Equilibration of hadrons in HICs via Hagedorn states

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Motivation

Bootstrap model

covariant formulation, conserved charges (B,S,Q)

detailed balance

Results and Outlook

Implementation into UrQMD / GiBUU

M.Beitel, KG, C.Greiner, PRC 90 (2014) 045203

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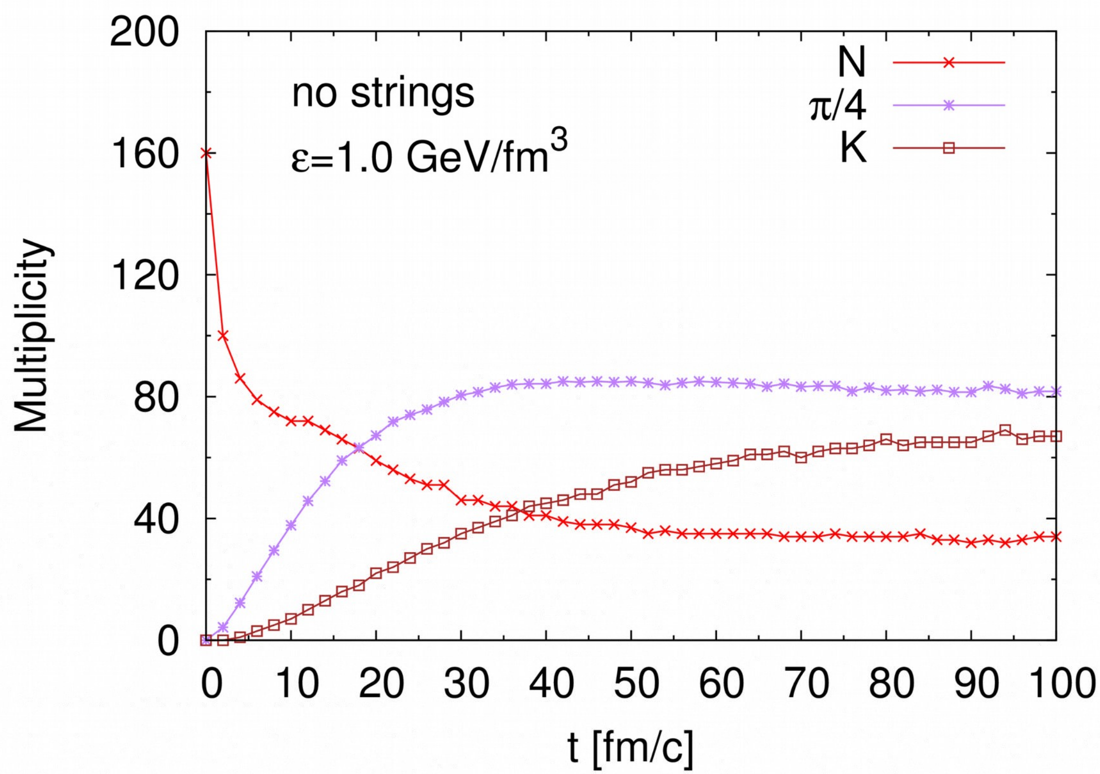
UrQMD Box

- UrQMD: hadronic transport model

Bass et al., Prog.Part.Nucl.Phys. 41 (1998), 255

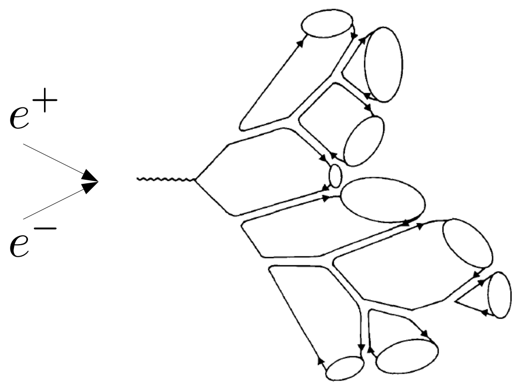
- Problem: chemical equilibration takes too long



Colorless Heavy Objects

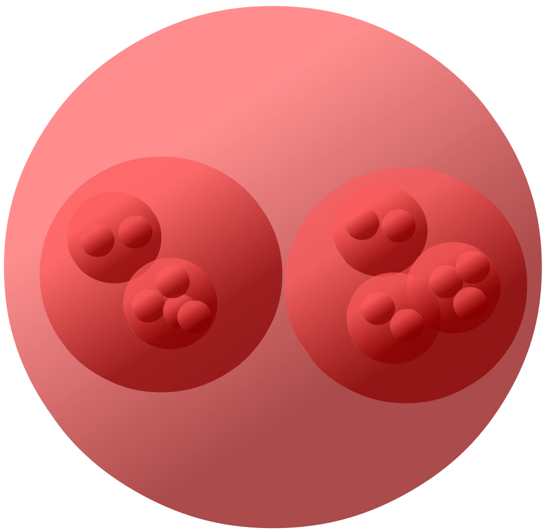
- Cluster (HERWIG)

  B. Webber, Nucl.Phys.B 238 (1984) 492



- Hagedorn states

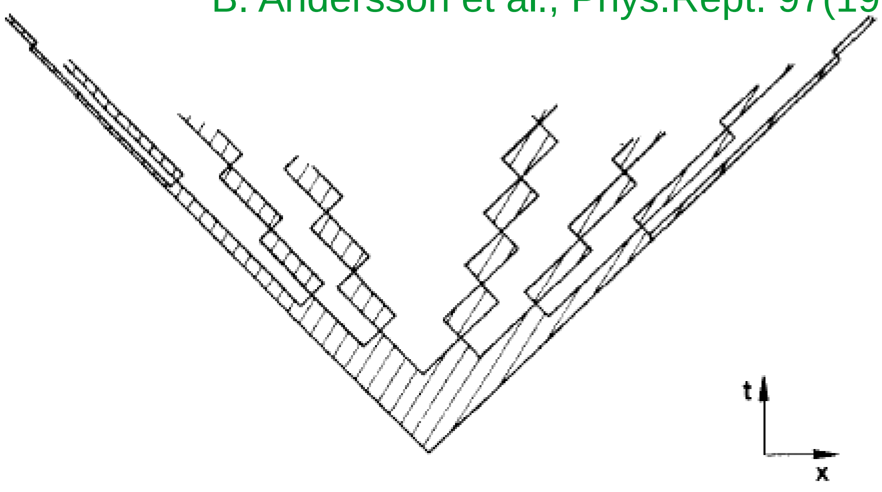
  R. Hagedorn, Nuovo Cim. Suppl. 3 (1965) 147



allow for
decay & recombination !!!

- Strings (Lund)

  B. Andersson et al., Phys.Rept. 97(1983) 31



Application of Hagedorn states

- at SPS energies chem. equilibration time is 1-3 fm/c

$$\mathrm{n}_1\pi + n_2 K \leftrightarrow \bar{Y} + p$$

C.Greiner, S.Leupold, 2000

- at RHIC energies chem. equilibration time is 10 fm/c (with same approach)

- fast chem. equilibration mechanism through Hagedorn states

$$\left(n_1\pi + n_2 K + n_3 \bar{K} \leftrightarrow\right)\ HS \leftrightarrow \bar{B} + B + X$$

- dynamical evolution through set of coupled rate equations leads to 5 fm/c for $B\bar{B}$ pairs

J.Noronha-Hostler et al., PRL100 (2008)
J.Noronha-Hostler et al., J.Phys.G 37 (2010)
J.Noronha-Hostler et al., Phys. Rev C81 (2010)

Bootstrap

cf.: S. Frautschi, PRD 3 (1971) 2821
C. Hamer, S. Frautschi, PRD 4 (1971) 2125
J. Yellin, NPB 52 (1973) 583

- Assumption: only 2-body (detailed balance!)
- Input: known hadrons (UrQMD/PDG)

$$\vec{C} = (B, S, Q)$$

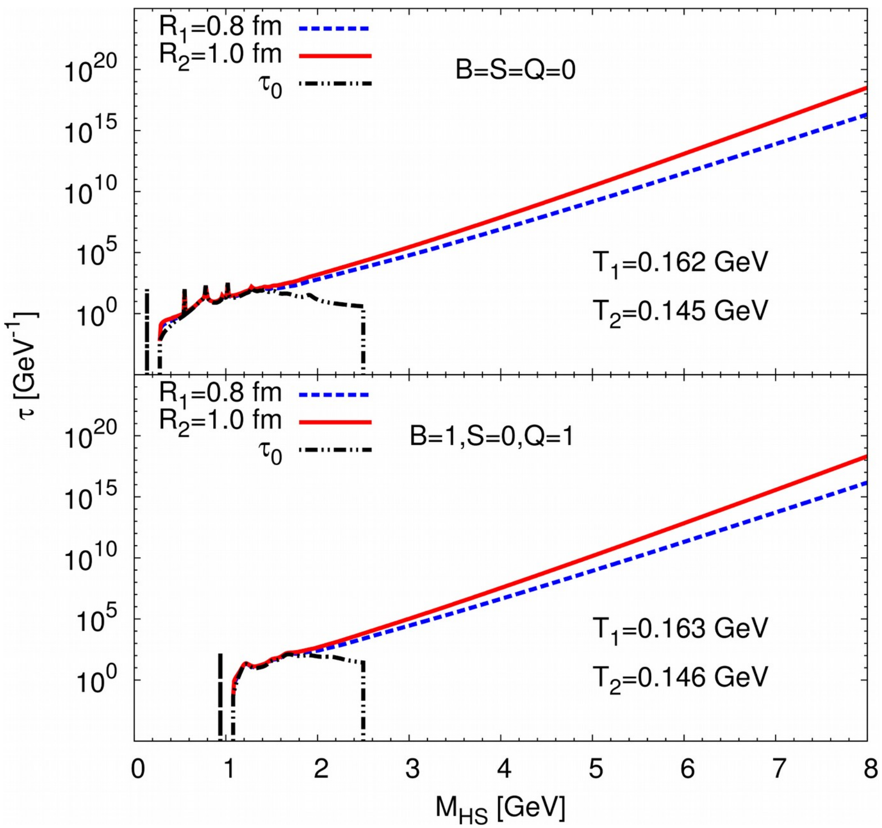
- Bootstrap equation

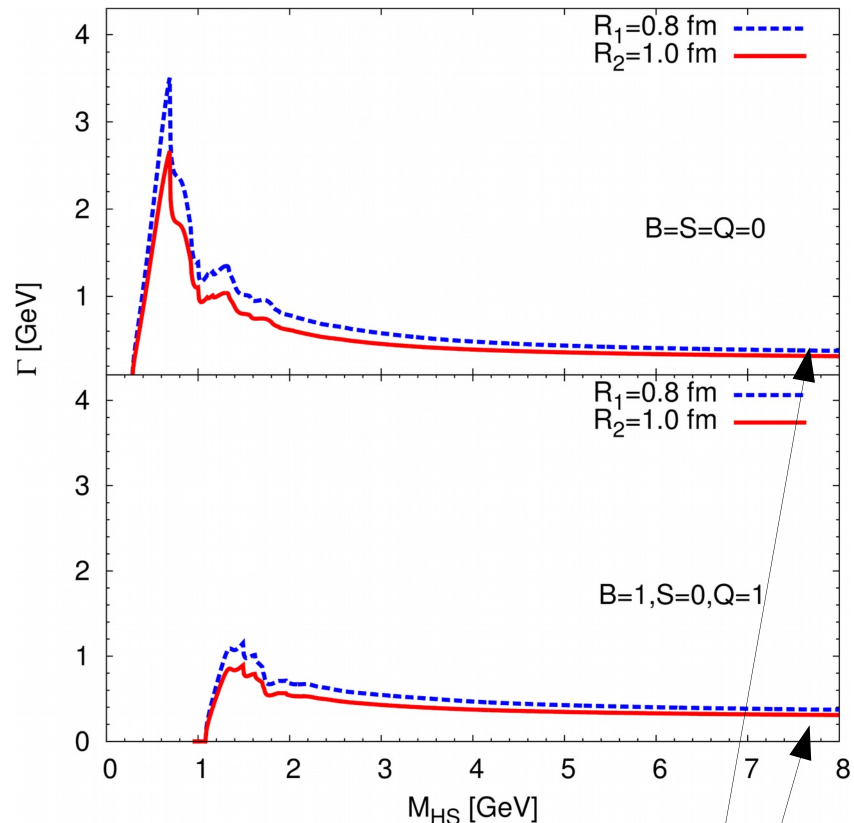
$$\tau_{\vec{C}}(m) = \frac{R^3}{3\pi\, m} \sum_{\vec{C}_1, \vec{C}_2} \iint \mathrm{d}m_1 \mathrm{d}m_2\, m_1 \tau_{\vec{C}_1}(m_1)\, m_2 \tau_{\vec{C}_2}(m_2)$$
$$\times\ p_{\mathrm{cm}}(m, m_1, m_2)\, \delta(\vec{C} - \vec{C}_1 - \vec{C}_2)$$

- Total decay width (via detailed balance)

$$\Gamma_{\vec{C}}(m) = \frac{\sigma}{2\pi^2\, \tau_{\vec{C}}(m)} \sum_{\vec{C}_1, \vec{C}_2} \iint \mathrm{d}m_1 \mathrm{d}m_2\, \tau_{\vec{C}_1}(m_1)\, \tau_{\vec{C}_2}(m_2)$$
$$\times\ p_{\mathrm{cm}}^2(m, m_1, m_2)\, \delta(\vec{C} - \vec{C}_1 - \vec{C}_2)$$

Spectra, Width





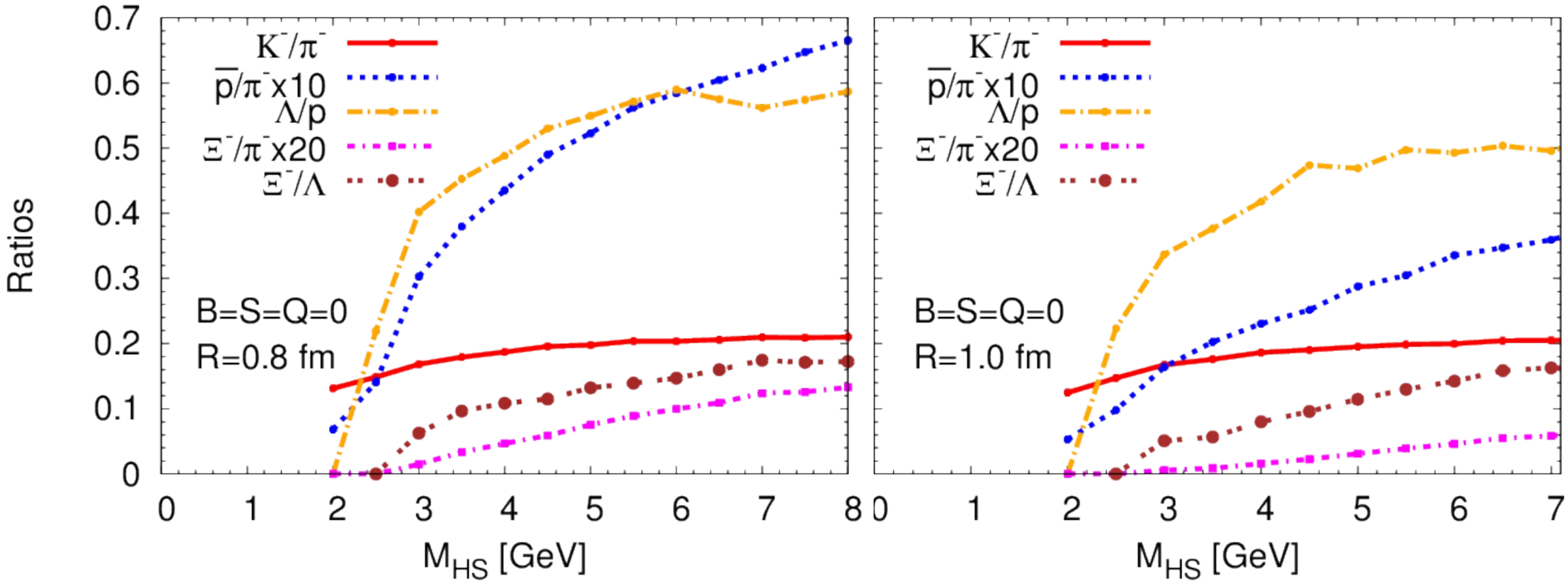
Radius $\nearrow$: Slope T $\searrow$

Radius $\nearrow$: Width Γ $\searrow$

T quite independent of charges

nonzero !

Single HS cascading decay: Multiplicity ratios



	p-p	Pb-Pb	4 GeV	8 GeV
K^-/π^-	0.123(14)	0.149(16)	0.187	0.210
$\overline{p}/\pi^-$	0.053(6)	0.045(5)	0.043	0.066
Λ/π^-	0.032(4)	0.036(5)	0.021	0.038
$\Lambda/\overline{p}$	0.608(88)	0.78(12)	0.494	0.579
Ξ^-/π^-	0.003(1)	0.0050(6)	0.0023	0.0066
$\Omega^-/\pi^- \cdot 10^{-3}$	—	0.87(17)	0.086	0.560

data: ALICE @ LHC

$$\mathrm{p-p}: \sqrt{s_{NN}} = 0.9\,\mathrm{TeV}$$

$$\mathrm{Pb-Pb}: \sqrt{s_{NN}} = 2.8\,\mathrm{TeV}$$

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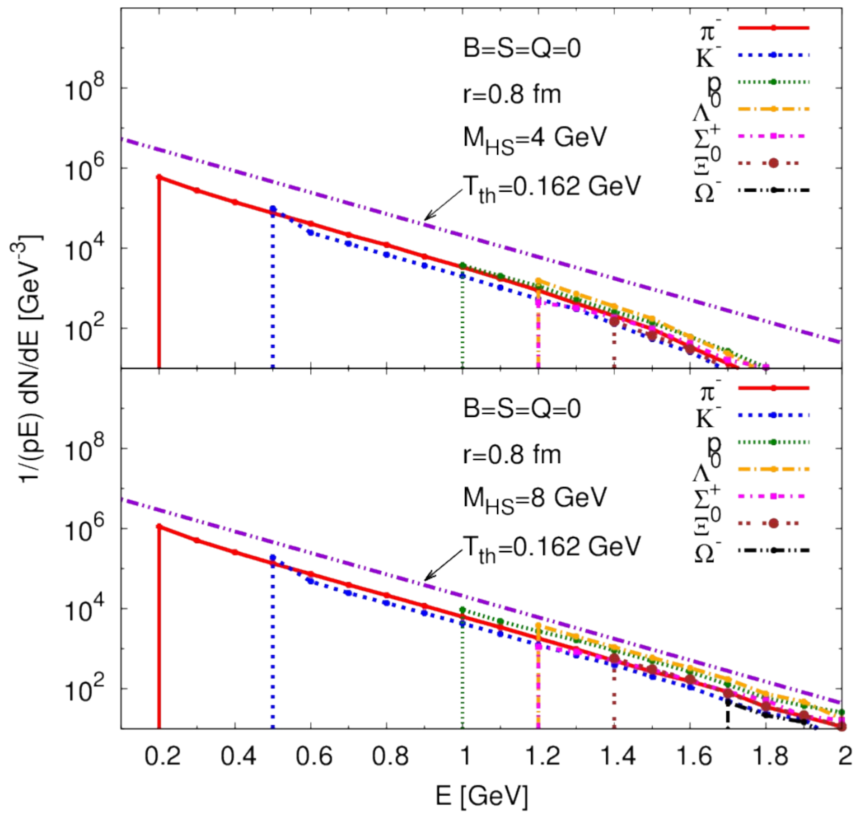
Single HS cascading decay: Spectra



- spectra of decay products of single HS cascading decay chain
  look (!) thermal !!!
- slope equals Hagedorn temperature
- slope independent of mass, radius, charges

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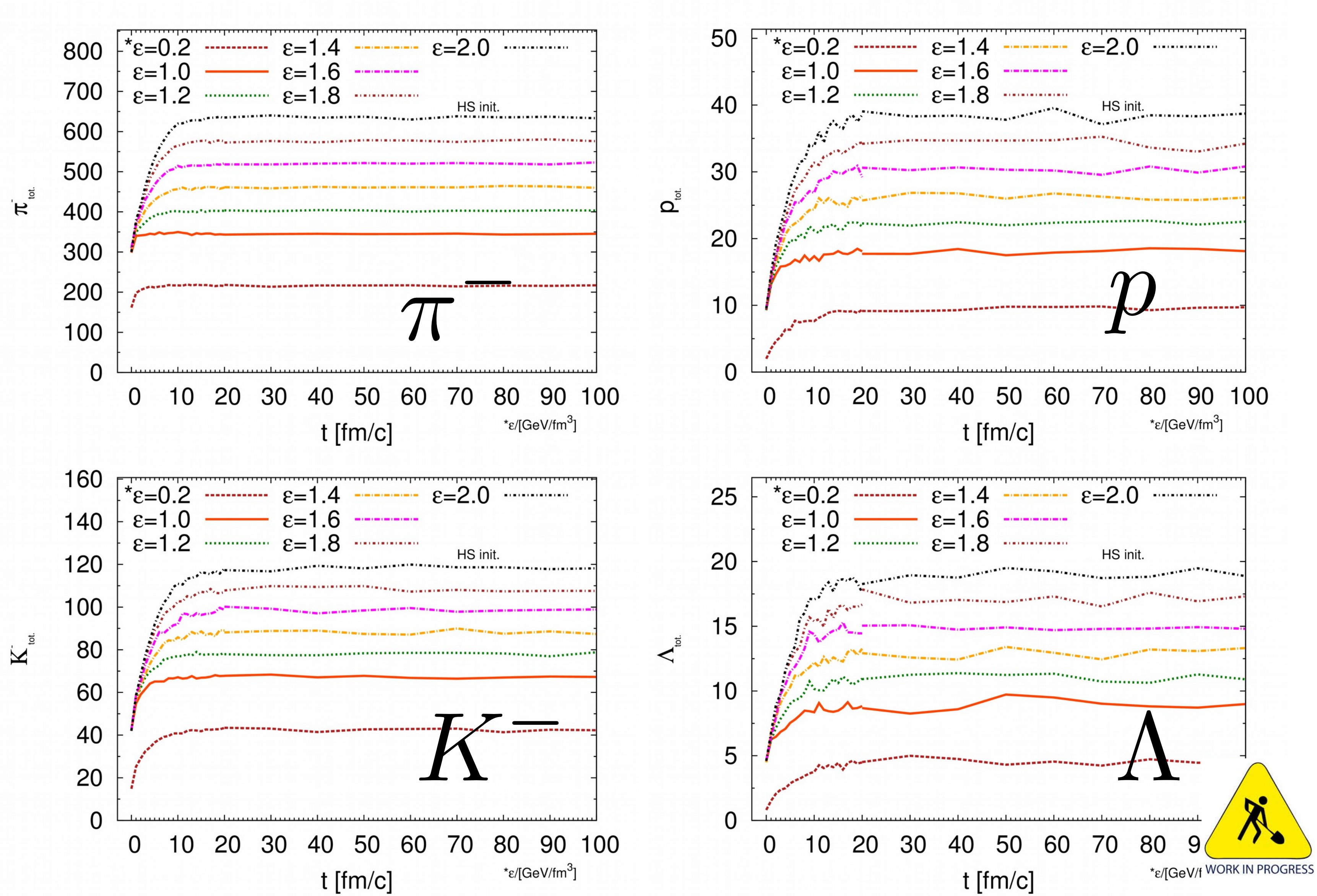
UrQMD Box calculations

- Implementation into UrQMD
- Creation of Hagedorns replaces string interactions
- Box calculations
- Different initialization scenarios
  - Only pions
  - Only hadrons
  - **Only Hagedorn states**

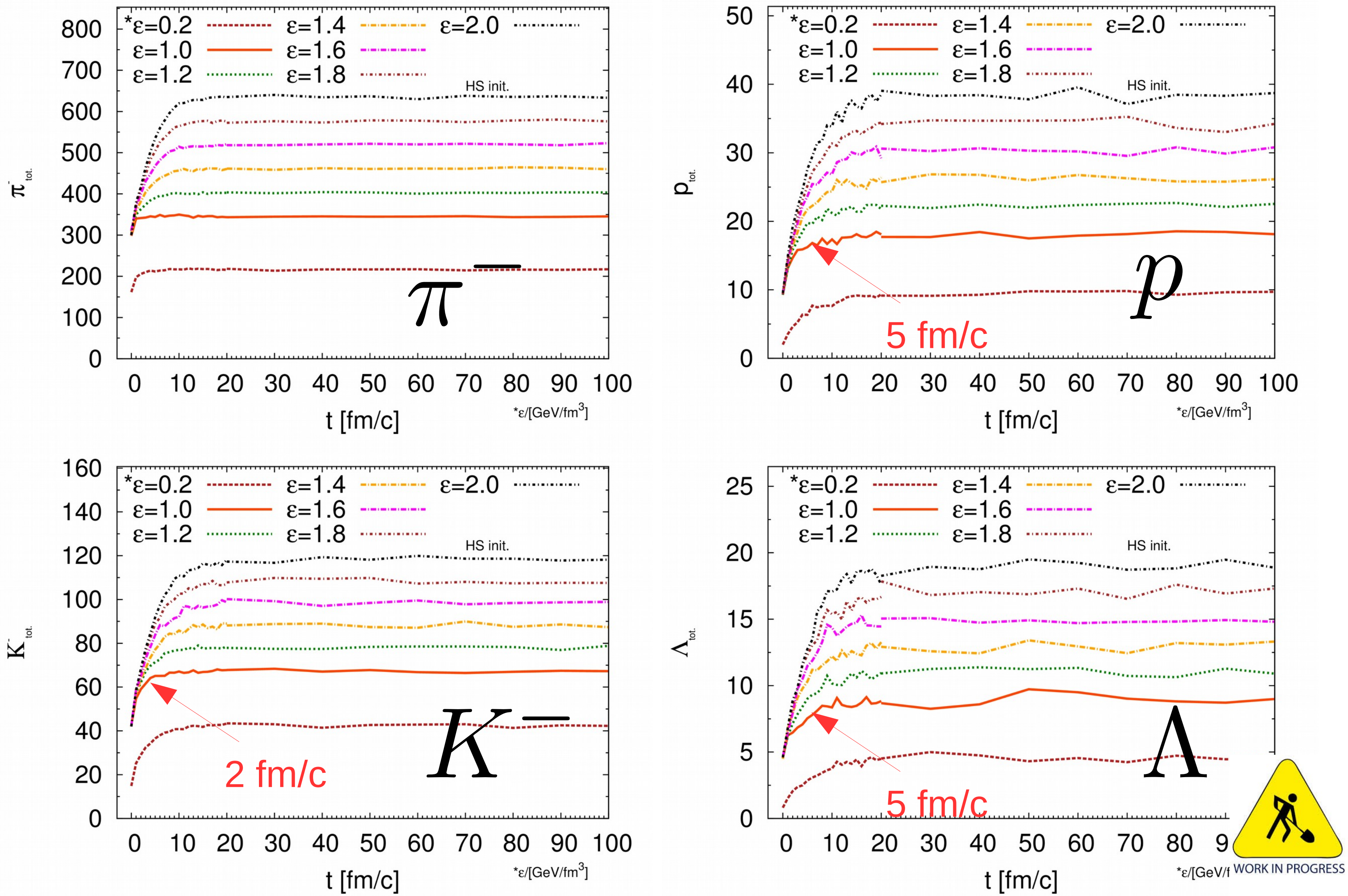
Bottom-up

Top-down

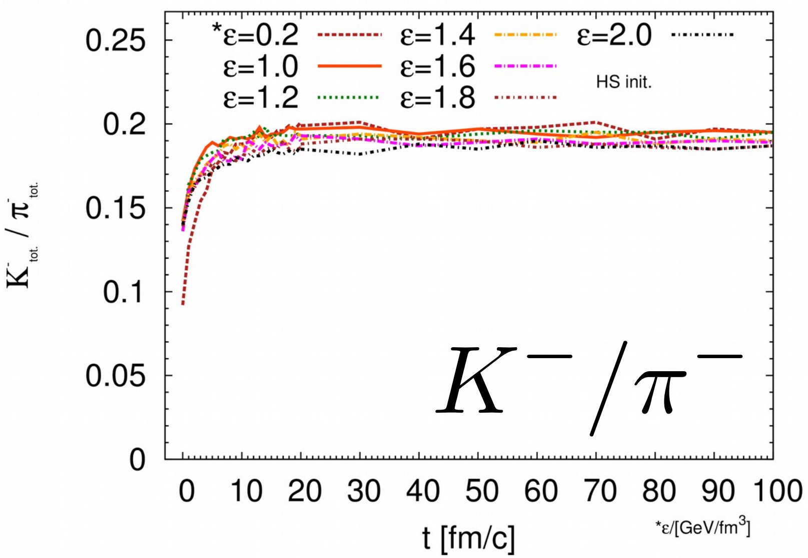
UrQMD-Box, HS init

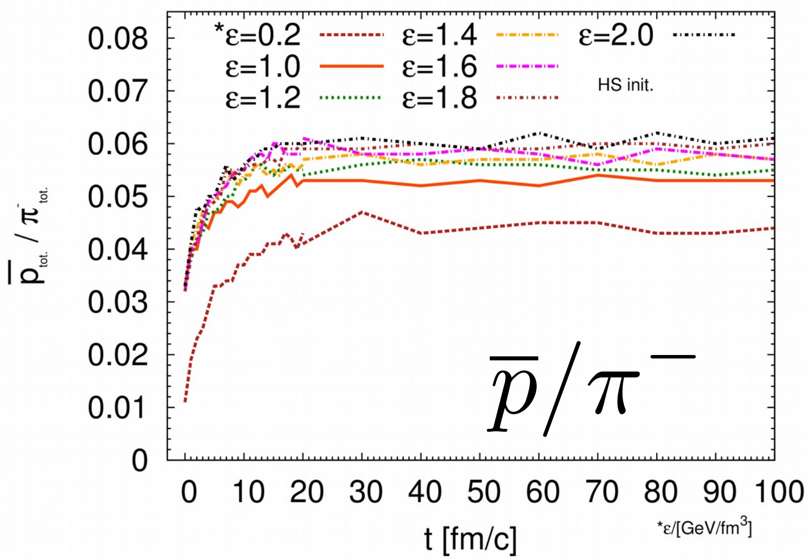


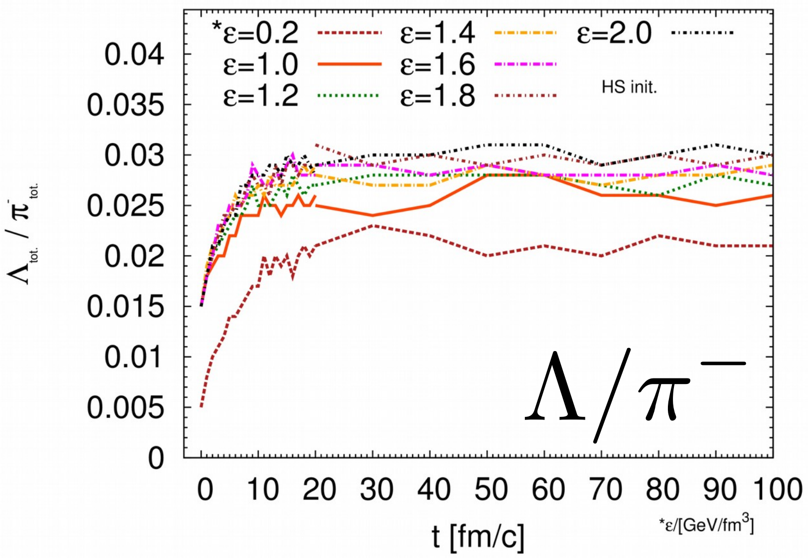
UrQMD-Box, HS init

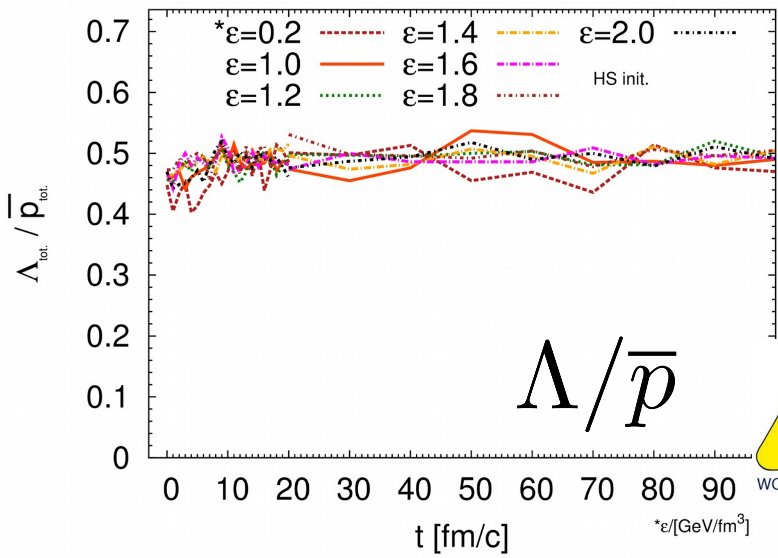


UrQMD-Box, HS init





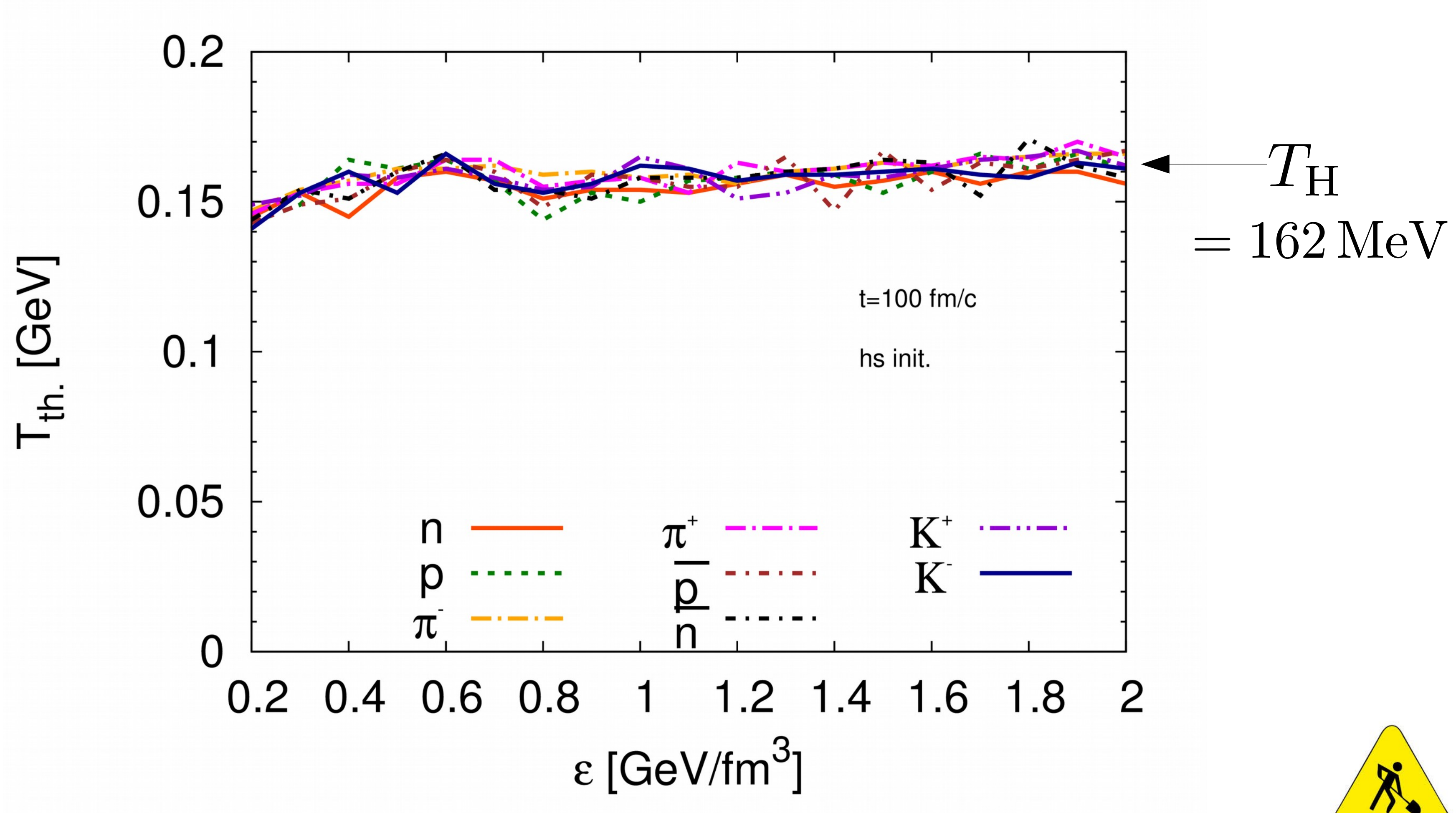




WORK IN PROGRESS

UrQMD-Box, HS init

- Kinetic equilibration, slopes:



WORK IN PROGRESS

Conclusions

- Microcanonical bootstrap implementation
- HS properties connected to UrQMD limitations
  - Input 'known hadrons' as implemented in UrQMD
  - Only 2-body processes

- Cascading decay chain of single HS:
  - Multiplicity ratios close to experimental values (ALICE@LHC)
  - Decay product spectra *look* thermal
  - Slope equals Hagedorn temperature

- Implementation into UrQMD, Box calculations
  - Fast equilibration: 2...5 (...10) fm/c
  - Kinetic slopes = T_H for all ε =0.2...2 GeV/c

- To be done:
  - Check (B,S,Q) vs. (B,S,I)
  - Implement into GiBUU; cross check!