COMPUTER AIDED MEDICAL DIAGNOSIS

An Alternative to an 'Expert System'

If an expert system is to be of use to a medical practitioner, then the rules as are defined by the expert must apply to the data and the patients of the practitioner. This is unlikely because the data and the patients of the expert are generally subsets of the data and the patients of the practitioner.

This report is of a method in which the intelligence is the frequency of each level of test result in each of the diagnostic categories and the rule is the repeated scaling of the frequency of each diagnosis as each test result indicates a frequency within each diagnostic category for that particular test result. Experience with this method in the classification of proteinuric glomerular disease will be presented. The is relevant to a discussion of the FORTH programming language because this computing application must be complex, fast, flexible and compact.

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Systems of artificial intelligence permit an 'expert' to define the current knowledge of a subject in terms of a set of rules that are then woven into the fabric of a computational system. A less experienced individual, by providing the pertinent data, arrives at the same conclusion as would this 'expert' for each individual case. Such a system is useful if the rules and data are universal and complete.

Knowledge in most fields is a dynamic process. Criteria change frequently, as in medicine where the new or refined diagnosis of disease is the result of rapidly advancing medical science. A great deal of effort is required to remain 'expert' in even a small area of medical practice. Delay exists between the availability of knowledge, an 'experts' assimilation of new knowledge, and the dissemination of an 'expert system' based upon these new observations and conclusions. In medicine, this process is complicated further because the rules as are applied to the subset of the patients and data of the 'expert' are often not the same as the rules that must be applied to the data and patients of the practitioner.

Each practitioner manages a **CASE** database which contains data and diagnoses for each patient. The data include the answers to specific questions (medical history), results of direct and indirect observation (physical examination) and the results of procedures such as laboratory tests. The **ALGORITHMS** relating data to diagnoses are learned and modified as the practitioner becomes more experienced with these data and diagnoses.

New methods of testing are defined by those engaged in medical research. The results of these new methods of testing are compared to the results of conventional testing in the subset of patients at the research institution. New algorithms are defined if the results of the new procedure are superior to the results of the conventional procedures. This knowledge is communicated from experts to practitioners in the form of lectures and scholarly publications. Unfortunately, the relevance of these new methods of diagnosis is often obscure to the practitioner.

The **CASE** database and the **ALGORITHMS** mentioned above exist within the mind of the practitioner. It is increasingly likely that both will exist within a computational system. What might be some of the ideal properties of this database and these algorithms?

The database must express complex information, probably by combining elements selected from a large knowledge base. Both the database and the knowledge base must be capable of virtually limitless extension. The system should be compact so that it can be as portable as a checkbook, because it must function within the working environment of the practitioner (patients bedside). It must be possible to define algorithms from the database and to test the response of the database to algorithms because a practitioner will commit to an 'expert system' only if convinced

that this system improves his capability to make the 'proper' diagnosis in each of his patients. A 'proper' diagnosis is not only an accurate diagnosis but also indicates a process of diagnosis that is efficient and minimizes both expense and risk to the patient.

One approach is detailed as follows:

1) Define a total of I pertinent tests, T, in terms of intervals of results each interval designated as i.
2) Define a total of J pertinent diagnoses, D , each designated as j.
3) Develop frequency distributions, F, for each test result interval in each diagnosis.

The frequency of each diagnosis after iteration i is then computed as:

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Dj [ F(i) ] = F [ Dj (Ti) ] * Dj [ F(i-1) ]

              / SUM(j) ( F [ Dj (Ti) ] * Dj [ F(i-1) ] )
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where F [Dj (Ti)] is the frequency of a result of test i, for diagnosis j,

Dj [F(i)] is the frequency of diagnosis j after the test i has been considered,

Dj [F(i-1)] is the frequency of diagnosis j before the test i has been considered. In the absence of bias, F(0) = 1/J; initial bias can reflect the distribution within a population or the frequencies passed from a previous processing of data.

Ideally, during each diagnotic process, the number of possibilities should decrease and converge to the most likely answer. If testing is not complete, then a modification of the equation noted above guides in the selection of the optimal path to a more precise appraisal of the patient, if a more precise appraisal is possible; the cost and risk in relation to the potential benefit are indicated concomitantly.

This method was applied to the results of sixteen clinical relevant tests (nine intervals defined for each) in 208 patients with one of twelve proteinuric glomerular diseases as were classified by the microscopic analysis of excised tissue (biopsy). Between 2 and 41 patients existed in each category. Frequency distributions prepared for each test for each diagnosis constituted the intelligence. When the rule (above equation) was applied retrospectively, 75 (62-100) per cent of cases were classified appropriately (Table I). Prospectively, seven of eleven patients have been properly classified (Table II).

This database also includes the results of a new method of understanding the pathophysiology of proteinuric glomerular disease. When data has been obtained from a sufficient number of cases, histograms will be generated based upon break points as are suggested from the results of Wilcoxon Rank Sum statistics. These will then be applied with the clinical data to see if the accuracy of diagnosis is improved. The goal is not only to better understand the pathophysiology of proteinuria, but also to define a cheaper, faster and safer method of diagnosing glomerular disease. The report of each case (Table III) indicates the results of conventional clinical tests (solid lines), the results of experimental testing (dashed lines), the probable diagnoses (results) compared to any initial bias (population), and a summary of the frequency of each test result in each of the diagnoses that were considered.

This application was initially written in BASIC. It has proved worthwhile to implement also in DBASE-III. Both applications are tediously slow; the DBASE-III application is not easily extensible. If this approach delineated in this paper is deemed to be worthwhile and is not currently available as an application in FORTH, it might be worth the effort to develop a suitable database and intelligence system to satisfy these criteria.

TABLE I.
DIAGNOSES INFERRED FROM THE RETROSPECTIVE TABULATION OF SIXTEEN TEST RESULTS

CALLED	MCD	MN	IGA	FSN	MPG	PGN	CGN	SLE	AMY	DM	MSP	LCD	TOTAL
MCD	28	6	1	3	1				1		1		41
MN	5	30	1		1		1				1		39
IGA	1	4	17	2			1				2		27
FSN	1	1	1	15	1	2							21
MPG					8						1		9
PGN		1				7	1	1			1		11
CGN			2	1			21			1	1		26
SLE			1					10					11
AMY									9				9
DM										5			5
MSP					1		1				5		7
LCD												2	2
TOTAL	35	41	23	21	11	9	25	11	10	6	12	2	208

TABLE II.
DIAGNOSES INFERRED BY PROSPECTIVE COMPARISON OF SIXTEEN TEST RESULTS

CALLED	MCD	MN	IGA	FSN	MPG	PGN	CGN	SLE	AMY	DM	MSP	LCD	TOTAL
MCD	3												3
MN	1	1											2
IGA													
FSN													
MPG													
PGN													
CGN							2						2
SLE			1					1					2
AMY													
DM							1						1
MSP													
LCD													
TOTAL	4	1	1				3	1		1			11

ABBREVIATE	DIAGNOSIS
MCD	Minimal Change Disease
MN	Membraneous Nephropathy
IGA	IgA Nephropathy
FSN	Focal Sclerosing Nephropathy
MPG	Membranoproliferative Glomerulonephritis
PGN	Proliferative Glomerulonephritis
CGN	Cresentic Glomerulonephritis
SLE	Systemic Lupus with Nephritis (WHO III,IV)
AMY	Amyloidosis
DM	Diabetic Nephropathy
MSP	Mesangial Proliferative Glomerulonephritis
LCD	Light Chain Glomerulopathy

[redacted] [240 , 281]
DATE OF BIRTH 08/24/44 43.0 M
[redacted]
/ / ANATOMICAL DIAGNOSIS MN

02/19/87 BIOPSY DISEASE ACTIVE COMPUTED DIAGNOSIS MN 0.3726

ANALYTE	CONCENTRATIONS mg/dl SERUM	URINE	CLEARANCE ml/min
CREATININE	1.2	65	135
AGP (OROSOMUCOID)	75	9.00	0.2633
ALBUMIN	2730	157.00	0.1262
TRF (TRANSFERRIN)	240	13.00	0.1189
IGG	450	0.00	0.0000
ANTITRYPSIN	200	12.00	0.1317
IGA	200	2.00	0.0219
HPT (HAPTOGLOBIN)	180	0.00	0.0000
LDL (LIPOPROTEIN)	220	0.00	0.0000
MACROGLOBULIN	240	0.00	0.0000
CC3	138	0.00	0.0000
CC4	30	0.00	0.0000
IGM	117	0.00	0.0000

Radius of GBM in A.U. 20.95 A.U. (20 - 30)
Fraction GFR diverted 0.0114 (0.001 < p < 0.01)
For a total of 4 Filtered Proteins.

Selectivity Index -1.88
Selectivity Degrees 61 (0.001 < p < 0.01)

Proteinuria of 6.6 gm/day is PARTLY-SELECTIVE .

DIAGNOSES IN ORDER OF PROBABILITY		results	population	
Membraneous Nephropathy	F(I)	0.37255	0.22273	F(∅)
Mesangio-proliferative GN		0.17372	0.06364	
Amyloidosis		0.15800	0.04545	
Minimal Change Disease		0.15059	0.15455	
Proliferative Glomerulonephritis		0.14244	0.05909	
IgA Nephropathy		0.00259	0.10909	
Cresentic Glomerulopathy		0.00016	0.10909	

frequency (per cent) of each diagnosis for each test result

DX	AGE	VEC	ALB	IGA	RAD	PRO	CLE	IGG	ANT	HPT	LDL	CC3	CC4	TRF	IGM	AGP	MAC
MCD	9	***	9	26	***	15	4	26	38	12	15	18	26	47	21	50	24
MN	20	***	29	19	***	38	11	19	4	6	31	10	31	58	19	29	33
FSN	25	***	8	21	***	24	0	12	8	17	29	17	38	12	17	17	17
MPG	0	***	22	0	***	14	0	33	0	33	22	22	22	33	44	33	22
PGN	8	***	25	8	***	9	11	17	8	17	58	33	50	42	33	25	25
CGN	8	***	35	13	***	8	0	9	0	0	35	22	48	65	13	0	4
SLE	0	***	9	9	***	0	0	9	9	36	18	18	9	18	0	9	27
AMY	0	***	20	0	***	22	11	30	30	0	50	20	0	70	0	33	30
DM	17	***	33	33	***	60	0	33	17	33	33	17	17	67	33	0	17
MSP	14	***	25	33	***	8	17	8	0	0	33	42	33	42	0	17	0
IGA	8	***	9	9	***	5	10	9	9	27	59	23	64	18	14	14	14
LCD	0	***	0	0	***	100	0	0	0	0	100	50	0	0	0	0	0