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An automatic document processing system for medical data extraction

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Abstract *– This paper illustrates an automatic document processing system for the extraction of data contained in medical laboratory results printed on paper. The final goal of the research is to automate the collection of medical data and to enable an efficient management and dissemination of the information. The following processing steps of the system are described in detail: image preprocessing; layout analysis for the identification of the tables contained in the document; extraction and classification of the laboratory results. Among the many features of the system there are the use of an open source OCR engine, as a basis of further processing, and the storage in XML format of the data retrieved, for ease of sharing. The knowledge base used to guide the data extraction is also explained. The proposed approach has been tested on several document formats and performance analyzed.*

Index terms **–** medical data, document image processing, medical services, performance evaluation

I. INTRODUCTION

Medical investigation is conducted to extend the life of people and to improve quality of life for patients with severe diseases; today it is common to run into doctors having different specializations which work together towards the common goal of curing a disease. This requires a multidisciplinary research organization utilizing advanced medical technologies and medical research institutes of different universities. Besides, in order to guarantee the statistical significance of the studies, a sufficient amount of data from clinical trials and medical examinations should be collected. Thus, the scientific communities of several medical fields are working on electronic databases containing clinical analyses and laboratory results useful for researches, medical investigations, epidemiological studies, quality control, and so on [1], [2], [3]. It should be stressed that an efficient and undistorted communication of medical research results and hospital data is one of the most important heritages of the medical scientific community.

As a matter of fact, however, a complete transition towards paperless practices has not been accomplished or, in some cases, is not possible at all, and paper continues to be used for diagnoses, laboratory results, and prescriptions. This constitutes and obstacle for the creation of electronic databases and electronic medical records [4]. Indeed, it has been noticed that the manual entry of data into medical records takes a long time and often produces errors [5], [6]. Moreover, the absence of common practices among various medical centers produces discrepancies and non-uniformity of data.

Therefore, the automatic conversion of paper documents into digital resources is an important and nontrivial task that greatly contributes to the preservation and dissemination of medical archives. In this paper an automatic system able to extract the data contained in tabular-like form

in printed medical laboratory results, converting them into an electronic form which can be stored in databases and further processed is proposed.

A review of algorithms for the automatic analysis of printed documents is presented in Sec. II, followed in Sec. III by a thorough description of the implemented system. Performance is analyzed in Sec. IV and final remarks are given in Sec. V.

II. RELATED WORK

Extracting information from printed medical laboratory results in an automated way is not a simple task, and requires several processing steps [3], [7], [8], [9]. Medical image archiving and management allows a fast and objective diagnosis even from remote locations [10]. There are many successful applications in this field [11], [12], [13], [14]. Document automation systems are available for other purposes, such as generating special printed forms to be compiled by hand and processed by OCR [15]. In [16] a method is proposed for the automatic text classification in biomedical research documents, based on the use of a support vector machine. However, a complete system tailored to laboratory results isn't available. In this work several components have been integrated with the aim of building such a system. In order to better understand the features of the proposed method, a short premise should be done about the components of the system and the processing flow.

The main components required for processing the document are: digitization, pre-processing, layout analysis, OCR, correction of the OCR results and document understanding. We consider these ones as components rather than consecutive steps, because they can be used several times with different working parameters in order to advance in the data extraction. For example, in our proposed approach, layout analysis and OCR are iterated two times in order to find column

headers in the printed table of laboratory results. A third OCR run is performed with parameters tailored to the contents expected in each table cell, which are predicted on the basis of the column and the row where each cell is located.

Layout analysis allows to retrieve the structure of the document by using, essentially, graphical features such as position, distance, orientation and size of the components being analyzed, which can be connected components, characters, words, text lines, paragraphs, and so on. Layout analysis has its roots in image segmentation algorithms, and is a fundamental step towards document understanding, in which the logical relations between document components are fully exploited. Image segmentation [17], [18] and text region extraction [19], [20], [21] are one of the most debated issues in the document images analysis [16] and many problems are currently unresolved. Over the last two decades, several techniques have been proposed, all referable to three classes; bottom-up algorithms, top-down algorithms and hybrid algorithms [22]. In the bottom-up approaches text components are identified starting at the character level, then characters are aggregated into words, and finally text lines, paragraphs and higher level components are built to reassemble the whole pages; examples are the use of the Voronoi diagram [23], the Docstrum algorithm [24], the Kruskal algorithm [25] and the probabilistic approach [26]. Alternatively, in the top-down approaches, the pages are split into columns, then into paragraphs and finally in the text lines and words. Examples are the XYcut [27] and whitespace analysis [28]. Finally, hybrid approaches can be regarded as a mix of the above two approaches in an attempt to overcome the limitations of these algorithms. Neural techniques have been applied not only to OCR and word recognition, but also to layout analysis [29]. Due to the importance of layout analysis in document image understanding, considerable effort has been dedicated to the performance evaluation of these algorithms [16], [30]. No single algorithm can

be considered optimal and different approaches should be chosen depending on the specific application.

In this work layout analysis is dedicated essentially to the analysis of tables, because this is the form in which laboratory results are generally reported. Table detection can be performed by analyzing gaps between words and rows, as described in [31]. However laboratory results often are not tabulated in a strict manner, for example some cells can span more than one column, and no cell box delimiters are printed. For this reason in our system a knowledge base is used, in order to extract table data.

We have explored the possibility of integrating in our system an open source OCR software. Really, any OCR could have been used because there aren't special requirements about advanced functions and the layout analysis is performed mainly by our system. The only OCR features used in this work, besides characters recognition, are the computation of the locations of the characters and the restriction of the characters set (letters, digits, special symbols, and so on). Matching scores for the recognized characters, which can be output by the OCR, are not used in our system. Optical character recognition is prone to errors, and several techniques have been proposed in literature to correct them [32]. This is useful in particular for the recognition of handwritings. For example in [33] the use of specific language models is discussed, based on statistical properties of words in text, morpho-syntactic characteristics of words and syntactic structures of the language. In our application, which is aimed at the recognition of tables, we use a different approach, based on a knowledge base of laboratory exams with their naming variants, common measurement units, and approximate string matching algorithms. Our approach should also be distinguished from other ones in which the knowledge-base contains only rules about the geometric structure of the document [35]. We exploit the knowledge base and the logical structure of the tables is order to correct OCR errors and recognize the laboratory exams, i.e. to

perform the document understanding. This method uses an explicit set of information to support the data extraction so it requires some work in order to expand the range of recognized laboratory exams but, for the same reason, it is relatively simple to implement and gives accurate results. In particular, it has a low rate of matching errors as regards the recognition of the names of the single exams contained in the document. Indeed, confusing one exam for another can be dangerous in this kind of application.

As regards the general aspects of the processing flow, it should be noted that the extraction and classification of data requires a lot of automatic decisions about where data are located and what is their meaning, and each decision may have deep consequences on subsequent processing [34]. This is in contrast with other industrial applications, where the authors have experienced less correlation between subsequent processing steps [36], [36], [38], [39], [40]. Nonetheless in the approach presented in this paper these decisions are taken sequentially and deterministically evaluating best scores, and a careful choice of the algorithms employed avoids the need of going back to reconsider past decisions. Even though walking backwards in the decision tree is a possibility left open in our system, it has not been implemented because the achieved results, reported in Sec. IV, are already satisfactory.

III. SYSTEM ARCHITECTURE

The conversion of paper and electronic documents into standard electronic forms is a key step in medical research. There are many advantages in using standard electronic records: compact and lossless storage, fast retrieval and transmission, easy data analysis and the possibility of comprehensive statistical studies. Unfortunately, medical documents are very different in terms of format, and medical lexicon is large; this leads to difficulties in the automatic creation or

conversion of records. In this paper we propose a method to automatically convert paper-based medical reports into XML documents. Being easy to retrieve, display and index information contained in XML documents, this will contribute to create a standard database useful to researchers and clinicians.

The main stages that allow the processing of a printed page containing the laboratory results, described in the following sub-sections, are: (Sec. A) image preprocessing, in which the document readability is enhanced; (Sec. B) layout analysis, in which the document layout is analyzed in order to identify columns and rows containing the information to be extracted, so discarding extraneous graphical elements such as "margins" and graphs; (Secs. C and D) data extraction and classification, in which text returned by the OCR is analyzed syntactically and semantically; (Sec. E) exportation in XML format of the extracted data. A knowledge base (KB), which assists layout analysis, data extraction and classification, is described in Sec. F.

A. Preprocessing

In this phase the image is prepared for subsequent processing steps. In particular, equalization, binarization and suppression of long lines are required to ease layout analysis and OCR, and to remove various artifacts which could give rise to misinterpretations. Let $\mathbf{A}_0 = [A_0(i,j)]$ be the gray-scale input image. An example image, obtained with a common scanner with resolution 300 dpi, is shown in Fig. 1. The procedure is as follows.

a) In a first step, if the skew angle is greater than 1.0°, $\mathbf{A}_0$ is deskewed, obtaining the image $\mathbf{A}_1$.

b) $\mathbf{A}_1$ is equalized in order to cover the full 256 gray-levels range, so obtaining the image $\mathbf{A}_2$.

c) $\mathbf{I}_3$ is then calculated by binarizing $\mathbf{A}_2$with a combination of thresholding techniques. In particular, a first image $\mathbf{I}_1$ is obtained with a threshold t_1 fixed at the 90% of the intensity range and inversion:

$$I_1(i,j) = \begin{cases} 0, \text{ if } A_2(i,j) > t_1 \\ 1, \text{ otherwise} \end{cases} \quad (1)$$

with $t_1 = 0.9 \times 255$.

A second image $\mathbf{I}_2$ comes from adaptive thresholding on $\mathbf{A}_2$ and inversion:

$$I_2(i,j) = \begin{cases} 0, \text{ if } A_2(i,j) > T_2(i,j) - c_2 \\ 1, \text{ otherwise} \end{cases} \quad (2)$$

where $T_2(i,j)$ is the mean of the $N_2 \times N_2$ neighbourhood of $A_2(i,j)$, with $N_2 = 7$ and $c_2 = -35$.

Finally, $\mathbf{I}_3$ is given by

$$\mathbf{I}_3 = \mathbf{I}_1 \cap \mathbf{I}_2 \quad (3)$$

d) Image $\mathbf{I}_5$ is obtained by deleting long horizontal and vertical lines, in order to avoid interference with OCR. Firstly, the thresholded image $\mathbf{I}_4$ is prepared,

$$I_4(i,j) = \begin{cases} 0, \text{ if } A_2(i,j) > T_4(i,j) - c_4 \\ 1, \text{ otherwise} \end{cases} \quad (4)$$

where $T_4(i,j)$ is the mean of the $N_4 \times N_4$ neighbourhood of $A_2(i,j)$, with $N_4 = 17$ and $c_4 = 6$. The lines are detected by applying to $\mathbf{I}_4$ the algorithm discussed next, so obtaining the image $\mathbf{I}_L$ which contains only horizontal and vertical lines. These lines are removed by performing the set difference

$$\mathbf{I}_5 = \mathbf{I}_3 - \mathbf{I}_L \quad (5)$$

When horizontal lines are being detected on the binary image $\mathbf{I}_4$, the following operations are accomplished:

- Connected components whose area is less than 2 pixels are filtered out.

- Morphological closure is performed with a horizontal structuring element of length 15 pixels, followed by morphological opening with a horizontal structuring element of length 20 pixels.
- The following characteristics are calculated for each connected component of the resulting image: minimum width *wm* in the vertical direction, maximum width *wM* in the vertical direction, length *len* in the horizontal direction. All characteristics are measured in pixels.
- A component is recognized as a line iff

$$len >= 50 \text{ and } \frac{len}{wM} > 30 \text{ and } \frac{wM - wm}{len} < 0.01 \tag{6}$$

The detection of vertical lines proceeds analogously.

e) Finally small size components are filtered out,

$$\mathbf{I}_6 = F[\mathbf{I}_5] \tag{7}$$

where the operator *F* filters connected components whose area is less than 3 pixels. The area is calculated by using the Green's formula applied to the component contours[41], as implemented in OpenCV (Open Source Computer Vision Library) [42].

B. Layout Analysis

In the layout analysis phase, the image is subdivided into blocks; text rows are processed by the OCR, and the text is compared with a list of column headers. The column headers identify those table columns which contain pertinent medical data. Those found by the algorithm in the example image of Fig. 1 are enclosed in red boxes in Fig. 2 and Fig. 3.

Successively, the rows are analyzed in order to identify the table cells and the semantic of words and group of characters. A distinction is performed between test names (enclosed in blue boxes in Fig. 2 and Fig. 3, numerical and alphanumerical results (green boxes), measurement units

(magenta boxes) and reference values (yellow boxes). Tests that are preceded by a header rows and multi-row tests, which extend over multiple rows, are also identified. Header rows are enclosed in blue boxes, as test names, in Fig. 2 and Fig. 3.

The algorithm is detailed in the remainder of this paragraph. The input image $\mathbf{I}_6$ is the one obtained at the end of the pre-processing.

Segmentation of table headers

a) A first segmentation of document rows is performed with the aim of identifying which one contains table headers. The segmentation is performed with the following steps: horizontal projection, so obtaining vertical regions; zero-padding of size 3 at both ends of the projection; morphological opening with a structuring element of size 6; deletion of the zero-padding; filling of empty regions of size 1 pixel; the resulting vertical regions, expanded horizontally up to the size of $\mathbf{I}_6$, constitute the binary mask which denotes document rows.

b) The rows are processed individually by the Tesseract OCR[43]. Let r_k be the text contained in the *k*-th row.

c) The previously processed rows are searched for columns headers by means of approximated string matching. Four column types are considered: test name, test result, test unit, test reference range. For each column type, a list of headers text variants is stored in the KB. Let h_{ij} be the *j*-th text variant associated with the *i*-th column type, where *i*=1,… N_C and $N_C = 4$. To find the row containing the column headers, firstly the Levenshtein distance (with deletion, insertion and substitution costs all equal to 1) between string h_{ij} and its best matching substring in r_k is computed and denoted as l_{ijk}. Then a cost function $c_{ijk} = l_{ijk}/\mathrm{len}(h_{ij})$ is calculated, where the function len returns the number of characters of its

argument. The lower cost text variant for each column class in calculated as $c'_{ik} = \mathrm{argmin}_j c_{ijk}$. The value c'_{ik} is calculated for each row *k*. A header row *K* is found if $\sum_i c'_{iK}/N_C \leq 0.34$ and $c'_{iK} \leq 0.7$ for each *i*. If there isn't one and only one such row, then an error is returned.

d) The coordinates of the boxes enclosing the column headers are calculated by examining the headers row *K*. Hence, for each column type *i*, the selection of the more appropriate text variant j is refined by using a new cost function $c''_{ij} = l_{ijK}/\mathrm{len}(h_{ij}) - 1.5 \cdot \mathrm{len}(s_{ij})/\mathrm{len}(r'_K)$, where r'_K is obtained from r_K by removing spaces, and s_{ij} is the substring of r'_K that best matches h_{ij}. After the text of each column headers is identified, the enclosing boxes are finally individuated.

Segmentation of table cells

To segment table cells in a robust manner, at the beginning only the text contained in the vertical projection of the column headers is taken into account (step e), then the cells are extended horizontally and vertically to include nearest text (step f). The fact that table cells can have variable sizes help in filtering out irrelevant graphical elements.

e) The table rows under the column headers are segmented as follows. Firstly, the pixels in the image $\mathbf{I}_6$ that are not under the boxes enclosing the column headers are zeroed, so obtaining the image $\mathbf{I}_7$. A binary mask $\mathbf{I}_8$ is then calculated by applying to $\mathbf{I}_7$ the same procedure described previously in step a). Finally, the table rows are obtained by masking $\mathbf{I}_6$ with $\mathbf{I}_8$.

f) Table cells in the previously found table rows are segmented by analyzing blanks with the following procedure. Each row separately is subjected to vertical projection, zero-padding of size 1 at both ends of the projection, morphological opening with a structuring element of

size 2, deletion of the zero-padding, and filling of empty regions of size less than 20 pixel. This gives, for each row, the horizontal extension of each table cell. The vertical extensions of table cells are expanded by considering the connected components of the horizontal projection of $\mathbf{I}_6$. In particular, each cell is vertically extended up to the size of the connected components that intersects it when the block is horizontally projected onto the *y*-axis.

Classification of cells

g) Table cells are tagged with the column types they belong to. For any given row, this classification procedure considers in turn each column type and tries to tag the cell that better corresponds to that column. Column types are examined with the following priority order: test name, test result, test unit, test reference range. The condition for tagging a table cell is that it should overlap with the column header box after projection on the *x*-axis and should not have been previously associated with another column type. If more cells overlap with the same header, then the wider cell is selected.

The rows are classified according to the cell tags they contain, following the rules described in *Table I*. Four classes are defined: test row, name row, result row, invalid row. A row is invalid if none of the rules specified in *Table I*

h) applies. This classification is based only on the layout analysis of rows one at time, while the logical relations among rows are detected in the data extraction phase, where KB is also used.

C. Data extraction

In this phase data are extracted from table cells.

a) The cells are processed by the OCR, which is configured to recognize a different set of characters according to the cell type. If a test result cell and a test unit cell are in the same row, then the set of characters recognized in the test result cell are those used to represent numbers.

b) The text retrieved by the OCR is then analyzed in order to recognize the laboratory tests it contains. In particular the data classification routine (DCR), which is described in the following section, is applied to *name rows* and *test rows*. The DCR is aimed at determining the test definition in the KB that matches the table row, that this to classify that row, and extract the relevant information. The KB contains the list of all medical tests (LMT) that the system is able to recognize, with details such as test names (including variants) and measurement units. It should be also taken into account that header rows can occur in a document to put in evidence the logical structure of the document, or to better specify the test name cell contained in another row when ambiguities can result. Hence the KB contains also a list of headers (LH), where each header can be of one of two types denoted as *H2* and *H1*. When *test rows* are analyzed, the DCR uses the LMT and the LH, while *name rows* are analyzed by using only the LH. Each test name variant specified in the LMT can be optionally associated (by the KB) with a header belonging to the LH.

When a table row contains a test name variant associated with an H2 header, this means that the table row should appear in a row after that header (separated by zero or more other rows), and otherwise it is discarded. Instead, if a test name variant is associated with an H1 header, then this header should appear immediately before that table row (separated by zero other rows), otherwise it is discarded. To allow more flexibility in data extraction, *test rows* which are recognized as H1 headers are considered valid even if they are not immediately followed by an associated row. In other words, H1 header rows can also carry complete test

information, while H2 headers should be necessarily associated with other rows in order to be interpreted as meaningful information. Moreover, if the table row contains a *test name* but not a *result cell*, then the result and/or measurement unit are eventually taken form the corresponding cells in the associated H1 header row.

Finally, the case is also considered in which the result is multi-row. This happens, for example, when the result is in the form of descriptive text spanning more rows, which are expected to be classified as *result rows*. These rows are processed by the DCR only if the preceding row is recognized in the KB as being part of a multi-row result, and in that case the test results from different rows are aggregated.

c) Special rules are applied selectively to some recognized tests, according to the KB. For example, categorical results are matched against a list of known words.

d) For each recognized test, a record is created which contains the raw OCR data, and the data normalized with the help of the KB. The normalized data include a unique test identifier, a standardized name (chosen among different variants that can occur in medical laboratory results), the result and, eventually, the measurement unit.

D. Data classification routine (DCR)

This section describes the data classification routine, which is called during the data extraction phase reported in the previous section.

In the following discussion, the test definitions are individuated by index i, with $i = 0, \dots I$. For simplicity, we assume here that naming variants of the same medical test count as separate entries in the KB.

Let $[k_i]$ be the list of test names and/or headers retrieved from the KB, and s be the string contained in the test name cell of the table row under analysis. For each string k_i in the list, the

substring s_i' of s best-matching k_i is found by considering the Levenshtein distance, with deletion, insertion and substitution costs all equal to 1. Let l_i be the Levenshtein distance between s_i' and k_i. For each string k_i in the list, a cost is then calculated as

$$c_i = \left[l_i + \frac{len(k_i) - len(s_i')}{len(s_i')} + \frac{len(s) - len(s_i')}{len(s_i')} \right] / len(k_i) \tag{8}$$

If the row being analyzed isn't a test row, then the classification proceeds by calculating $i' = \mathrm{argmin}_i c_i$.

Otherwise the three KB definitions that correspond to the least costs, denoted as $[c_j]$ with $j \in J$, are further processed by taking into account measurement units. The string contained in the measurement unit cell, which can eventually be empty, is parsed by eliminating spaces and the 'x' multiplier symbol, if they are present. At this point the measurement unit string is compared with a list of possible measurement units (including variants) described in the test definition j. Let l_j' be Levenshtein distance of the best matching measurement unit. If no measurement unit is specified in the KB, then l_j' is zero. A cost l_j'' is then calculated as $l_j'' = c_j + l_j' / 3$, and finally the row is classified with the KB definition $i' = \mathrm{argmin}_{j \in J} l_j''$.

If the classification has cost c_i, greater than 0.51, then the procedure fails and the row is discarded.

The content of the *result cell* is stored internally as a floating point number, if possible. Otherwise it is interpreted as a generic alphanumeric string.

E. Exportation in XML format

In this phase, the data extracted from the document are saved in an XML output file. An excerpt of a typical output file is shown in Fig. 4.

The most relevant elements in the XML output have tag <test>. A <test> element contains the following elements:

- <testId> and <name> are, respectively, the unique test identifier and the test name. The available identifiers and test names are listed in the KB.
- <result> and <unit> are the result and the measurement unit of the test.
- <nameRaw>, <resultRaw>, <unitRaw> are the raw results of the OCR (without KB-driven post-processing), indicating respectively the test name, the test result, and the measurement unit.
- <nameIm>, <resultIm>, <unitIm>, are the coordinates of the boxes which bound the corresponding elements in the image. The attribute *array* indicates the size, 1 x 4, of the array containing the coordinates. This array is serialized to a string that can be easily parsed.

The previously mentioned elements have an attribute, *type*, with values “numeric” or “string”, that indicate the class of the data contained inside the element.

This XML output has been conceived in order to share medical laboratory results in a simple manner.

F. Knowledge base (KB)

The KB contains the definitions of the medical tests and the test headers that the system is able to recognize. For simplicity, each definition corresponds to a table row in a spreadsheet file, an excerpt of which is given in Table II.

Each definition consists of a set of attributes:

- *testId*: unique test or header identifier;
- *name*: normalized test name;

- *unit*: normalized test unit;
- *nameAliases*: list of test name variants;
- *unitAliases*: list of measurement unit variants;
- *testHeaderId*: list of *id* headers associated to test name variants;
- *headerType*: specifies if it is an header, and which type of header (H1 or H2);
- *multiRow*: specifies if the result is multi-row;
- *specialParsing:* specifies post-processing functions for handling particular tests.

Since medical tests may be given different names in different laboratories, it is necessary to relate each variant to a unique test identifier (*testId* attribute) and descriptive name (*name* attribute). The possible textual variants of the test name, which comprise also abbreviations and different spellings, are collected in a list (*nameAliases* attribute). The same reasoning applies to normalized units (*unit* attribute) and their variants (*unitAliases* attribute). The use of the KB is particularly useful for the correct recognition of the measurement units, because OCRs, if not properly trained or configured, can have high error rates due to the presence of non-Latin characters (e.g. µ) that are wrongly recognized.

Three other attributes, *testHeaderid, headerType*, *multiRow*, allow the system to handle cases in which the data relevant to a given test should be extracted by examining multiple lines. For any given name variant of a medical test, an associated header can eventually be specified by using the *testHeaderId* attribute. For header definitions, the *headerType* attribute differentiates between H1 and H2 headers, whose meanings have been explained in Sec. III.C. The *multiRow* attribute is used to specify that the result can occupy more than one row as happens, for example, for the microscopic analysis of the urine sediment, which often occurs in form of some descriptive text.

The *specialParsing* attribute is aimed at handling tests, such as *Urine specific gravity*, in which the measurement unit is often not given and should be deduced by the numerical result choosing among ‘g/mL’ and ‘g/L’.

IV. SYSTEM PERFORMANCE

In this Section experimental results are illustrated. The system performance has been analyzed in detail by applying the proposed method to the recognition of printed laboratory tests, and quantitative results are reported.

The KB used in this experimentation included about 120 definitions, tailored for recognizing four different kinds of documents coming from different laboratories. These documents contained laboratory test prescribed regularly to patients by nephrologists. The algorithm parameters were chosen by means of experimentation on a few pages.

The final evaluation procedure consisted in the following steps:

- Selection of 20 pages of laboratory tests, in Italian language. Each page, whose size is A4, has been digitalized at 300 dpi by an off the shelf scanner, giving grayscale image files in PNG format.
- Creation of a ground-truth database containing the medical tests present on each page. Each record, which will be referred later as *true test*, contains the following fields: *testId*, normalized test *name*, test *result*, normalized measurement *unit*, page identifier *pageId*. The ground-truth database contained 480 *true tests*.
- Processing of the images with the proposed system, and creation of output XML files containing the extracted data. Creation of a database of extracted data, with the same

structure of the ground-truth database, containing what will be referred as *estimated tests* in the following discussion. Image skew was not corrected.

- Comparison between *true tests* and *estimated tests*, and automatic creation of a report.

Total processing time was about 18 minutes using a notebook with an Intel Core 2 X9100 3 GHz processor and 4 GB of RAM.

Global statistics relevant to the entire set of documents are illustrated in Table III.

The definition of each event counted by the statistics and their relative frequency of occurrence (obtained dividing by the number of *true tests*) are reported.

The *test mismatch* error rate, which counts *true tests* that doesn't match any *estimated test* on the same page, is 4.8%.

Test name mismatches were almost due to excessively bad character recognition, with only one case of wrong segmentation in which the test *name* and the test *result* were merged in a single cell. Hence, the algorithm was selective in discarding test *names* recognized with too many character errors, according to the threshold illustrated in Sec. III.D .

Two *numeric mismatches* were due to the decimal separator (a comma in Italian) interpreted as a digit.

Two *string mismatches* occurred. In the first case, an anomalous result, ">400", has been extracted as "5400". In the second case, a long alphanumeric result has been extracted with some OCR errors, but it is still readable (in Italian): "ESAME MICROSCOPICO DEL SEDIMENTO Alcune cellule basse vie;0-5 Leuccciti per campo;0-5 Emazie per campo;Diversi cristalli ossalatc di calcio".

It should be noted that the *spurious test names* statistic is zero, meaning that the system has never interpreted some characters as tests when they are not.

This is true also for a page, included in the experiment, which contained only the laboratory template and no tests to extract.

V. CONCLUSION

The manual insertion of laboratory results by the medical or nursing staff is time consuming and produces errors. However the use of electronic medical records and databases has many benefits, among which the possibility of improving treatments of diseases more readily and accurately, and the availability of clinical data for research purposes.

The algorithm presented here, which has been experimented on laboratory results of patients with renal problems, overcomes the limitations of manual entering and is able to extract and interpret data originated from different laboratories.

This kind of automation is not a simple task, as it requires many processing steps and several parameters to be tuned. However the fact that the problem has been subdivided in to steps with fine granularity simplifies the tuning of the system and make the algorithm applicable, in prospective, to a large set of typologies of laboratory results.

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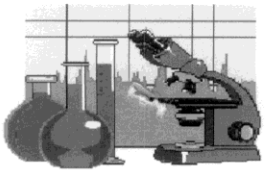
LIST OF FIGURES



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Sistema Gestione Qualita' certificato UNI EN ISO 9001:2000
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Pag. 1/3

Numero Pratica: **Del:** MARIO ROSSI
Data di Nascita: **Sesso:** VIA DANTE 1/a
Provenienza: Esterno ROMA RM
Ente: ASL BA/4
Punto prelievo: Ambulatorio

Esame Richiesto		Risultato	U.M.	Valori di Riferimento
Sg-EMOCROMO				
WBC		9,04	x10^3/µL	4,00-10,00
RBC		4,63	x10^6/µL	4,00-5,50
HGB		13,3	g/dL	12,0-16,0
HCT		41,1	%	38,0-48,0
MCV		88,8	fl	80,0-96,0
MCH		28,7	pg	27,0-34,0
MCHC		32,4	g/dL	32,0-37,0
PLT		286	x10^3/µL	140-500
RDW-SD		40,1	fl	37,0-45,0
RDW-CV		12,5	%	11,0-14,0
PDW		13,1	fl	10,0-16,0
MPV		10,6	fl	9,0-12,0
P-LCR		30,8	%	18,0-44,0
PCT		0,30	%	0,17-0,35
NEUT		4,74	x10^3/µL	1,70-7,20
LYMPH		2,92	x10^3/µL	0,50-4,00
MONO	*	0,88	x10^3/µL	0,10-0,80
EO	*	0,46	x10^3/µL	0,00-0,30
BASO		0,04	x10^3/µL	0,00-0,10
NEUT		52,5	%	40,0-70,0
LYMPH		32,3	%	20,0-40,0
MONO		9,7	%	1,0-10,0
EO		5,1	%	0,0-6,0
BASO		0,4	%	0,0-1,0
MORFOMETRIA CELLULARE		Nulla da segnalare		
S-GLUCOSIO *Enzimatico*		96	mg/dL	75-115
S-UREA *Enzimatico-UV*		28	mg/dL	10-50
S-URATO *Enzimatico colorimetrico*	*	2,07	mg/dL	2,40-5,70
S-CREATININA *Cinetico*		0,73	mg/dL	0,50-1,20

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Stampato il: xxxxxxxx
Validato il: IL DIRETTORE
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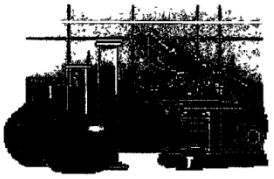
Fig. 1. Example image of medical laboratory tests.



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Numero Pratica: **Del:**
Data di Nascita: **Sesso:**
Provenienza: Esterno
Ente: ASL BA/4
Punto prelievo: Ambulatorio

MARIO ROSSI
VIA DANTE 1/a
ROMA RM

Esame Richiesto	Risultato	U.M.	Valori di Riferimento
Sg-EMOCROMO			
WBC	9,04	x10^3/µL	4.00-10.00
RBC	4,63	x10^6/µL	4.00-5.50
HGB	13,3	g/dL	12.0-16.0
HCT	41,1	%	38.0-48.0
MCV	88,8	fl	80.0-96.0
MCH	28,7	pg	27.0-34.0
MCHC	32,4	g/dL	32.0-37.0
PLT	286	x10^3/µL	140-500
RDW-SD	40,1	fl	37.0-45.0
RDW-CV	12,5	%	11.0-14.0
PDW	13,1	fl	10.0-16.0
MPV	10,6	fl	9.0-12.0
P-LCR	39,6	%	18.0-44.0
PCT	0,30	%	0.17-0.35
NEUT	4,74	x10^3/µL	1.70-7.20
LYMPH	2,92	x10^3/µL	0.50-4.00
MONO	0,88	x10^3/µL	0.10-0.80
EO	0,46	x10^3/µL	0.00-0.30
BASO	0,04	x10^3/µL	0.00-0.10
NEUT	52,5	%	40.0-70.0
LYMPH	32,3	%	20.0-40.0
MONO	9,7	%	1.0-10.0
EO	5,1	%	0.0-6.0
BASO	0,4	%	0.0-1.0
MORFOMETRIA CELLULARE	Nulla da segnalare		
S-GLUCOSIO *Enzimatica*	96	mg/dL	75-115
S-UREA *Enzimatico-UV*	28	mg/dL	10-50
S-URATO *Enzimatico colorimetrico*	2,07	mg/dL	2,40-5,70
S-CREATININA *Cinetico*	0,73	mg/dL	0,50-1,20

e-mail:xxxxxxxxxxxxxxxxxxxxxxxxxxx visitate il nostro sitoxxxxxxxxxxxxxxxxxxxxxxxxxx

Stampato il xxxxxxxx
Validato il IL DIRETTORE
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xxxxx

Fig. 2. Segmentation of the most relevant data. The page footer is discarded by subsequent processing.

Esame Richiesto	Risultato	U.M.	Valori di Riferimento
Sg-EMOCROMO			
WBC	9,04	x10^3/µL	4,00-10,00
RBC	4,63	x10^6/µL	4,00-5,50
HGB	13,3	g/dL	12,0-16,0
HCT	41,1	%	38,0-48,0
MCV	88,8	f	80,0-96,0
MCH	28,7	pg	27,0-34,0
MCHC	32,4	g/dL	32,0-37,0
PLT	286	x10^3/µL	140-500
RDW-SD	40,1	f	37,0-45,0
RDW-CV	12,5	%	11,0-14,0

Fig. 3. Expanded view of Fig. 2.

```
<?xml version="1.0" encoding="utf-8"?>
<medicalRecord version="2.0"><folder><labResults>
   <test>
      <nameRaw type="string">WBC</nameRaw>
      <nameIm array="[1 4]" type="numeric">[[ 247 1000  328 1036]]</nameIm>
      <name type="string">WBC</name>
      <resultRaw type="string">9,04</resultRaw>
      <resultIm array="[1 4]" type="numeric">[[1025 1000 1092 1036]]</resultIm>
      <result type="numeric">9.04</result>
      <unitRaw type="string">x1 O^3/pL</unitRaw>
      <unitIm array="[1 4]" type="numeric">[[1412 1000 1556 1037]]</unitIm>
      <unit type="string">10^3/uL</unit>
      <testId type="numeric">17</testId>
   </test>
   …
   <test>
      <nameRaw type="string">S-CREATININA</nameRaw>
      <nameIm array="[1 4]" type="numeric">[[ 185 2761  434 2800]]</nameIm>
      <name type="string">S-CREATININA</name>
      <resultRaw type="string">0,73</resultRaw>
      <resultIm array="[1 4]" type="numeric">[[1022 2761 1089 2800]]</resultIm>
      <result type="numeric">0.73</result>
                                                <unitRaw type="string">mg/dL</unitRaw>
      <unitIm array="[1 4]" type="numeric">[[1410 2761 1506 2800]]</unitIm>
      <unit type="string">mg/dL</unit>
      <testId type="numeric">32</testId>
   </test>
</labResults></folder></medicalRecord>
```

Fig. 4. An excerpt of an output XML file containing data extracted from medical laboratory tests of Fig. 1.

LIST OF TABLES

	Test name cell	Test result cell	Test measurement unit cell	Test reference range cell
Test row	Present	present	don’t care	don’t care
Result row	Absent	present	absent	absent
Name row	Present	absent	don’t care	don’t care

Table I. Row classification according to the cell types it contains

testId	*name*	*unit*	*nameAliases*	*unitAliases*	*testHeaderId*	*headerType*	*multiRow*	*specialParsing*
1	RBC	10^6/uL	RBC	10^6/uL				
2	HGB	g/dL	HGB	g/dL				
10	RDW	%	RDW	%				
11	PLT	10^3/uL	PLT	10^3/uL				
21	LYMPH%	%	LYMPH%	%				
31	S-URATO	mg/dL	S-URATO	mg/dL				
44	CLEARANCE CREATININA	mL/min	CLEARANCE DELLA CREATININA, CLEARANCE CREATININA	mL/min,mL/minute				
51	BILIRUBINA TOTALE	mg/dL	BILIRUBINA TOTALE	mg/dL				
1052	BILIRUBINA FRAZIONATA		BILIRUBINA FRAZIONATA			2		
52	BILIRUBINA FRAZIONATA DIRETTA	mg/dL	BILIRUBINA FRAZIONATA DIRETTA, DIRETTA	mg/dL	0, 1052			
53	BILIRUBINA FRAZIONATA INDIRETTA	mg/dL	BILIRUBINA FRAZIONATA INDIRETTA, INDIRETTA	mg/dL	0, 1052			
1062	CICLOSPORINA	ng/mL	CICLOSPORINA	ng/mL		1		
62	CICLOSPORINA T0	ng/mL	CICLOSPORINA T0, T0	ng/mL	0, 1062			
63	CICLOSPORINA T2	ng/mL	CICLOSPORINA T2, T2	ng/mL	0, 1062			
103	SODIO	mEq/L	SODIO	mEq/L, mmoli/L				
109	COLORE		COLORE					
120	PESO SPECIFICO	g/L	PESO SPECIFICO					1
121	ESAME MICROSCOPICO DEL SEDIMENTO		ESAME MICROSCOPICO DEL SEDIMENTO			1	1	

Table II. Knowledge base excerpt

Statistic name	Relative frequency	Absolute frequency	Description of the event counted by the statistic
Test matches	95.2 %	457	The *true test* matches an *estimated test* on the same page.
Test mismatches	4.8 %	23	The *true test* doesn't match any *estimated test* on the same page.
Test names matches	97.9 %	470	The *true test name* (or, equivalently, *testId*) matches an *estimated test name* on the same page.
Test names mismatches	2.1 %	10	The *true test name* (or, equivalently, *testId*) doesn't match any *estimated test name* on the same page.
Numeric mismatches	2.3 %	11	The *true test name* matches an *estimated test name* on the same page, but the *result*, which is expressed in numeric form, differs.
String mismatches	0.4 %	2	The *true test name* matches an *estimated test name* on the same page, but the *result*, which can't be expressed in numeric form, differs.
Spurious test names	0.0 %	0	The *estimated test name* (or, equivalently, *testId*) doesn't match any *true test name* on the same page.
Aggregated errors	*4.8 %*	23	Any event that contributes to *Test mismatches* or *Spurious test names* statistics.

Table III. Performance evaluation