$$LR = 2 * \ln \left( \frac{L_B}{L_U} \right) \quad (19)$$

can be computed. The likelihood function  $L_U$  has the form

$$L_U = \prod_{i=1}^N \frac{1}{\sqrt{2 * \pi * C1^2}} \exp \left( - \frac{(x_i - B1)^2}{2 * C1^2} \right) \quad (20)$$

and for  $L_B$  is valid

$$L_B = \prod_{i=1}^N A1 * \exp \left( - \frac{(x_i - B1)^2}{2 * C1^2} \right) + A2 * \exp \left( - \frac{(x_i - B2)^2}{2 * C2^2} \right) \quad (21)$$

Statistics  $LR$  has approximately  $\chi^2(4)$  distribution i.e. for  $LR \leq 9$  the unimodal simple normal distribution can be accepted. For the case of sample yarn Compact 30 tex is  $LR = 244.3$  and bimodality is proved.

### 3. RESULTS AND DISCUSSIONS

It is clear from figure (8) that all yarns are bimodal distributed. The plot of the probability density function  $s$  for all yarns fit quit well.

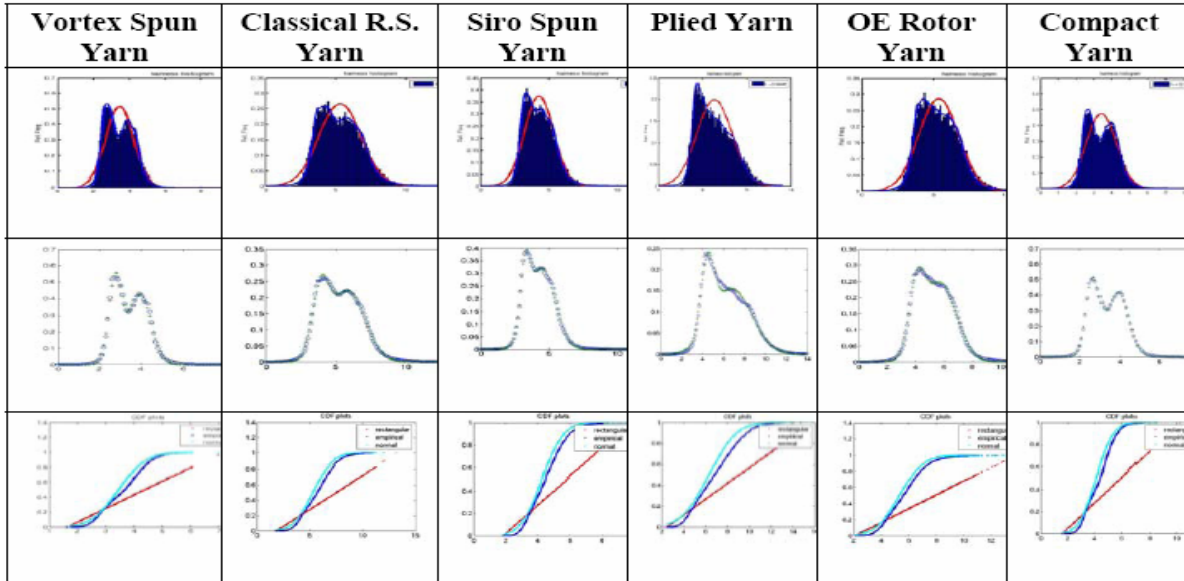


Fig. 8: The kernel PDF and fitted mixture of normal distribution

Table 1 shows the different values obtained from H-yarn program. It obvious that the lowest values for long hairs are due to vortex yarns followed by compact yarns and siro spun. The highest values are due to plied yarns. This may be due to the plied yarns passes more stages during processing. This result is also valid for the length of the long hairs and also for the total yarn hairiness  $H$ . The percentage of short fibers for both vortex and compact yarns are comparable and has the highest values. The standard deviation, which is a measure of the variation in yarn hairiness distribution for both components the short and long hairs, has the same trend.

	<b>Vortex</b>	<b>RS</b>	<b>Siro</b>	<b>Plied</b>	<b>OE</b>	<b>Compact</b>
<b>Mean short hairs</b>	<b>2.75</b>	<b>3.9</b>	<b>3.24</b>	<b>4.4</b>	<b>4.08</b>	<b>3.21</b>
<b>Mean long hair</b>	<b>3.46</b>	<b>5.87</b>	<b>4.48</b>	<b>6.8</b>	<b>5.75</b>	<b>4.31</b>
<b>S.D short hairs</b>	<b>0.32</b>	<b>0.61</b>	<b>0.36</b>	<b>0.63</b>	<b>0.56</b>	<b>0.41</b>
<b>S.D. long hairs</b>	<b>0.52</b>	<b>1.21</b>	<b>0.95</b>	<b>1.89</b>	<b>1.14</b>	<b>0.66</b>
<b>Portion short hairs</b>	<b>0.42</b>	<b>0.32</b>	<b>0.27</b>	<b>0.22</b>	<b>0.27</b>	<b>0.41</b>
<b>Portion long hairs</b>	<b>0.57</b>	<b>0.67</b>	<b>0.73</b>	<b>0.77</b>	<b>0.70</b>	<b>0.57</b>
<b>Total hair length H</b>	<b>3.46</b>	<b>5.30</b>	<b>4.26</b>	<b>6.32</b>	<b>5.34</b>	<b>4.12</b>
<b>S.D of total H</b>	<b>0.77</b>	<b>1.49</b>	<b>1.07</b>	<b>1.99</b>	<b>1.39</b>	<b>0.76</b>
<b>Bi-modal. Separation</b>	<b>0.70</b>	<b>0.54</b>	<b>0.47</b>	<b>0.46</b>	<b>0.49</b>	<b>0.57</b>
<b>t- test statistics</b>	<b>189.6</b>	<b>146.24</b>	<b>127.56</b>	<b>125.23</b>	<b>130.4</b>	<b>190.73</b>

Table 1 Sample results of yarn hairiness of different spun yarns of 20 tex.

## 6. YARN HAIRINESS AS A STOCHASTIC PROCESS:

The data extracted from Uster is taken in equidistance (time interval), so that it can be used for more complex evaluation of hairiness characteristics in the time and frequency domain. The yarn hairiness can be described according to the:

- *Periodic components*
- *Random variation*
- *Chaotic behavior*

For these goals, it is possible to use system based on the characterization of long term and short-term dependence of variance. The so-called Hurst exponent or fractal dimension can describe especially long-term dependence. Here we shall deal with a limited functions from many characteristics computed in our H-Yarn Program. Details are found in [4].

As an example, the autocorrelation, which simply can be described as a comparison of a signal with itself as a function of time (distance) shift (lag) is illustrated in Figure (9).

Also, concerning frequency domain analysis, we demonstrate the FFT, which is also used for transforming time domain function into frequency domain and its inverse. The signal is decomposed to different sine waves. There are many types of spectrum, PSD, amplitude spectrum, and many other types. The power spectrum output from H-Yarn program is illustrated in figure (9). The cumulative of white identically distribution noise is known as Brownian motion or random walk. The Hurst exponent is a good estimator for measuring the fractal dimension. The Hurst equation is given by:  $R/S = K^*(N)^H$ . This can be seen in the same figure (last row).

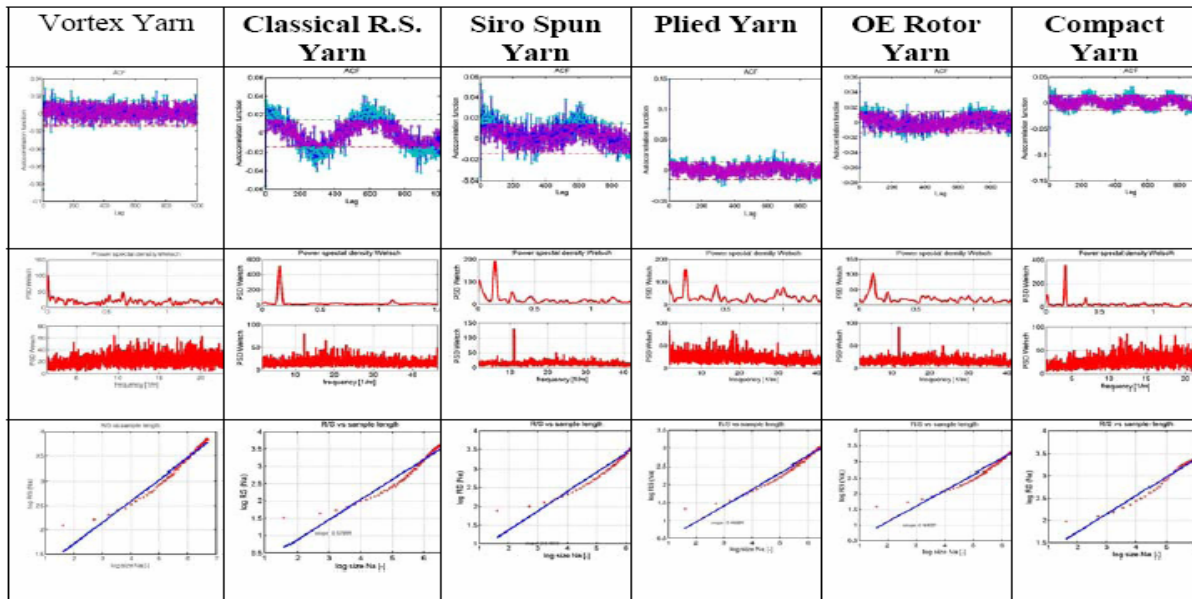


Figure 9: Sample from H-Yarn program, Autocorrelation (upper graph), Power spectrum (middle graph), and Hurst diagram (lower graph) for yarns of 20 tex

## 7. CONCLUSIONS:

- The yarn hairiness distribution can be described by two Gaussian, the portion, mean and the standard deviation of each component leads to deeper understanding and evaluation of hairiness.
- The Hyarn system is a powerful program for evaluation and analysis of yarn hairiness as a dynamic process, in both time and frequency domain.
- H-yarn program is capable of estimating the complexity of this process.
- Great deal of effort should be undertaken due to Zweigle system for evaluation of yarn hairiness.
- Comparing the results of different systems for yarn hairiness evaluation are of great help for industry.

**Acknowledgement:** This work was supported by the research project 1M4674788501 - “Textile Center” of Czech Ministry of Education.

## 8. REFERENCES:

- [1] Celik P. and Kadoglu H. : “A Research on the Compact Spinning for Long Staple Yarns”, *Fibers & Textiles in Eastern Europe*, vol. 4, No. 4(48).
- [2] Basal G. and Oxenham W. : “Comparison of Properties and Structure of Compact and Conventional Spun Yarns”, *Textile Research Journal* Vol. 76(7); 567-575.
- [3] Meloun M. Militky J. and Forina M.: "*Chemometrics for Analytic Chemistry vol.I and II, Statistical models building*", Ellis Horwood, Chichester, (1992 and 1994).
- [4] Militky J., Ibrahim S.: “*Yarn Hairiness Complex Characterization*”, Proc. Annual Fiber Soc. Conf., St Galen, May 2005.
- [5] Parzen E.: Statistical methods mining and non parametric quantile domain data analysis, Proc Ninth int. conf. on quantitative methods for environmental science, July 1988, Melbourne