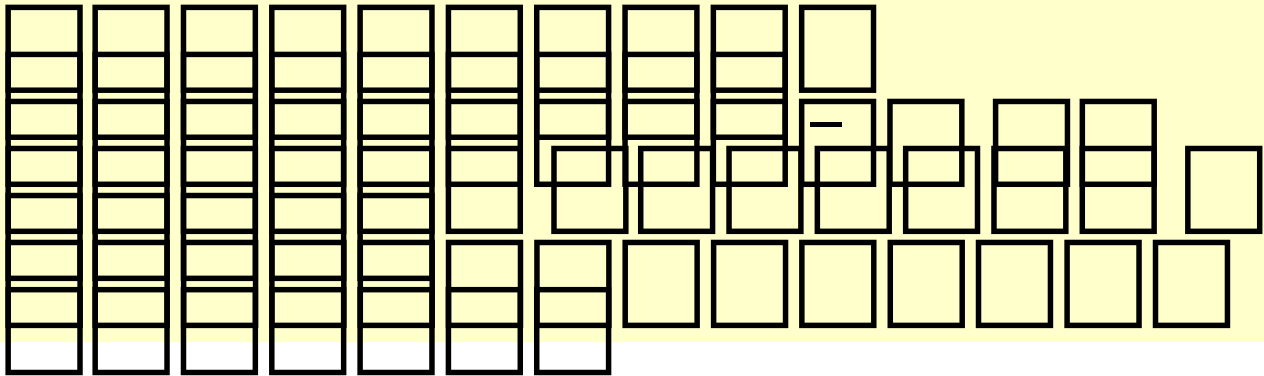
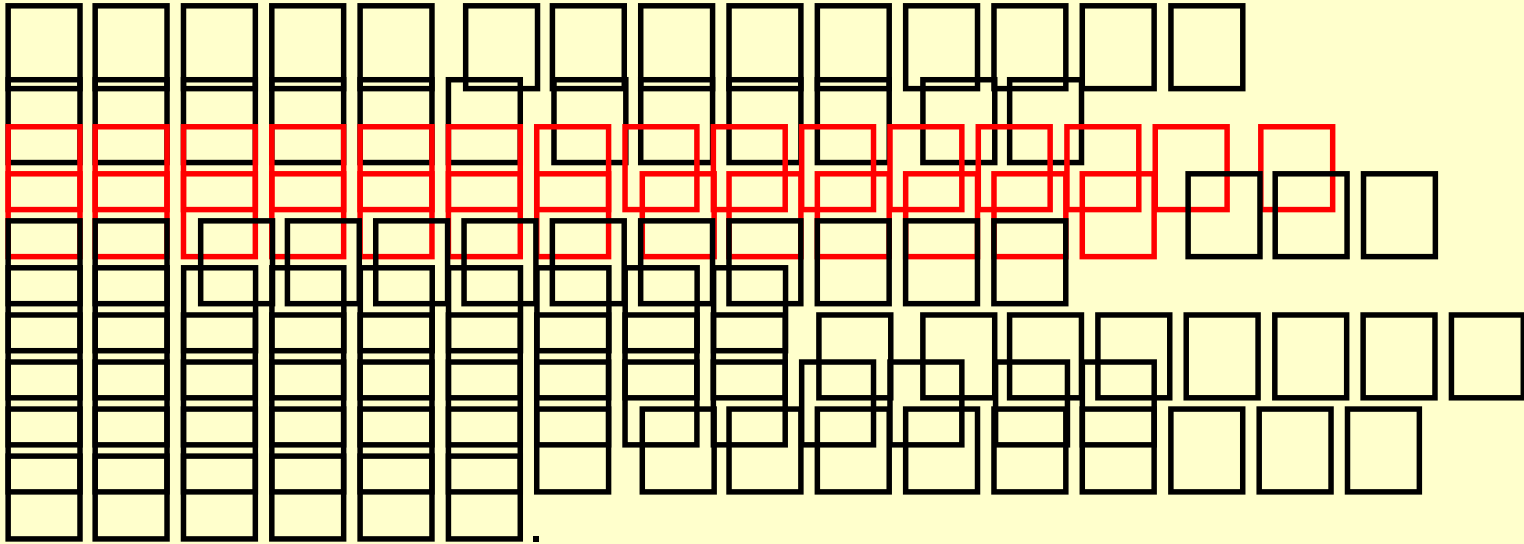


Белодробниот микробиом и неговата улога кај респираторни инфекции

**Асс. др. Ирина Ангеловска
Клиника за Пулмологија и алергологија**

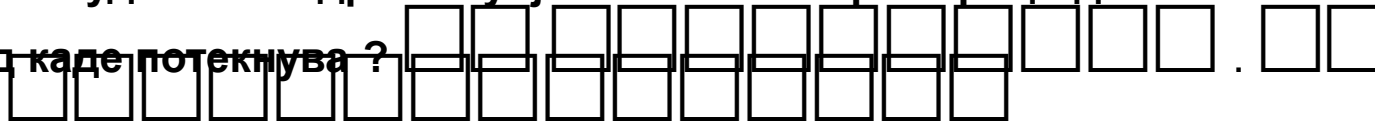


Дали белите дробови се стерилни ?

Не-стара теорија

>25 студии >700 здрави субјекти. Во сите примероци докажана бактериска ДНК

Од каде потекнува ?

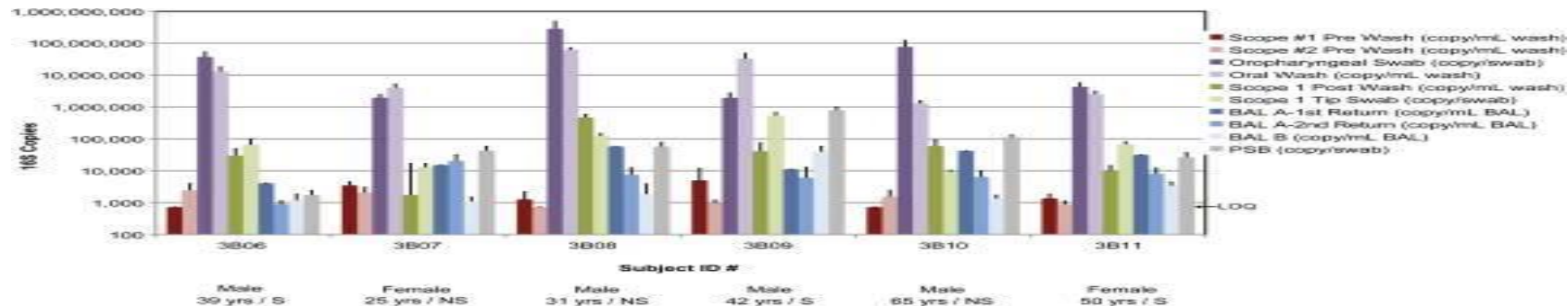


Начин на земање на примероци

спутум, индуциран спутум

- бронхоалвеоларен лават, брашинг,


- заштитено земени примероци (Protected sampling)



Charlson, Emily S. et al. "Topographical Continuity of Bacterial Populations in the Healthy Human Respiratory Tract." *American Journal of Respiratory and Critical Care Medicine* 184.8 (2011)

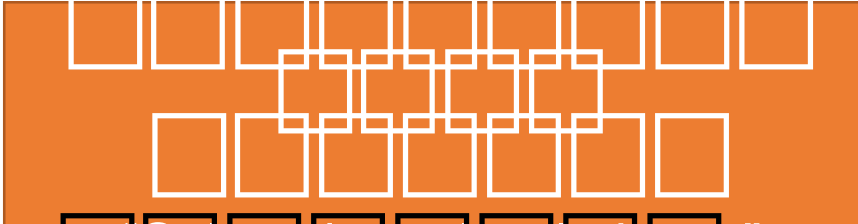
Нови молекуларни техники

Анализа на сите микроорганизми и на оние недектибилни со досегашни микробиолошки анализи



“OmniChip”

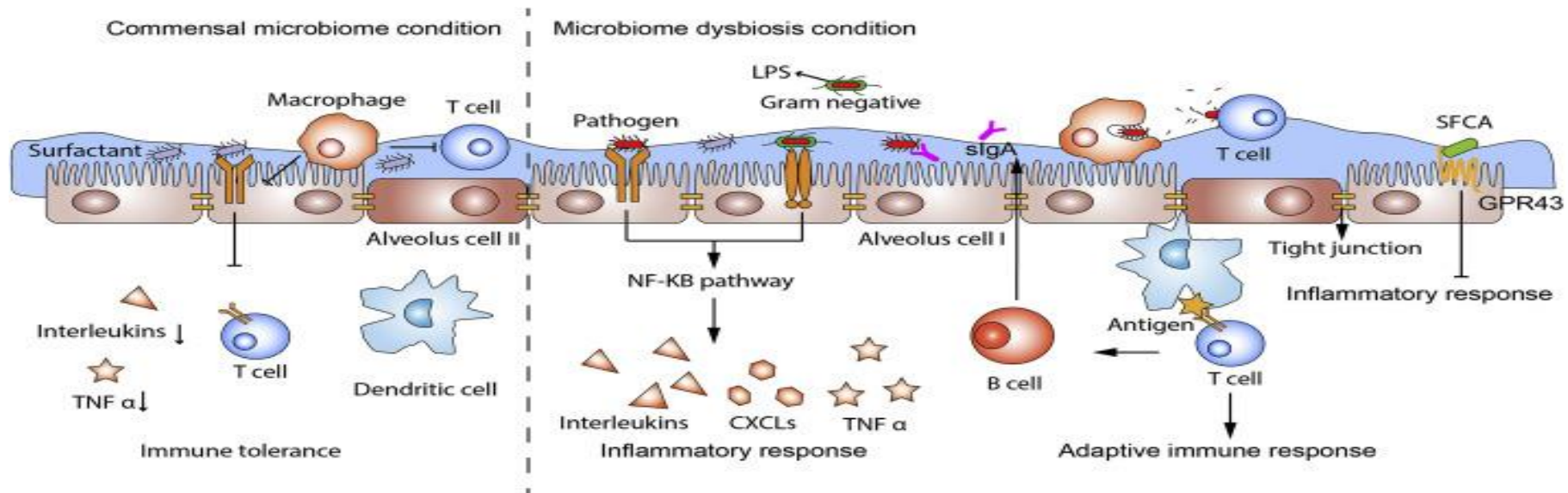
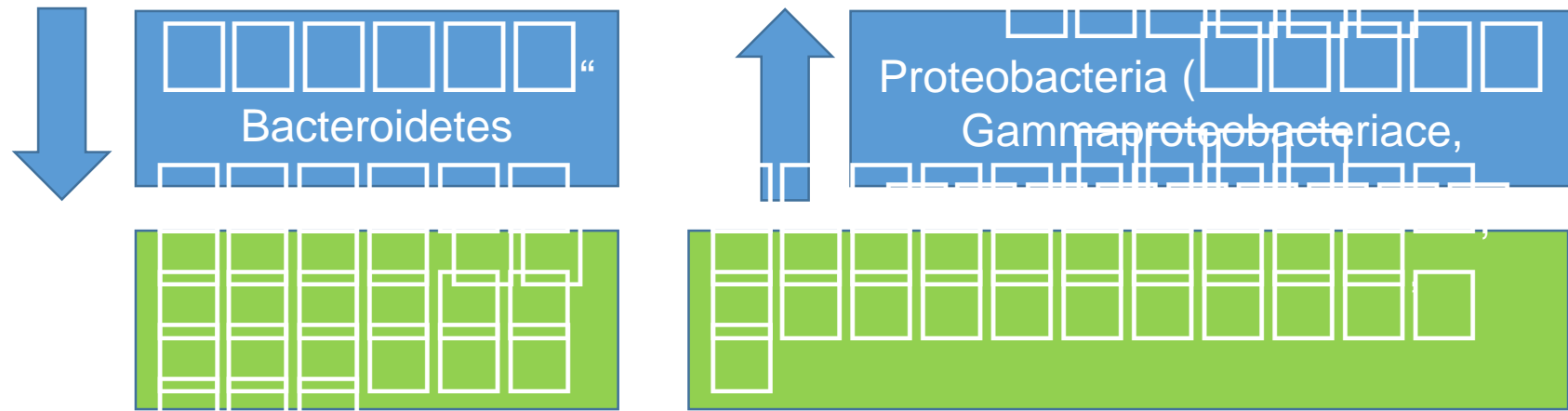
- секвенционирање на 16S r RNA
- Метагеномски (микробна DNA)
- Метатранскриptomски (микробна mRNA)



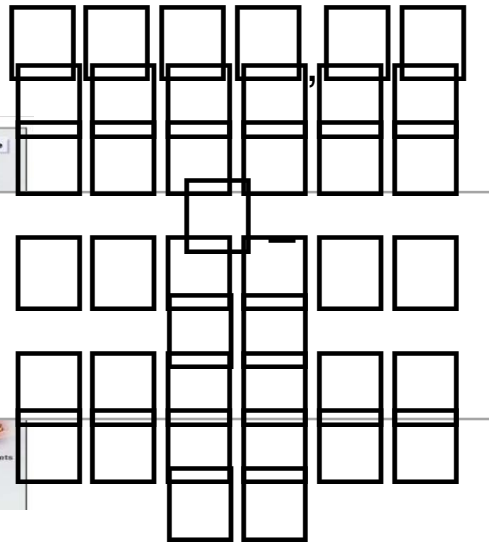
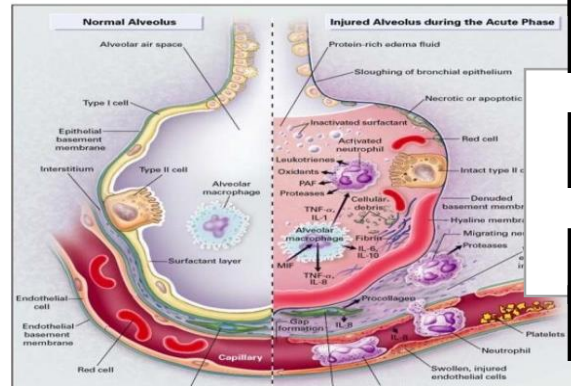
“OmniChip”

(Haemophilus influenzae, ...)

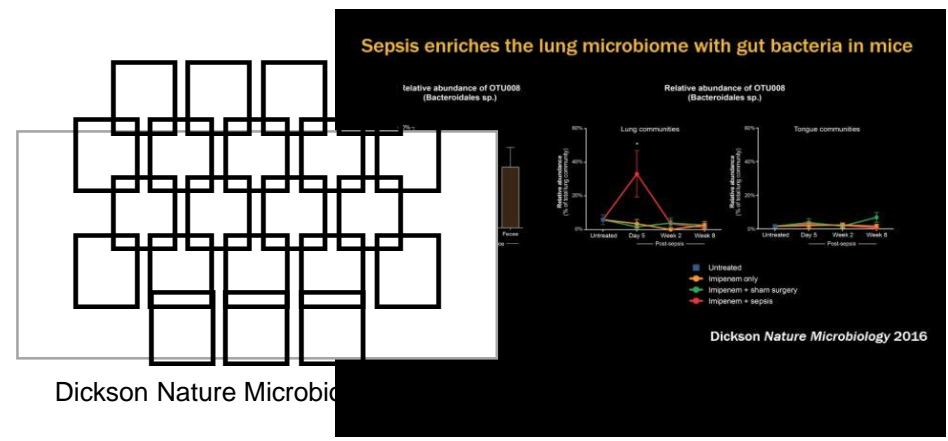
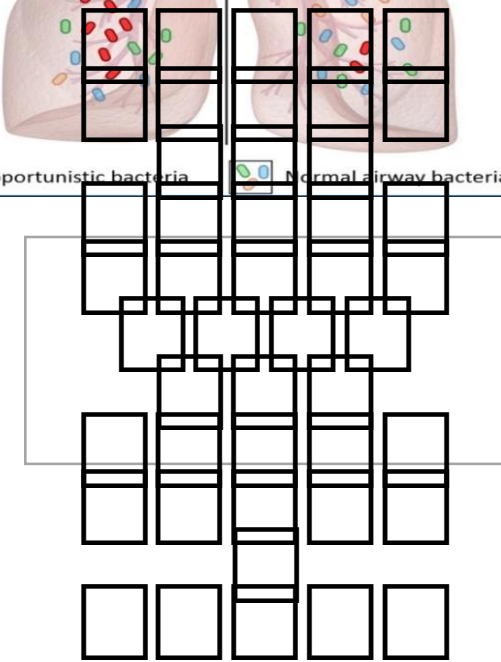
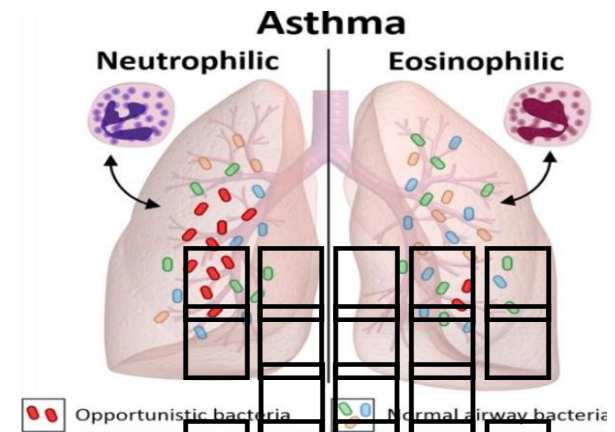
Промена на композиција и/или бројност Дисбиоза



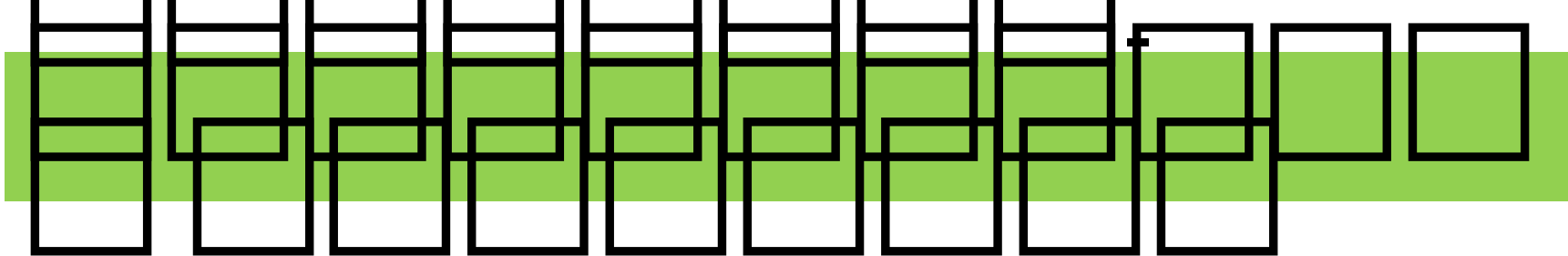
Респираторни заболувања и белодробен микробиом



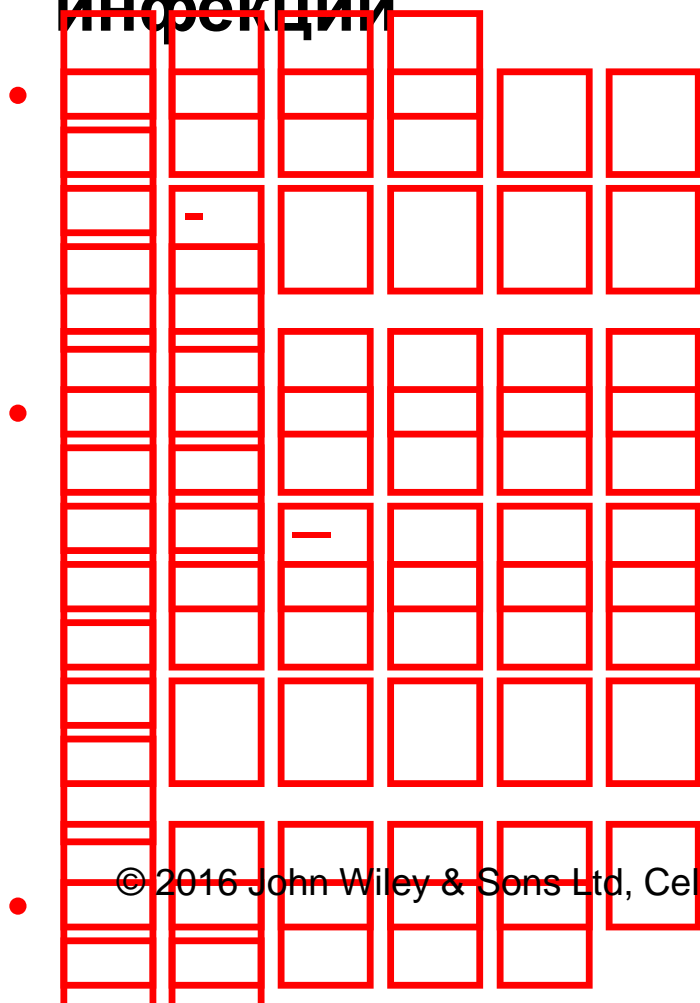
Ware NEJM 2000



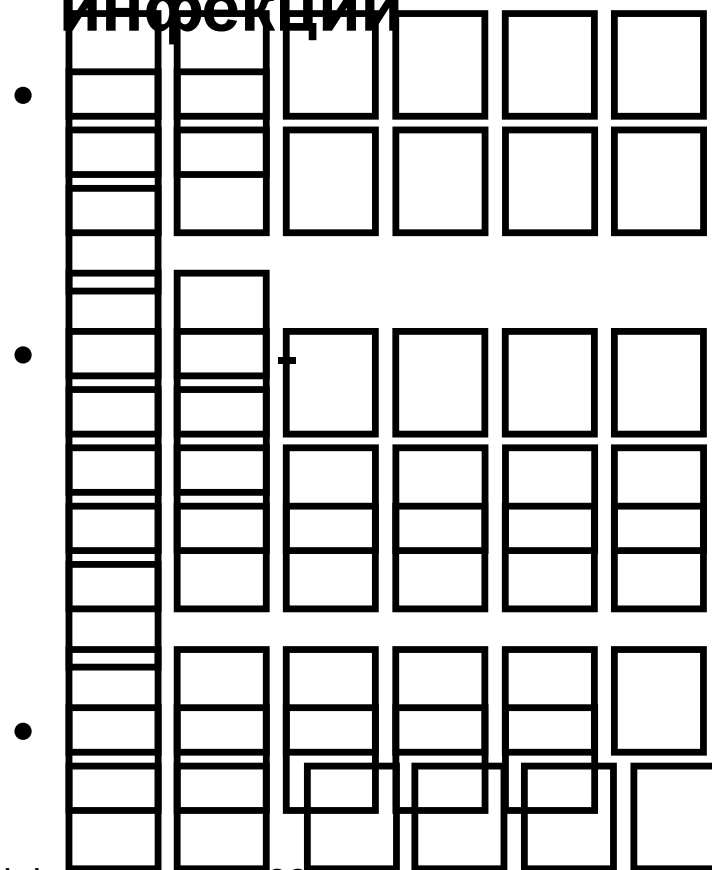
Dickson Nature Microbi

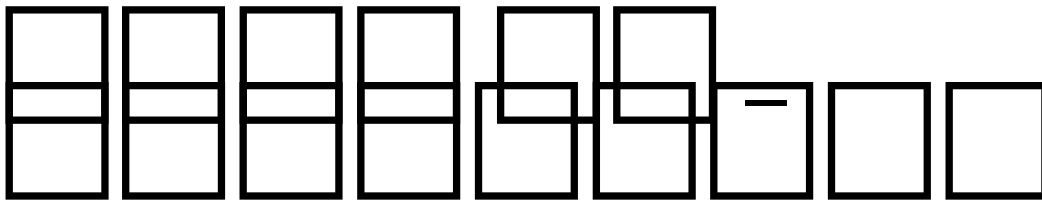


- **Акутни долнореспираторни инфекции**

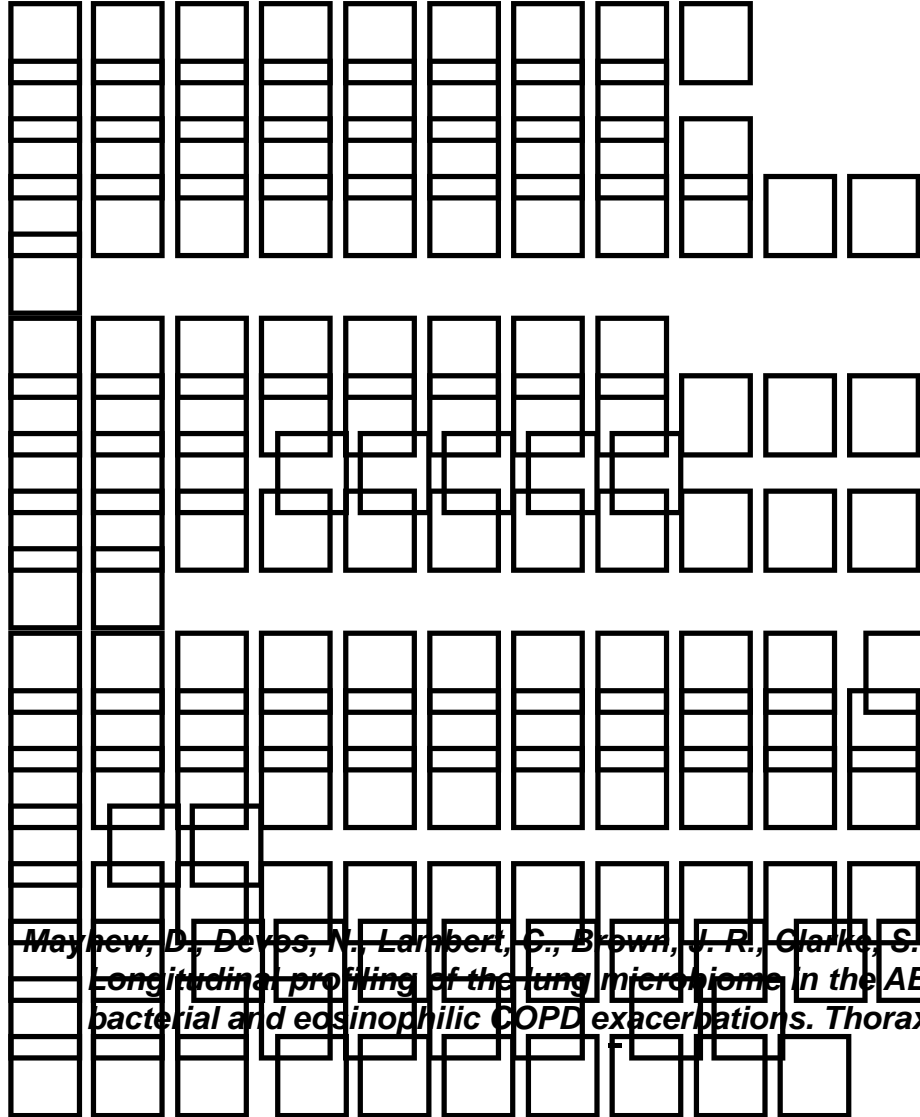


- **Хронични долнореспираторни инфекции**





(AERIS study)



Chronic obstructive pulmonary disease



ORIGINAL ARTICLE

Longitudinal profiling of the lung microbiome in the AERIS study demonstrates repeatability of bacterial and eosinophilic COPD exacerbations

David Mayhew,¹ Nathalie Devos,² Christophe Lambert,² James R Brown,¹ Stuart C Clarke,^{3,4} Viktoriya L Kim,² Michal Magid-Slav,² Bruce E Miller,² Kristoffer K Ostridge,⁴ Ruchi Patel,⁴ Ganesh Sathe,⁴ Daniel F Simola,¹ Karl J Staples,^{3,4,7} Ruby Sung,² Ruth Tal-Singer,² Andrew C Tuck,² Stephanie Van Horn,⁶ Vincent Weynants,² Nicholas P Williams,² Jeanne-Marie Devaster,² Tom M A Wilkinson,^{3,4,7} on behalf of the AERIS Study Group

Additional material is published online only. To view please visit the journal online (<https://doi.org/10.1136/thoraxjnl-2017-210408>).
For numbered affiliations see end of article.

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DM and ND contributed equally.
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INTRODUCTION

COPD is a chronic inflammatory disorder resulting in irreversible decline in lung function as a consequence of inhalation of tobacco smoke or other irritants.¹ One of the difficulties in treating and managing COPD is the heterogeneity of the

Mayhew D, et al. *Thorax* 2018;73:422-430. doi:10.1136/thoraxjnl-2017-210408

Key messages

What is the key question?
► What is the composition and stability of the lung microbiome in patients with COPD when longitudinally sampled at stable and exacerbation events?

What is the bottom line?
► The composition of the lung microbiome shows unique profiles within subtypes of COPD exacerbations, and the exacerbations experienced by an individual over time are non-random.

Why read on?
► These results describe a unique examination of the stability of the lung microbiome in COPD and predictability of future exacerbations available within a large cohort containing longitudinal sampling and clinical measurements over 1 year.

complex disease in terms of severity, progression, exercise tolerance and nature of symptoms.² This complexity is also evident in acute exacerbations of COPD (AECOPD), which are transient and apparently stochastic periods of increased COPD symptoms requiring additional medical treatment and, often, hospitalisation.³ Known subtypes of exacerbations are classified by the nature of key triggers including bacterial or viral infections, and/or high eosinophil levels, and these events are typically treated with a combination of antibiotics and steroids in a non-specific manner.⁴

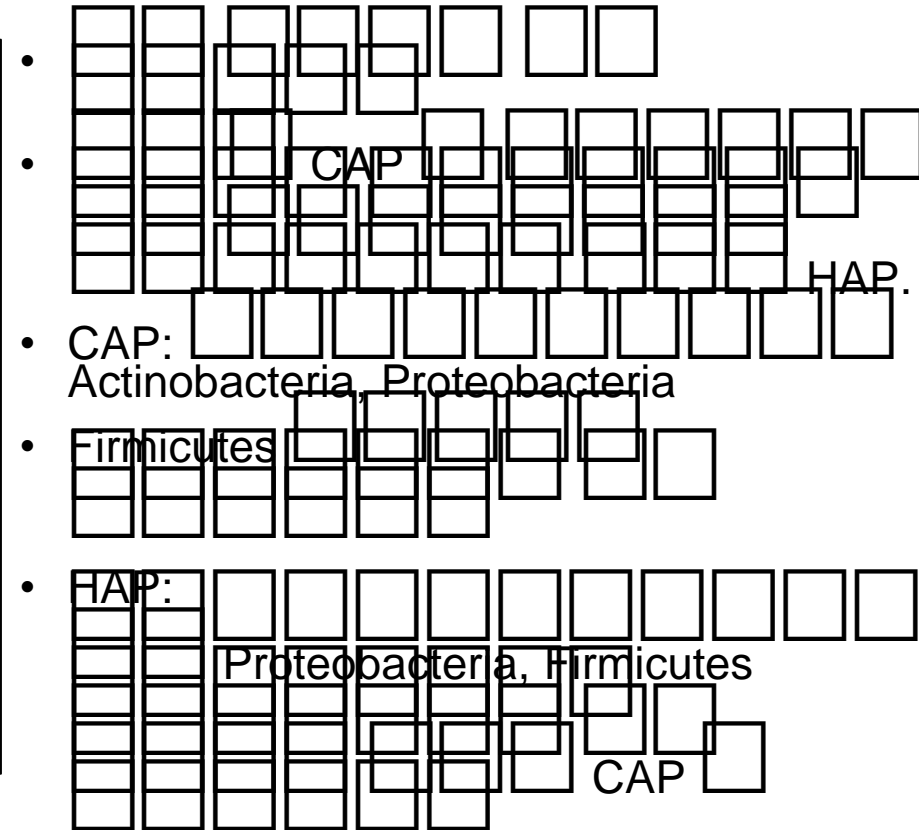
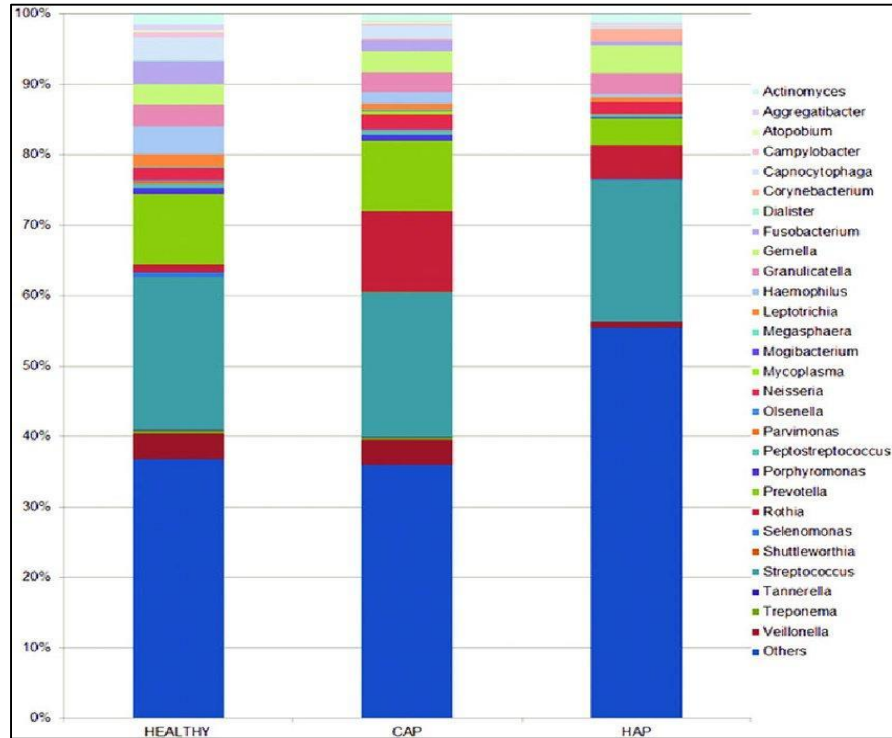
The lung microbiome represents an emerging opportunity to understand COPD heterogeneity and exacerbations. The healthy human lung contains a variety of commensal microorganisms throughout the respiratory tract, and these bacteria can show substantial heterogeneity between individuals, across regions within the lung and over time within an individual.⁵⁻⁷ Alterations in the taxonomic composition of the lung microbiome, known

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BMJ

Mayhew D, Devos N, Lambert C, Brown J R, Clarke S C, Kim V L, ... Wilkinson T M A. (2018). Longitudinal profiling of the lung microbiome in the AERIS study demonstrates repeatability of bacterial and eosinophilic COPD exacerbations. *Thorax*. <https://doi.org/10.1136/thoraxjnl-2017-210408>

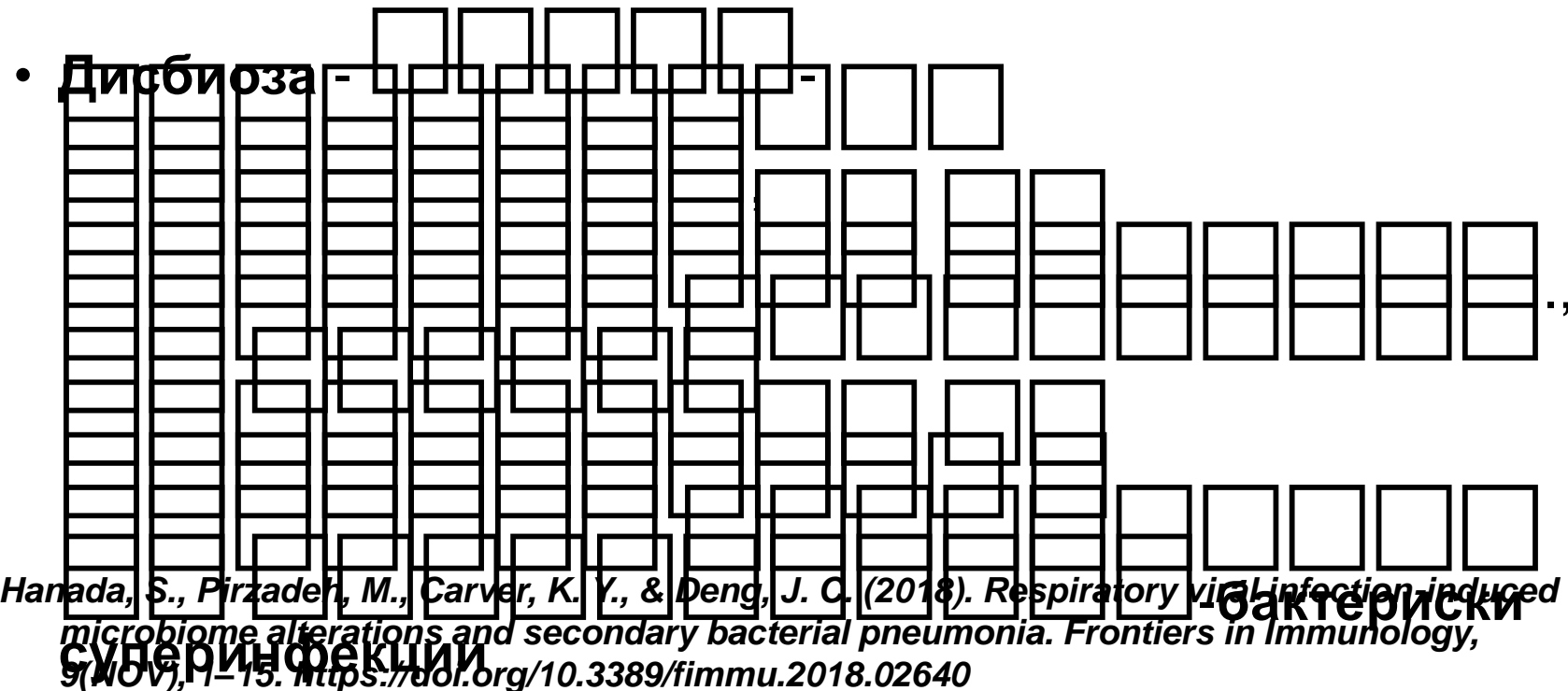
Пневмонија-микробиом разлики



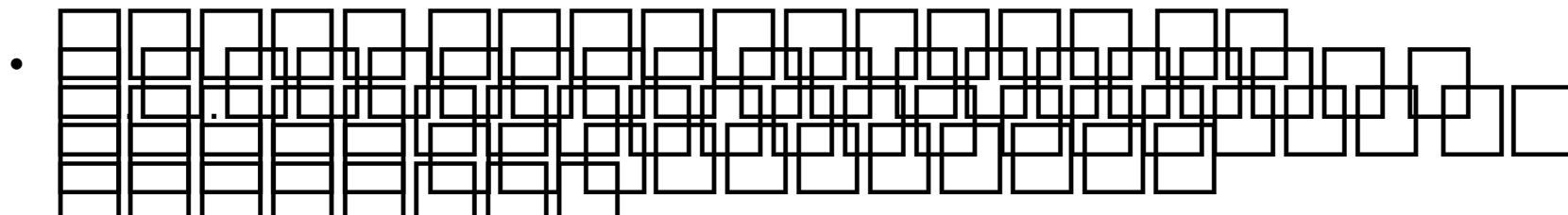
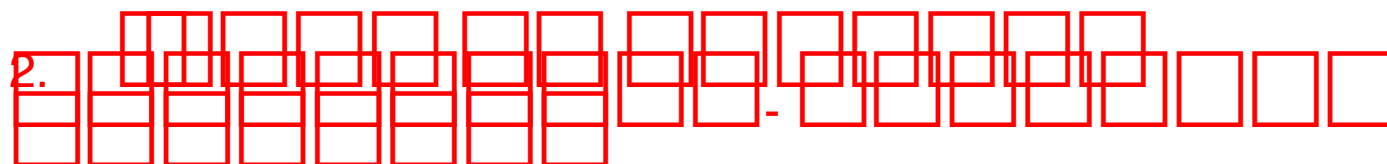
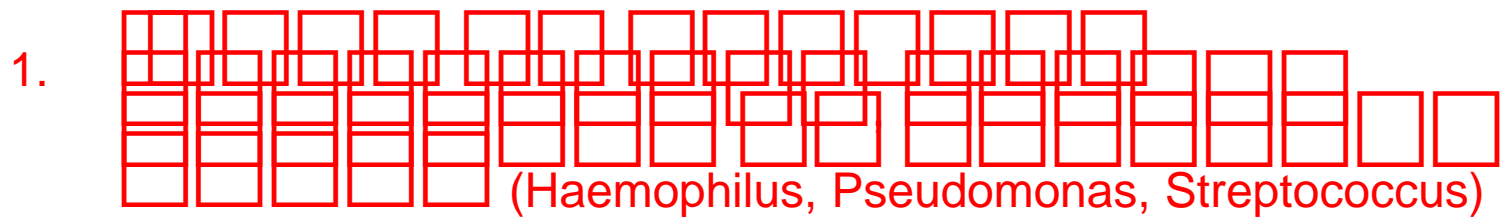
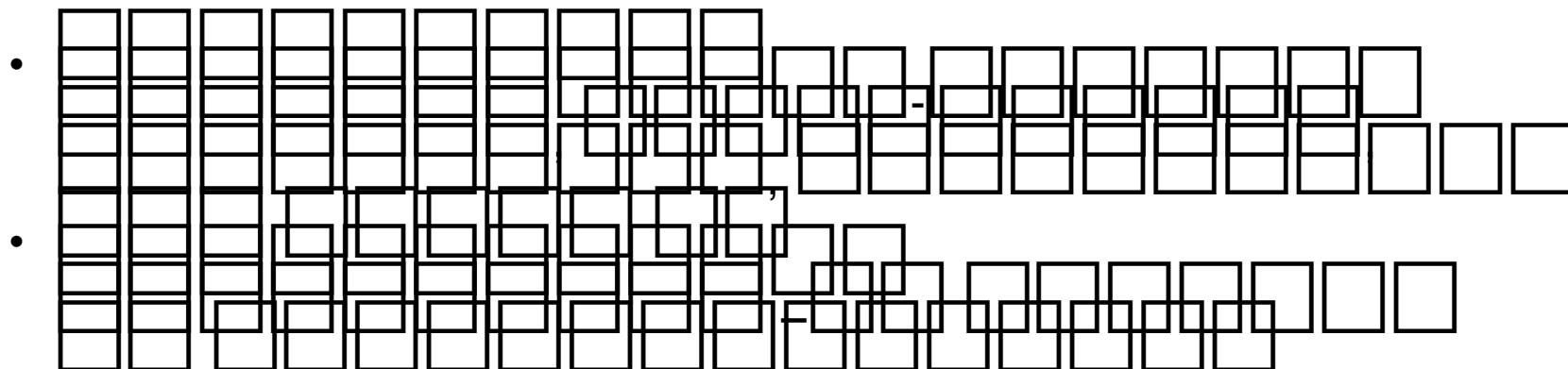
Shen, T., Guo, X., Xue, M., Zhou, Y., Ye, J., Zhang, Y., Chen, C. (2013). New microbiota found in sputum from patients with community-acquired pneumonia. *Acta Biochimica et Biophysica Sinica*, 45(12), 1039–1048. <https://doi.org/10.1093/abbs/gmt116>

Респираторни вирусни инфекции-алтерација на микробиом

- **Influenza A :**
- **Proteobacteria** (*Pseudomonas* spp, *Acinetobacter*), **Firmicutes** (*Staphylococcus* , *Streptococcus* spp).



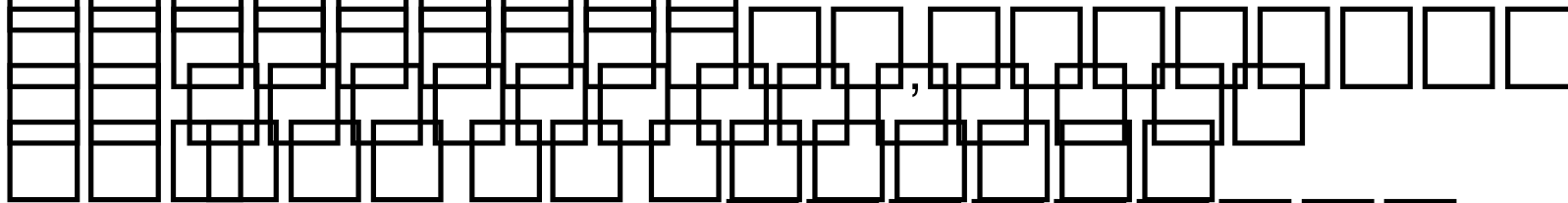
Бронхиектазии-микробиом (Non CF)



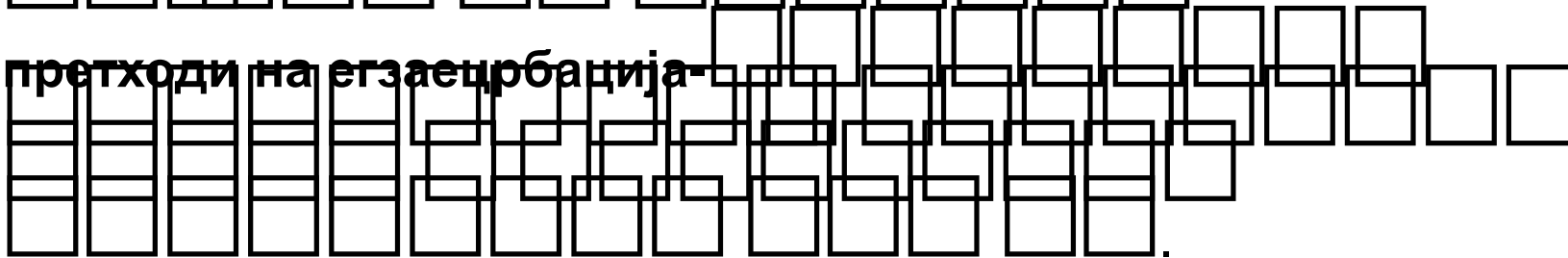
Микробиом кај цистична фиброза

- Намаена диверзибилност- зголемен однос Firmicutes / Bacteroides:

- прогресија на болеста и колонизација со патогени,

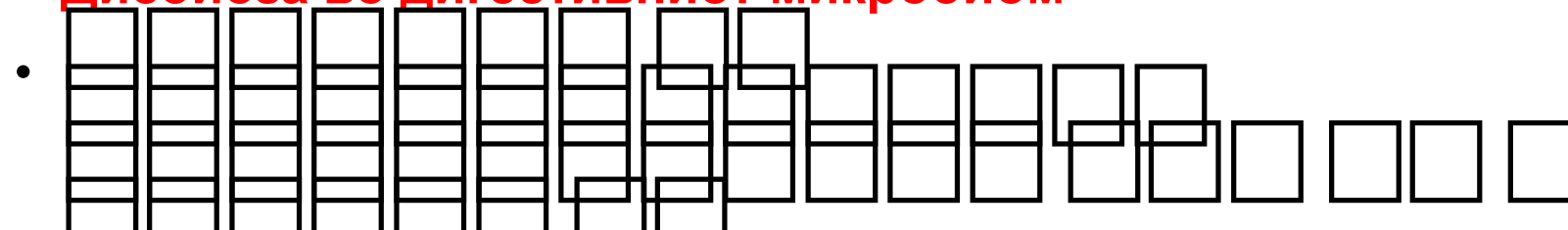


- претходи на егзацербација



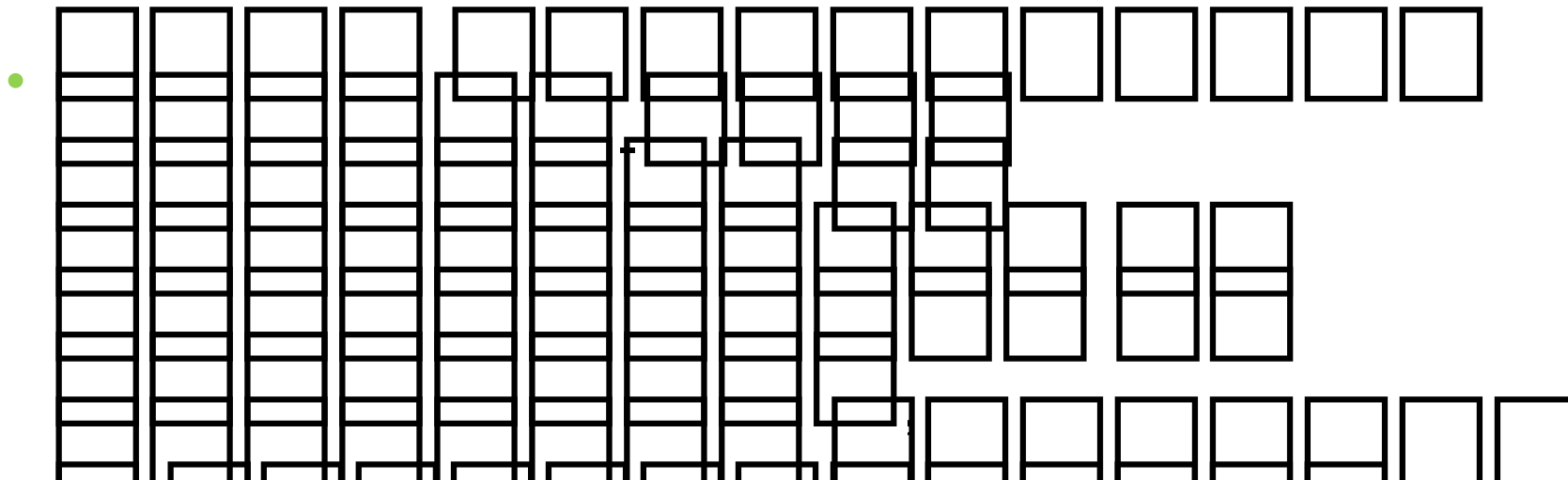
- Доминација на еден патоген и честа употреба на антибиотици- во рана возраст

- Дисбиоза во дигестивниот микробиом



Заклучок

- Намалена диверзибилност на микробиомот кај респираторните инфекции
- Зголемување на бројноста на патогените и намалување на протективните бактериски таксони мали промени со кумулативен ефект.
- Дисбиоза-Заболувања



Можен менаџмент на белодробниот микробиом

