

Machine learning - could it help in the RIGVIR case?

Manfred Sneps-Sneppe

Ventspils University of Applied Sciences,
manfreds.sneps@gmail.com

Dmitry Namiot

Lomonosov Moscow State University, Moscow, Russia
dnamiot@gmail.com

FRUCT 2023

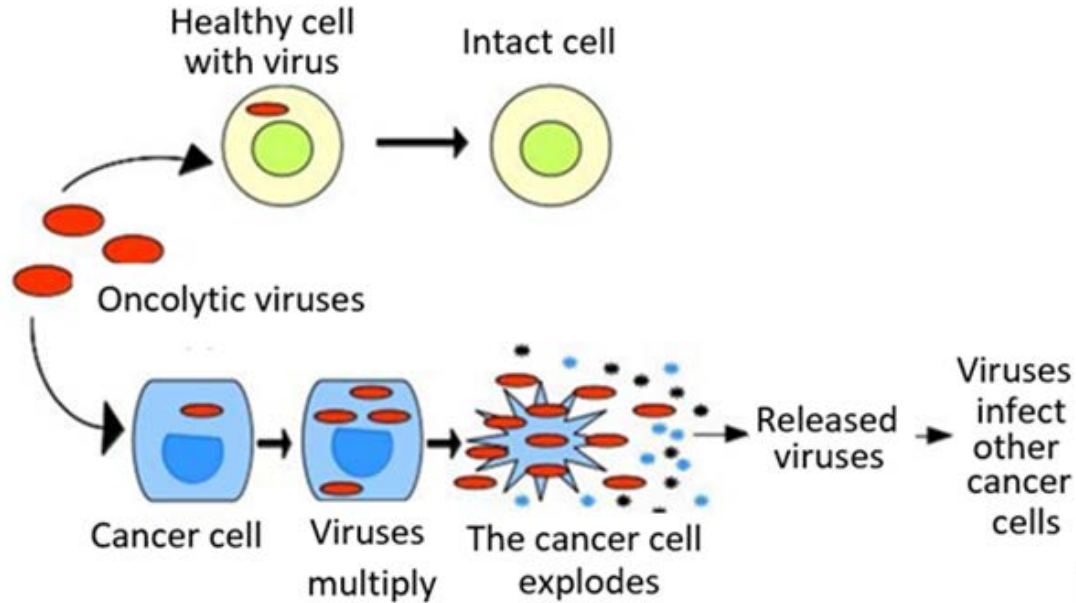
Riga, Nov 16, 2023

Content

- Introduction
- The RIGVIR story
- Machine learning for skin disease diagnoses
- How to interpret machine learning features
- Discriminant Analysis for automation of diagnoses

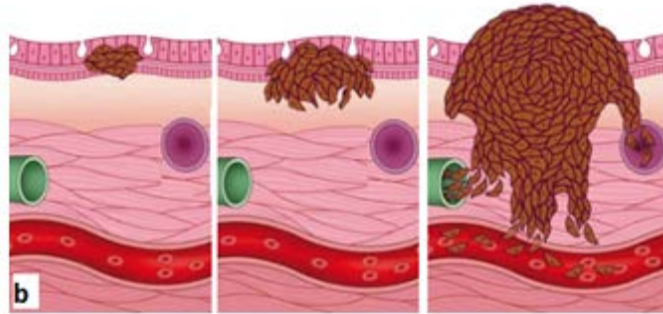
Introduction

Schematic representation of oncolytic virotherapy



Viruses can specifically infect cancer cells and then multiply until the cancer cells burst. The newborn viruses are then released to infect (and then burst!) other cancer cells.

Melanoma is the most dangerous type of skin cancer



- a) Melanoma starts from pigment-producing cells,
- b) three stages of melanoma, in the third stage it produces metastases.

Approved oncolytic viruses up to 2021

Year	Oncolytic virus	Type of tumor
2004	ECHO-7-Rigvir (Latvia)	melanoma
2005	H101 (China)	late-stage-refractory-nasopharyngeal-cancer
2015	T-VEC (USA)	advanced-melanoma
2021	Teserpaturev (Japan)	malignant-glioma

The first oncolytic virus in the world was the genetically unmodified enterovirus RIGVIR, which was approved in Latvia in 2004 for the treatment of skin melanoma.

All other three viruses are genetically modified ones.

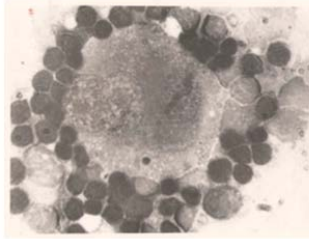
RIGVIR is some kind of miracle of nature.

Bifulco, M., Zazzo, E.D., Napolitano, F., et al. "History of how viruses can fight cancer: From the miraculous healings to the approval of oncolytic viruses". Biochimie. Vol 206, March 2023

The RIGVIR story

The research started in Latvia in 1959. The Latvian virologist team isolated 60 different viruses from the gastrointestinal tract of healthy children. One of these viruses called RIGVIR turned out to be the most suitable for oncology. The first RIGVIR clinical trial was approved in 1968.

The pre-registration clinical studies were performed from 1968 to 1991. The first genetically unmodified oncolytic virus RIGVIR was approved in Latvia in 2004 for the treatment of skin melanoma.



Melanoma cell surrounded
by lymphocytes during RIGVIR therapy

RIGVIR activates immune cells (lymphocytes) - T-cells and B-cells.

RIGVIR administration was based on the changes in CD4⁺, CD8⁺, and CD38⁺ lymphocytes.

Alberts, P., Tilgase, A., Rasa, A., et al. "The advent of oncolytic virotherapy in oncology: The Rigvir story". European Journal of Pharmacology. Vol 837, 15 Oct 2018

KĀ VĒRTĒT IMUNITĀTI (melanomas modelis)

Melanomas gaitas raksturojums		Perifēro asiņu imūnšūnu skaita (mm3) un attiecību						Imūnšūnu savstarpējo attiecību simboli						
		Ly	>	CD3	>	CD4	>	CD8	CD3/CD4	CD3/CD8	CD3/CD38	CD4/CD8	CD4/CD38	CD8/CD38
Kontrole – imūnšūnu skaits/attiecības		1900		1265		772		490	1,6	2,6	2,5	1,6	1,5	1,0
>, < par 27%		2400-1400	1,5	1600-925	1,6	970-570	1,6	620-360	2,0-1,2	3,3-1,9	3,2-1,8	2,0-1,2	1,9-1,1	1,3-0,7
Primārā melanoma	I A stadijā (CI II)	1900	>	1315	>	733	>	582	N	N	N	N	N	N =
	I B stadijā (CI III)	1900	>	1147	>	693	>	454	N	N	N	N	N	N =
	II A stadijā (CI IV)	1700	>	1107	>	714	>	393	N	N	N	N	N	N =
	Reaktīvs limfmezgls	2000	>	1407	>>	718	=	689	N	±↓	N	±	N	↑
Primārā melanoma 3 mēnešus pēc radikālas ekscīzijas	I A stadijā	2200	>	1440	>	806	>	632	N	N	N	N	N	N =
	I A, I B, II A stadijā	2100	>	1330	>	795	>	523	N	N	N	N	N	N =
	3-5 gadu stabilizācija	1800	>	1108	>	664	>	444	N	N	N	N	N	N =
Limfmezglu raksturojums pēc primārā perēkļa ekscīzijas 1 gada laikā	Limfmezgli kliniski normāli	2125	>	1419	>	851	>	568	N	N	N	N	N	N =
	Limfmezgli reaktīvi	2500	>	1682	>	1024	>	658	N	N	N	N	N	N =
	Limfmezgli metastāžu periodā	2700	>	1825	>	1164	>>	661	N	N	N	N	N	N =
	6-12 mēn. pirms limfadenektomijas	2151	>	1409	>	936	>>	470	N	N	±	±	↑	N =
	I A, I B, II A stadijā: limfmezglos	1600	>	1030	>	580	>	446	N	N	N	N	N	±
	metastāzes reģionālos limfmezglos	1600	>	1046	>	626	>	417	N	N	N	N	N	N =
Melanomas progresija	metastāzes ādā	1500	>	970	>>	490	=	480	±	±↓	N	±	N	↑
	Metastāzes plaušās	1600	>	926	>	504	>	422	N	N	N	±↓	N	↑
	Recidīvs	1600	>	1030	>	631	>	400	N	N	↑	N	↑	↑
	Metastāzes aknās	1400	>	890	>	575	>	313	N	N	±↑	N	N	↓
	Totāla progresija	2450	>	1789	>>	950	>	735	N	N	↓	N	↓↓	↓↓

Paskaidrojumi: – protekcijas simptomi – reaktīvo limfmezglu simptomi – progresijas simptomi – indikācijas bioterapijai

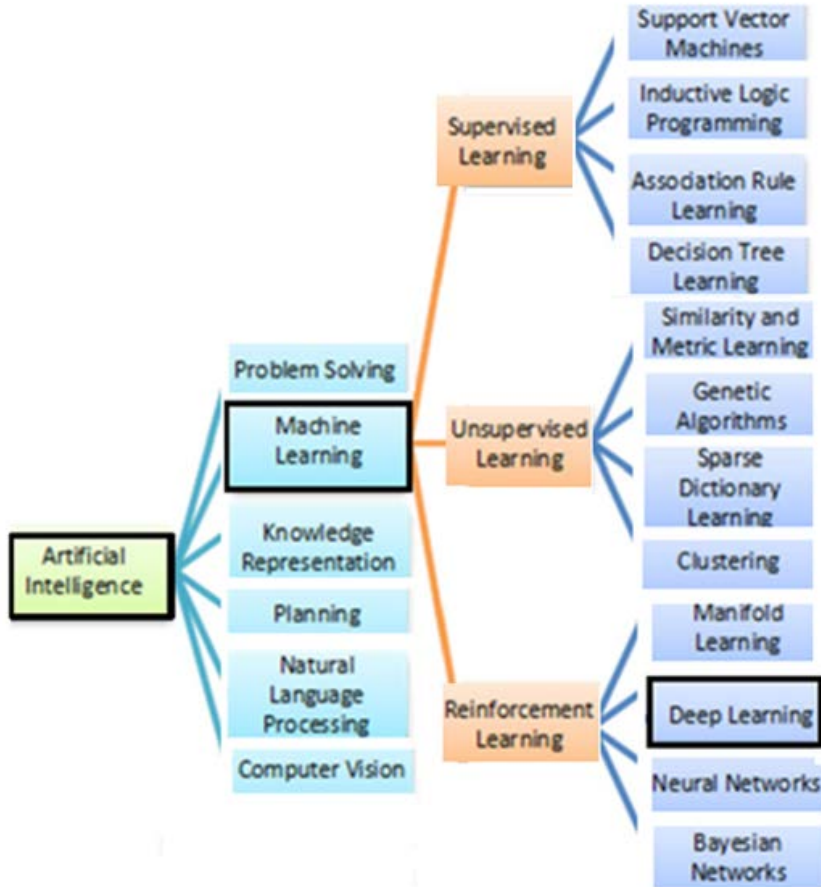
Muceniece, Aina,
and Venskus, Dita.
How to assess
immunity
(melanoma model).
Riga, 2007
(in Latvian).

Artificial intelligence

Machine learning is the heart of artificial intelligence, and its more promising research area is represented by deep learning

Machine-learning models have demonstrated great success in learning complex.

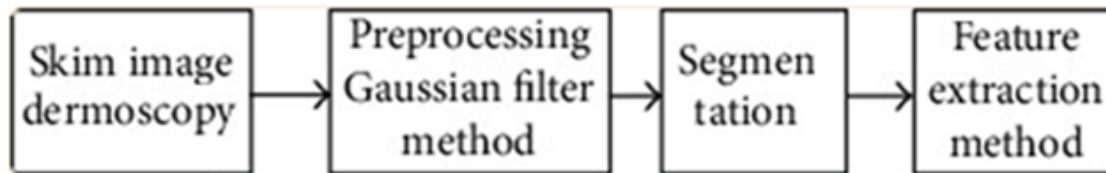
However, this increased focus has led to considerable confusion about **the notion of interpretability**.



Machine learning for skin disease diagnoses



Simple images extracted from the database



The skin disease detection using the feature-based method

DL model considered 13 statistical features: contrast, correlation, energy, homogeneity, mean, standard deviation, entropy, RMS, variance, smoothness, kurtosis, and skewness.

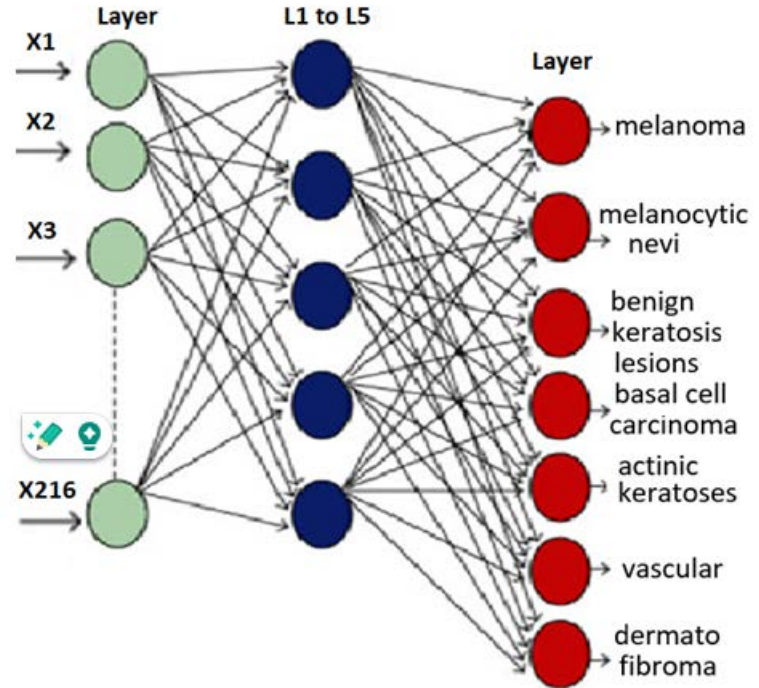
216 significant features were selected for training.

The architecture of artificial neural network (ANN)

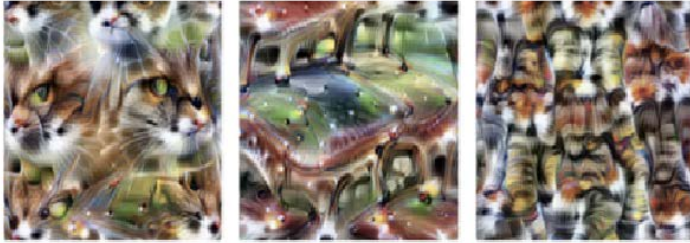
DL model considered 13 different statistical features: 216 significant features were selected for training.

Excellent results have been achieved in the diagnosis of skin diseases. The ANN model achieved the accuracy (98.35%).

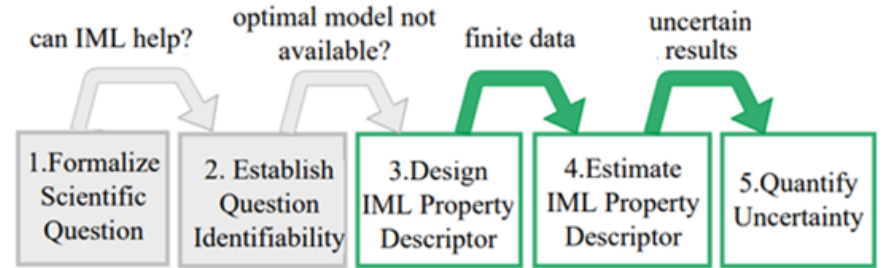
They can certainly speed up the work of doctors (like how an excavator works faster than a man with a shovel). Does it have any value for physician education? Unfortunately, **the doctor is unable to understand 216 computer-generated signs.**



On interpretable machine learning (IML)



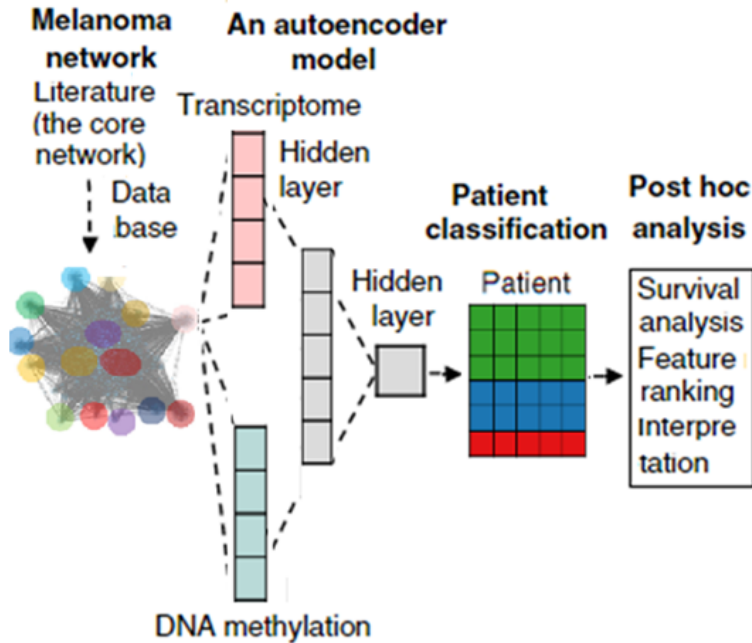
ML models are not elementwise representations
heads of cats (left image), car bodies (center), or bees (right)



An epistemic foundation for scientific inference

Freiesleben, T., König, G., Molnar, Ch., Tejero-Cantero, A. "Scientific Inference with Interpretable Machine Learning: Analyzing Models to Learn About Real-World Phenomena". June 2022.

On melanoma genomics and deep learning



Integration of The Cancer Genome Atlas data into a melanoma network

The resulted melanoma network contains 5860 molecules and 14 494 interactions.

Category	No. of gene symbols	No. of nodes
Transcriptome (gene expression)	55 500	4983
DNA methylation	33 487	5193
Somatic mutation	19 303	5015
Copy number variation	19 059	4952

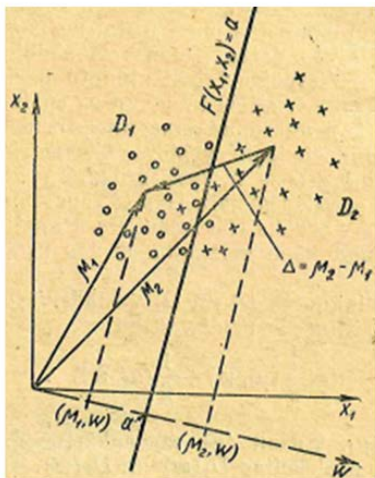
Overview of the genomics data

The studied example shows that melanoma genetic research has a very long way to medical practice.

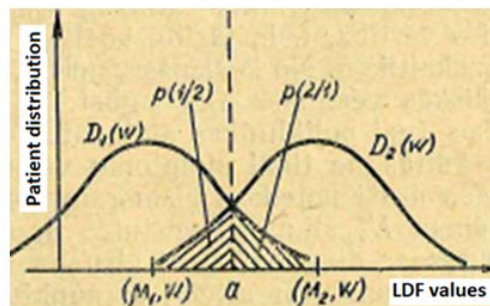
Discriminant Analysis for automation of diagnoses

Linear discriminant functions (LDF):

$$F = \omega_1 x_1 + \omega_2 x_2 + \dots + \omega_m x_m$$



Construction of LDF for two symptoms



Distribution of numerical values of LDF and selection scheme of diagnoses D_1 and D_2

Sneps-Sneppe, M. A. Mathematics, and Health Care. Moscow, 1982 (in Russian).

Medical example (1965-1978): Lung Cancer Moscow Oncology Research Institute's database



A chest X-ray showing a tumor in the lung
(marked by arrow)

How computers can improve diagnostic accuracy

Diagnostic result	Computer diagnosis	Radiologist diagnosis
Correct answer	87.8%	65%
Wrong answer	4.4%	10%
Refusal to diagnose	7.8%	25%

Statistical analysis, first of all, showed that out of 82 signs (answers to questions) and 240 symptoms of the disease, it is enough to leave 28 signs and 76 symptoms, i.e. 32% of the original data set.

Second, and more importantly, a nurse can fill out a medical chart and receive a diagnosis from a computer without the involvement of a doctor, and this diagnosis turns out to be much more accurate than the decision of a radiologist.

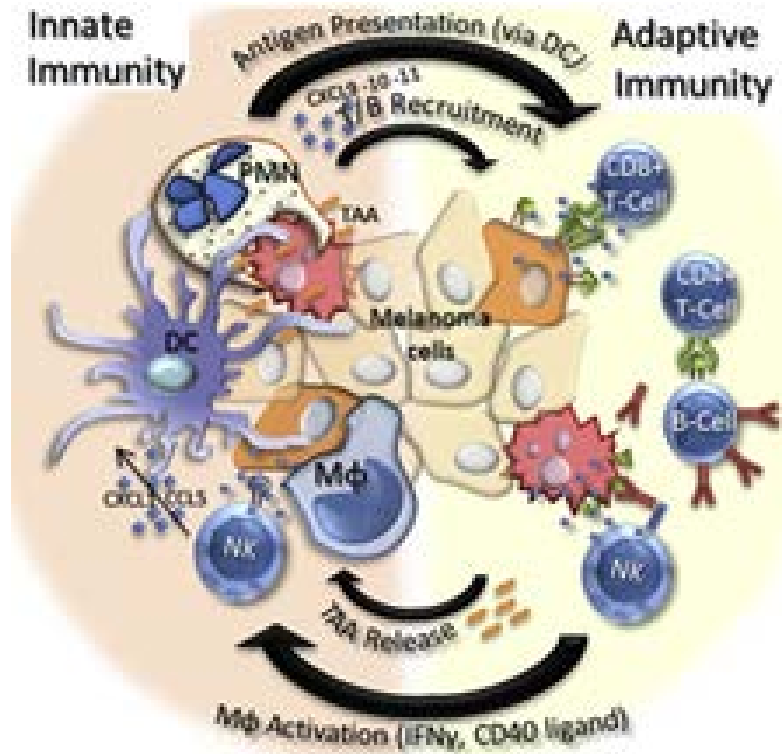
KĀ VĒRTĒT IMUNITĀTI (melanomas modelis)

Melanomas gaitas raksturojums		Perifēro asiņu imūnšūnu skaita (mm3) un attiecību						Imūnšūnu savstarpējo attiecību simboli						
		Ly	>	CD3	>	CD4	>	CD8	CD3/CD4	CD3/CD8	CD3/CD38	CD4/CD8	CD4/CD38	CD8/CD38
Kontrole – imūnšūnu skaits/attiecības		1900		1265		772		490	1,6	2,6	2,5	1,6	1,5	1,0
>, < par 27%		2400-1400	1,5	1600-925	1,6	970-570	1,6	620-360	2,0-1,2	3,3-1,9	3,2-1,8	2,0-1,2	1,9-1,1	1,3-0,7
Primārā melanoma	I A stadijā (CI II)	1900	>	1315	>	733	>	582	N	N	N	N	N	N =
	I B stadijā (CI III)	1900	>	1147	>	693	>	454	N	N	N	N	N	N =
	II A stadijā (CI IV)	1700	>	1107	>	714	>	393	N	N	N	N	N	N =
	Reaktīvs limfmezgls	2000	>	1407	>>	718	=	689	N	±↓	N	±	N	↑
Primārā melanoma 3 mēnešus pēc radikālas ekscīzijas	I A stadijā	2200	>	1440	>	806	>	632	N	N	N	N	N	N =
	I A, I B, II A stadijā	2100	>	1330	>	795	>	523	N	N	N	N	N	N =
	3-5 gadu stabilizācija	1800	>	1108	>	664	>	444	N	N	N	N	N	N =
Limfmezglu raksturojums pēc primārā perēkļa ekscīzijas 1 gada laikā	Limfmezgli kliniski normāli	2125	>	1419	>	851	>	568	N	N	N	N	N	N =
	Limfmezgli reaktīvi	2500	>	1682	>	1024	>	658	N	N	N	N	N	N =
	Limfmezgli metastāžu periodā	2700	>	1825	>	1164	>>	661	N	N	N	N	N	N =
	6-12 mēn. pirms limfadenektomijas	2151	>	1409	>	936	>>	470	N	N	±	±	↑	N =
	I A, I B, II A stadijā: limfmezglos	1600	>	1030	>	580	>	446	N	N	N	N	N	±
	metastāzes reģionālos limfmezglos	1600	>	1046	>	626	>	417	N	N	N	N	N	N =
Melanomas progresija	metastāzes ādā	1500	>	970	>>	490	=	480	±	±↓	N	±	N	↑
	Metastāzes plaušās	1600	>	926	>	504	>	422	N	N	N	±↓	N	↑
	Recidīvs	1600	>	1030	>	631	>	400	N	N	↑	N	↑	↑
	Metastāzes aknās	1400	>	890	>	575	>	313	N	N	±↑	N	N	↓
	Totāla progresija	2450	>	1789	>>	950	>	735	N	N	↓	N	↓↓	↓↓

Paskaidrojumi: – protekcijas simptomi – reaktīvo limfmezglu simptomi – progresijas simptomi – indikācijas bioterapijai

Muceniece, Aina,
and Venskus, Dita.
How to assess
immunity
(melanoma model).
Riga, 2007
(in Latvian).

Melanoma Clearance by Functioning Immune Cells



Conclusion

The main means of evaluating the effectiveness of melanoma treatment remains the analysis of leukocytes, as in the time of the oncolytic virus RIGVIR discoverer, Aina Muceniece (1924 – 2010).